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OM nucleic - nucleic search, using sw model

Run on: January 7, 2003, 01:52:18 ; Search time 201 Seconds
(without alignments)

7791.534 Million cell updates/sec

Title: US-10-032-717-1

Perfect score: 3621

Sequence: 1 atgagtcacaaataacaaaa.....tgattgtagacgtagagtaa 3621

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 381593 seqs, 216252194 residues

Total number of hits satisfying chosen parameters: 763186

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a
Score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3621	100.0	3621	12	US-10-032-717-1
2	3621	100.0	4874	12	US-10-032-717-27
3	3151.8	87.0	3633	12	US-10-032-717-3
4	3151.8	87.0	6613	12	US-10-032-717-28
5	2008.4	55.5	2010	12	US-10-032-717-15
6	2003	55.3	2003	12	US-10-032-717-5
7	1987.4	54.9	2013	12	US-10-032-717-23
8	1986.4	54.9	2022	12	US-10-032-717-11
9	1986.4	54.9	2022	12	US-10-032-717-21
10	1986.4	54.9	2022	12	US-10-032-717-39
11	1985.8	54.8	2013	12	US-10-032-717-43
12	1848.4	51.0	1860	12	US-10-032-717-19
13	1827.4	50.5	1854	12	US-10-032-717-33
14	1826.4	50.4	1863	12	US-10-032-717-29
15	1825.8	50.4	1854	12	US-10-032-717-45
16	1824.8	50.4	1863	12	US-10-032-717-31
17	1821.6	50.3	1863	12	US-10-032-717-41
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19	1521.8	42.0	2003	12	US-10-032-717-7

20 983.6 27.2 2010 12 US-10-032-717-9 Sequence 9, Appli

21 658 18.2 6930 10 US-09-756-526A-1 Sequence 1, Appli

22 555.2 15.3 3534 10 US-09-873-873-27 Sequence 27, Appl

23 548.8 15.2 3531 10 US-09-873-873-9 Sequence 9, Appli

24 548.8 15.2 3531 10 US-09-873-873-11 Sequence 11, Appl

25 548.8 15.2 3531 10 US-09-873-873-13 Sequence 13, Appl

26 548.8 15.2 3534 10 US-09-873-873-33 Sequence 33, Appl

27 547.2 15.1 3534 10 US-09-873-873-25 Sequence 25, Appl

28 544.4 15.0 3579 10 US-09-873-873-29 Sequence 29, Appl

29 542.8 15.0 4300 10 US-09-851-194-1 Sequence 1, Appli

30 540.6 14.9 4359 9 US-10-120-544A-3 Sequence 3, Appli

31 518.2 14.3 3522 10 US-09-826-660-5 Sequence 5, Appli

32 493.8 13.6 4360 10 US-09-756-643-1 Sequence 1, Appli

33 447.6 12.4 4188 9 US-10-120-544A-5 Sequence 5, Appli

34 439.2 12.1 3558 10 US-09-826-660-22 Sequence 22, Appl

35 413.8 11.4 4896 10 US-09-756-526A-3 Sequence 3, Appli

36 411.4 11.4 3468 10 US-09-826-660-12 Sequence 12, Appl

37 410.4 11.3 4359 9 US-10-120-544A-17 Sequence 17, Appl

38 390.6 10.8 3489 10 US-09-826-660-20 Sequence 19, Appl

39 379 10.5 4366 9 US-10-120-544A-19 Sequence 19, Appl

40 325.8 9.0 3468 10 US-09-826-660-14 Sequence 14, Appl

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42 321.4 8.9 2615 10 US-09-943-692-1 Sequence 1, Appli

43 285.2 7.9 3444 10 US-09-826-660-1 Sequence 1, Appli

44 263.2 7.3 1929 10 US-09-826-660-24 Sequence 24, Appl

45 227.8 6.3 1175 10 US-09-851-194-3 Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-10-032-717-1

; Sequence 1, Application US/10032717

; Patent No. US20020151709A1

; GENERAL INFORMATION:

; APPLICANT: Andre R. Abad

; APPLICANT: Nicholas B. Duck

; APPLICANT: Xiang Peng

; APPLICANT: Ronald D. Flannagan

; APPLICANT: Theodore W. Kahn

; APPLICANT: Lynn E. Sims

; TITLE OF INVENTION: Genes Encoding No. US20020151709A1 Proteins With
Pesticidal Activity Against Coleopterans

; FILE REFERENCE: 35718/237005

; CURRENT APPLICATION NUMBER: US/10/032,717

; CURRENT FILING DATE: 2001-10-23

; PRIOR APPLICATION NUMBER: 60/242,838

; PRIOR FILING DATE: 2000-10-24

; NUMBER OF SEQ ID NOS: 48

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 3621

; TYPE: DNA

; ORGANISM: Bacillus thuringiensis

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)...(3621)

; NAME/KEY: misc_feature

; LOCATION: (0)...(0)

; OTHER INFORMATION: Cyl1218-1

US-10-032-717-1

Query Match 100.0%; Score 3621; DB 12; Length 3621;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 3731 TATACCAAGTTTACAGAAATTAACAGATCGACTCCAAACAGCGTGGAGTTGTATGATCAG 3060
Qy 3061 CGAAATGCCATACCAATGCTGATTTTCGAAATGGGTTAAGTAAATTCGGAATGCAAGCCCT 3120
Db 3791 CGAAATGCCATACCAATGCTGATTTTCGAAATGGGTTAAGTAAATTCGGAATGCAAGCCCT 3180
Qy 3121 GCGGTAGAAAGTACAAACAAATCAATCATACATCTGCTCTGTTGATTCGAAATCGGATGAG 3180
Db 3851 GCGGTAGAAAGTACAAACAAATCAATCATACATCTGCTCTGTTGATTCGAAATCGGATGAG 3240
Qy 3181 CAAGTTTCGCAACAGTTTACAGTTTCAACCGAATCAAAAGATATGTGTTACGAGTTACTGCG 3240
Db 3911 CAAGTTTCGCAACAGTTTACAGTTTCAACCGAATCAAAAGATATGTGTTACGAGTTACTGCG 3240
Qy 3241 AGAAAGAGAGGGGTAGGAAATGATATGTAAGTATCGGTGATGTTGGAATCAAAACAGAA 3300
Db 3971 AGAAAGAGAGGGGTAGGAAATGATATGTAAGTATCGGTGATGTTGGAATCAAAACAGAA 4030
Qy 3301 AGCTTTACTTTTATAGTCAACGGATATGATACAAATGGAATGATATAGCAAGTGTCC 3360
Db 4031 AGCTTTACTTTTATAGTCAACGGATATGATACAAATGGAATGATATAGCAAGTGTCC 4090
Qy 3361 AATACAAAATGGAATATACAAATTAATGCGTATATTAACAAGCATCGATACAAACGGA 3420
Db 4091 AATACAAAATGGAATATACAAATTAATGCGTATATTAACAAGCATCGATACAAACGGA 4150
Qy 3421 TATAACGCAAAATTAATGATATATACCAAGATCGATATCGAATCAAAACGGAATTAACAAT 3480
Db 4151 TATAACGCAAAATTAATGATATATACCAAGATCGAATCAAAACGGAATTAACAAT 4210
Qy 3481 AGTGTGTACAATGATCAAAACCGGTATATCAAAACAGTGCATTCATCCCGTATACA 3540
Db 4211 AGTGTGTACAATGATCAAAACCGGTATATCAAAACAGTGCATTCATCCCGTATACA 4270
Qy 3541 GATCAAAATGGAATGAGATGAGAGACAGAAAGGTTACATTTATATATAGAAAGTGTAGAA 3600
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Db 4271 GATCAAAATGTGGATTGAGATTGAGATGAGACAGAAAGGTACATTTCTATATAGAAAGTGTAGAA 4330
Qy 3601 TTGATTGTAGACGTAGAGTAA 3621
Db 4331 TTGATTGTAGACGTAGAGTAA 4351

RESULT 3
US-10-032-717-3
; Sequence 3, Application US/10032717
; Patent No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Peng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
; FILE OF INVENTION: Pesticidal Activity Against Coleopterans
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032,717
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3633
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3633)
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Cry12I8-2
US-10-032-717-3
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Query Match 87.0%; Score 3151.8; DB 12; Length 3633;
Best Local Similarity 92.1%; Pred. No. 0;
Matches 3353; Conservative 0; Mismatches 262; Indels 24; Gaps 2;

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Qy 61 TCCAATGATTTTAAACAGATACCCCTTTTGCAGATGAGCCCAAAATGCGCTACAAATATG 120
Db 61 TCCAATGATTTTAAACAGATACCCCTTTTGCAGATGAGCCCAAAATGCGCTACAAATATG 120
Qy 121 GATTATAAGATTTTAAATAATGCTCTGCGGAAATGCTAGTGAATACCCCTGTTCACT 180
Db 121 GATTATAAGATTTTAAATAATGCTCTGCGGAAATGCTAGTGAATACCCCTGTTCACT 180
Qy 181 GAAGTACTTTGTAGCGGACAAAGATGAGCTAAGGCCGCAATTCATATAGTAGTAAATTA 240
Db 181 GAAGTACTTTGTAGCGGACAAAGATGAGCTAAGGCCGCAATTCATATAGTAGTAAATTA 240
Qy 241 CTATCAGGTTTATAGGGTCCCATTTTGTGGCCGATAGTGAATCTTTATCTCAACTTATT 300
Db 241 CTATCAGGTTTATAGGGTCCCATTTTGTGGCCGATAGTGAATCTTTATCTCAACTTATT 300
Qy 301 GATATTTCTGTGGCTTCAGGGGAAAGAGTCAATGGGAAATTTTATGGAAACAGTAGAA 360
Db 301 GATATTTCTGTGGCTTCAGGGGAAAGAGTCAATGGGAAATTTTATGGAAACAGTAGAA 360
Qy 361 GAACCTATTAAATCAAAAAATAGCAGAAATGCAAGAAATTAAGCGCTTTTCGGAAATAGAA 420
Db 361 GAACCTATTAAATCAAAAAATAGCAGAAATGCAAGAAATTAAGCGCTTTTCGGAAATAGAA 420
Qy 421 GGATTAGGTAATTAATTAACCAATTTATATCTAACTGCGCTTTGAAGAAATGGGAAGAAATCCA 480
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Db	421	GGATTAGGTAAATAATTAACCAATTATTAICTAACTCGCGCTTGAAGAAATGGAAAGAAAATCCA	480
Qy	481	AATGGTTTCAAGAGCCTTACGAGATGCGAAATCGAATTTGAATCCTCGGATAGTTATTTT	540
Db	481	AATGGTTTCAAGAGCCTTACGAGATGCGAAATCGAATTTGAATCCTCGGATAGTTATTTT	540
Qy	541	ACGCAATATATGCCATCTTTTAGAGTGACAAATTTTGAAGTACCAATTCCTTACTGTTATAT	600
Db	541	ACGCAATATATGCCATCTTTTAGAGTGACAAATTTTGAAGTACCAATTCCTTACTGTTATAT	600
Qy	601	GCAATGSCAGCCAACTTCATTTTACTGTTATTAAAGGACGGCTCAATTTTGGAGAGAA	660
Db	601	ACACAGCGACCAACCTTCATTTACTGTTATTAAAGGACGGCTCAATTTTGGAGAGAA	660
Qy	661	TGGGGATGGTCAACAACTACTATTAACTATTAATGATCGTCAAAATGAAATCTTACTGCA	720
Db	661	TGGGGATGGTCAACAACTACTATTAACTATTAATGATCGTCAAAATGAAATCTTACTGCA	720
Qy	721	GAATATTCGATCACTGTGTAAAGTGGTATGAAACTGGTTAGCAAAATTAAGAGGCACG	780
Db	721	GAATATTCGATCACTGTGTAAAGTGGTATGAAACTGGTTAGCAAAATTAAGAGGCACG	780
Qy	781	AGCGCTAAACAATGGGTGCACTATACCAATTCGTTAGAGAAATGCACATCGCGGTTTTA	840
Db	781	AGCGCTAAACAATGGGTGCACTATACCAATTCGTTAGAGAAATGCACATCGCGGTTTTA	840
Qy	841	GATGTTGTTCATATTCCCAAATTAAGACACACGCGTACCCAAATGGAAACGAAAGCA	900
Db	841	GATGTTGTTCATATTCCCAAATTAAGACACACGCGTACCCAAATGGAAACGAAAGCA	900
Qy	901	CAACTAAACAAGGAAGTATATACAGATCCACTGGGCGGGTAAAGTGCTTCAATTTGGT	960
Db	901	CAACTAAACAAGGAAGTATATACAGATCCACTGGGCGGGTAAAGTGCTTCAATTTGGT	960
Qy	961	TCCTGGTATGCAAAAGCACCCTCTTCGAGGTGATAGAAATCATCCGTTATTTCGACCAACC	1020
Db	961	TCCTGGTATGCAAAAGCACCCTCTTCGAGGTGATAGAAATCATCCGTTATTTCGACCAACC	1020
Qy	1021	CATGTATTGATTATATAACGGGACTCACAGTGTATACAAATCAAGAAGCATTTCTTCC	1080
Db	1021	CATGTATTGATTATATAACGGGACTCACAGTGTATACAAATCAAGAAGCATTTCTTCC	1080
Qy	1081	GCTCGCTATATAAGACATTTGGGCTGTCTACAAATAAGCTACATCGGTGCTAGTAGGGT	1140
Db	1081	GCTCGCTATATAAGACATTTGGGCTGTCTACAAATAAGCTACATCGGTGCTAGTAGGGT	1140
Qy	1141	AGTAACTCTCAAACAATGTATGAACTAATCAAAATCTACACAGCACTAGTACCTTTGAT	1200
Db	1141	AATAATATAAACAAGATGTATGAACTAATCAAAATCTACACAGCACTAGTACCTTTGAT	1200
Qy	1201	TTTACGAATTTGATATTTTACAAGACTCTATCAAAAGGATGCAGTACTCCTTGATATTGTT	1260
Db	1201	TTTACGAATTTGATATTTTACAAGACTCTATCAAAAGGATGCAGTACTCCTTGATATTGTT	1260
Qy	1261	TACCCTGGTTATACGTATATTTTTTGGAAATGCCAAGATCGAGTTTTTTCATGTTAAAC	1320
Db	1261	TTTTCTCGTTTATACGTATATTTTTTGGAAATGCCAAGATCGAGTTTTTTCATGTTAAAC	1320
Qy	1321	CAATTGAATTAATACGAAAGAGCTTAAAGTATTAATCAGTTTCCAAAGATATTTATAGCG	1380
Db	1321	CAATTGAATTAATACGAAAGAGCTTAAAGTATTAATCAGTTTCCAAAGATATTTATAGCG	1380
Qy	1381	AGTACAAGAGATTTCCGAATTTAGAAATTTACCTCCAGAAACTTCAGATCAACCAAAATTATG	1440
Db	1381	GGGACAAGAGATTTCCGAATTTAGAAATTTACCTCCAGAAACTTCAGATCAACCAAAATTATG	1440
Qy	1441	TCATATAGCCATAGATTATGTCATATACAAAGTATTTCCCGCGACGGGTAAACCTACCGGA	1500
Db	1441	TCATATAGCCATAGATTATGTCATATACAAAGTATTTCCCGCGACGGGTAAACCTACCGGA	1500
Qy	1501	TTAGTACCTGTATTTTCTGGACACATCGAAGTGCAGATTTTAAACAATACAATATATTCA	1560
Db	1501	TTAGTACCTGTATTTTCTGGACACATCGAAGTGCAGATTTTAAATATGCAAGTCAATCA	1560

Qy	1561	GAT	AAAAATC	ACT	CAAAATTC	CGGCGCT	TAAATG	TGGGGG	TAATAT	TACCGTTGT	-----	1513								
Db	1561	GAT	AAAAAT	TACT	CAGATTT	CCGCTCG	TAAAGG	TTTCT	GATTTT	TGGCTCC	CTCTATA	CACGGA	1520							
Qy	1614	-----	TCC	AGTGT	TAAAGCA	CACGAC	ACATAC	GAGG	GGGATTT	TATAC	AGTAT	1562								
Db	1621	GG	CCCAAT	ATATAC	CGTTGT	ATCGGG	TCTCG	ATTTAC	GGGGGG	GGGATAT	ATAA	AGTA	1580							
Qy	1663	AAT	AGAAG	TACT	TGGTTCT	GAGAA	ACCTTTAT	TTCT	TAGCT	CGAATAT	GCC	TAGCA	ATGAAA	1722						
Db	1681	ATA	GAAGAT	TGGAGT	TAATAT	TATAC	ATATG	CGGTG	TAAAAAT	TTTC	GAGAC	ATTTAA	CAGAGAA	1740						
Qy	1723	AA	AGCAGG	GAATAT	TCGTCT	AGAC	GTG	AGATAT	CTGCT	GATG	CAGATAT	TTGTT	ATGTCAT	1782						
Db	1741	TAT	AGTAT	GAGGAT	TCGGTAT	CTCCG	TATAT	ATATCT	GATTTT	TATATA	ATAT	CTCTCT	1800							
Qy	1783	GT	AACGAT	CTC	CAGATTC	CAGATG	CCAAAA	CAATG	AACCC	AGTGAGG	ATCTG	CACATCT	1842							
Db	1801	GA	AAAAAC	CGTTAA	ATCTC	ACGCT	CAAAAA	CTATG	ATATGAG	GTGAAG	CTTTAA	CATAT	1860							
Qy	1843	AAA	CTTTTAA	AGTTT	GCAGAT	CTCTAT	CAAC	ATTTAA	ATTTT	TAGCA	ACAGAT	AGTTT	CGCTA	1902						
Db	1861	AATA	AAATTTAA	TTATG	CGACTTT	GGCCCC	TATTA	AAATTTAC	CGAC	CAACCG	CAACCTTT	CAIT	1920							
Qy	1903	GC	ATTGAAA	CATAA	TTAGGT	GAA	ACCC	TAAATTC	CAAC	ATATCT	GTGTAT	AGTTT	TAGCTT	1962						
Db	1921	ACT	TAGGG	CTATATTT	GAC	GGGAG	AC	TCTTCT	TGG	AT-----	TGA	AGCTTAT	ATA	1974						
Qy	1963	GAC	CGAAT	CGAAT	TCATCC	AGTAG	ATAG	AGACAT	ATATG	AGCGG	AA	CAAGATTT	TAGA	AGCA	2022					
Db	1975	GAC	CGAAT	CGAAT	TTATCC	AGTAG	ATAG	AGACAT	ATATG	AGCGG	AA	CAAGATTT	TAGA	AGCA	2034					
Qy	2023	GCG	AGAA	ACG	AGTGA	TCC	TTGTTT	TAC	GAATAC	AAAGAT	GCTTAC	CGAC	CAAGG	CGTA	2082					
Db	2035	GCG	AGAA	ACG	AGTGA	TCC	TTGTTT	TAC	GAATAC	AAAGAT	GCTTAC	CGAC	CAAGG	CGTA	2094					
Qy	2083	AC	GGA	TATG	AGATG	GAAT	CA	AGCGG	CAAACTT	TAGT	TGG	AAATGC	CTTAT	CGG	ATGATTT	CTGTAT	2142			
Db	2095	AC	GGA	TATG	AGATG	GAAT	CA	AGCGG	CAAACTT	TAGT	TGG	AAATGC	CTTAT	CGG	ATGATTT	CTGTAT	2154			
Qy	2143	CC	AAATG	AAAA	ACG	ATGTTAT	TTC	ATG	CTAGT	GAG	AGG	CAAA	CGCT	CAGT	GAGCA	2202				
Db	2155	CC	AAATG	AAAA	ACG	ATGTTAT	TTC	ATG	CTAGT	GAG	AGG	CAAA	CGCT	CAGT	GAGCA	2214				
Qy	2203	CG	TAA	TTTGT	CTTCA	GATCC	CAGATTT	CCA	GAGAT	TAAATG	GAGAAAA	TGG	CTG	CA	CGCA	2262				
Db	2215	CG	TAA	TTTGT	CTTCA	GATCC	CAGATTT	CCA	GAGAT	TAAATG	GAGAAAA	TGG	CTG	CA	CGCA	2274				
Qy	2263	AG	TACGG	AAATTT	GAGGTT	ATAG	AGGG	ATGCTTT	TTAT	CCA	AGGG	CGTTAT	CT	AC	CGCTTA	2322				
Db	2275	AG	TACGG	AAATTT	GAGGTT	ATAG	AGGG	ATGCTTT	TTAT	CCA	AGGG	CGTTAT	CT	AC	CGCTTA	2334				
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Db	2335	CC	AGGTG	CG	GAG	AGAAAT	TAGAT	AC	GGAA	CGTAT	CCA	CGTATCT	GTAT	CA	AAAG	ATGATAG	2394			
Qy	2383	GA	AGGTG	TAT	TAA	ACC	ATAC	AC	AGATAT	TAG	ATTG	AGAGGG	TTTGT	CG	GAAG	CAGTCAA	2442			
Db	2395	GA	AGGTG	TAT	TAA	ACC	ATAC	AC	AGATAT	TAG	ATTG	AGAGGG	TTTGT	CG	GAAG	CAGTCAA	2454			
Qy	2443	GG	ATTG	G	AAATTTT	T	CA	AAATTT	CGT	CA	T	CA	ACG	AAATTTG	T	AAAAAT	TGTA	CCGGAT	2502	
Db	2455	GG	ATTG	G	AAATTTT	T	CA	AAATTT	CGT	CA	T	CA	ACG	AAATTTG	T	AAAAAT	TGTA	CCGGAT	2514	
Qy	2503	GA	TTTGT	CG	CG	AGAT	CTATCT	CT	CTGT	TAACT	CG	GAATG	GTAGT	TAT	CA	AT	CG	ATG	CAGCGAA	2562

QY 2623 TCTATTCCTATTGATACAGGTGAAATCGATTACAAATGAAATGCGAATATGGTTGGA 2682
DB 2635 TCTATTCCTATTGATACAGGTGAAATCGATTACAAATGAAATGCGAATATGGTTGGA 2694
QY 2683 TTTAAGATTACGACCGCAGAGGGATATGCAACACTCGGAACCTAGATTGGTCGAGAG 2742
DB 2695 TTTAAGATTACGACCGCAGAGGGATATGCAACACTCGGAACCTAGATTGGTCGAGAG 2754
QY 2743 GGAACCTTTATCAGGAGACGATAGAAACGCTTGCAAGAGAGAAACCAACAGTGGAGATT 2802
DB 2755 GGAACCTTTATCAGGAGACGATAGAAACGCTTGCAAGAGAGAAACCAACAGTGGAGATT 2814
QY 2803 CAATGACAGAGACGCTGAAGAAACAGATAGAGGTATATGGCATGCAAAACAGCGGTA 2862
DB 2815 CAATGACAGAGACGCTGAAGAAACAGATAGAGGTATATGGCATGCAAAACAGCGGTA 2874
QY 2863 GATCGTTTATATCCGANTATCAGGATCAGCACTGAACTGATCTGATGTAGAGATTACAGAT 2922
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QY 2923 CTTPACTGCGGCCCAAGATCTGATACAGTCCATTCTTACGTATATACGAAATGTTCCCA 2982
DB 2935 CTTPACTGCGGCCCAAGATCTGATACAGTCCATTCTTACGTATATACGAAATGTTCCCA 2994
QY 2983 GAAATACCGAGGATGAACTATACGAAGTTTACGAATTAACAGATCGACTCCAAACAGCG 3042
DB 2995 GAAATACCGAGGATGAACTATACGAAGTTTACGAATTAACAGATCGACTCCAAACAGCG 3054
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DB 3115 AATTTGAATGCAACGCGCTGGCTGAGAGTACAAACAAATCAATCATATCATCTGCTCTGTG 3174
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QY 3223 GTGTTACGAGTTACTCGGAGAAAGAGGGGTAGGAAATGGATATGTAAGTATCCGTGAT 3282
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QY 3283 GGTGGAATCAACAGAAACGCTTACTTTTGTGCAAGCGATTTATGATACAAATGGAATG 3342
DB 3295 GGTGGAATCAACAGAAACGCTTACTTTTGTGCAAGCGATTTATGATACAAATGGAATG 3354
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QY 3463 AACGGATATAACAAATAGTGTGATCAATGATCAACCGGCTATATACAAACAGAGTG 3522
DB 3475 AACGGATATAACAAATAGTGTGATCAATGATCAACCGGCTATATACAAACAGAGTG 3534
QY 3523 ACATTCATCCCGTATACAGATCAAAATGTGGATTGAGATGAGTACAGAGGATACATTC 3582
DB 3535 ACATTCATCCCGTATACAGATCAAAATGTGGATTGAGATGAGTACAGAGGATACATTC 3594
QY 3583 TATATAGAAAGTGTAGAAATGATTGATGAGGTAGGTAGGTAA 3621
DB 3595 TATATAGAAAGTGTAGAAATGATTGATGAGGTAGGTAA 3633

RESULT 4

US-10-032-717-28
; Sequence 28, Application US/10032717
; Patent No. US20020151709A1

GENERAL INFORMATION:

APPLICANT: Andre R. Abad
APPLICANT: Nicholas B. Duck
APPLICANT: Xiang Feng
APPLICANT: Ronald D. Flannagan
APPLICANT: Theodore W. Kahn
APPLICANT: Lynn E. Sims
TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
Pesticidal Activity Against Coleopterans
FILE REFERENCE: 35718/237005
CURRENT APPLICATION NUMBER: US/10/032,717
CURRENT FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: 60/242,838
PRIOR FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PastSeq for Windows Version 4.0
SEQ ID NO 28
LENGTH: 6613
TYPE: DNA
ORGANISM: Bacillus thuringiensis
NAME/KEY: misc feature
LOCATION: (0)...(0)
OTHER INFORMATION: Genomic Cry12Ib-2
US-10-032-717-28

Query Match 87.0%; Score 3151.8; DB 12; Length 6613;

Best Local Similarity 92.1%; Pred. No. 0; Mismatches 262; Indels 24; Gaps 2;

Matches 3353; Conservative 0;

QY 1 ATGAGTCCAAATTAATCAAAATGAATATGAAATTTATAGATGCGACACCTTCTTCTCTGTA 60
DB 1254 ATGAGTCCAAATTAATCAAAATGAATATGAAATTTATAGATGCGACACCTTCTTCTCTGTA 1313
QY 61 TCCATGATTTCAACAGATACCCCTTTTGGCAATGAGCCAAACAAATGCGCTACAAAATATG 120
DB 1314 TCCATGATTTCAACAGATACCCCTTTTGGCAATGAGCCAAACAAATGCGCTACAAAATATG 1373
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DB 1374 GATTATAAGATTATTAATAATGCTCGGGAAATGCTAGTGAATACCTGGTTCACCT 1433
QY 181 GAAGTACTTTGTAGCGGACAGATGAGCTAAGCGCGCAATTTGATATAGTAAATTA 240
DB 1434 GAAGTACTTTGTAGCGGACAGATGAGCTAAGCGCGCAATTTGATATAGTAAATTA 1493
QY 241 CTATCAGGTTTAGGGTCCCATTTGTGGCCGATAGTCAGTCTTTTATCTCAACTTAT 300
DB 1494 CTATCAGGTTTAGGGTCCCATTTGTGGCCGATAGTCAGTCTTTTATCTCAACTTAT 1553
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QY 361 GAACCTATTAAATCAAAAATATGCAAGATATCAAGGAATAAAGCGCTTTCGGAATTAGAA 420
DB 1614 GAACCTATTAAATCAAAAATATGCAAGATATCAAGGAATAAAGCGCTTTCGGAATTAGAA 1673
QY 421 GGATAGGTAATTAATTAACCAATTTATCTAACTGCGCTTTGAAGAAATGGGAAGAAATCCA 480
DB 1674 GGATAGGTAATTAATTAACCAATTTATCTAACTGCGCTTTGAAGAAATGGGAAGAAATCCA 1733
QY 481 AATGTTTCAAGAGCTTTACGAGATGCGAAATCGAATTTGAAATCTCGATAGTTTATTT 540
DB 1734 AATGTTTCAAGAGCTTTACGAGATGCGAAATCGAATTTGAAATCTCGATAGTTTATTT 1793
QY 541 ACGCAATATATGCCATCTTTTGAAGTGAACAAATTTTGAAGTACCATTCTTCTACTGTATAT 600
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QY 601 GCAATGGCAGCCAACTCTCATTTACTTGTATTATAAGGACGCGCTCAATTTTGGAGAGAA 660
DB 1854 ACACAGGACCCAACTCTCATTTACTTGTATTATAAGGACGCGCTCAATTTTGGAGAGAA 1913

QY 661 TGGGATGGTCAACAACTACTATTAACTAATTAATGATCGTCAAAATGAAATCTACTGCA 720
DB 1914 TGGGATGGTCTACAACTACTATTAACTAATTAATGATCGTCAAAATGAAATCTACTGCA 1973
QY 721 GAATATCTGATCACTGTTGTAAGTGGTATGAATCTGGTTAGCAAAATTAAGAGCACG 780
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DB 2034 AGCGCTAAACAACTGGTGTGACTATAACCAATTCGTAGAGAAATGACACTGGCGTTTGA 2093
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Db 1981 CCAGTAGATGAGACATATGAAGCGGAATAA 2010
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RESULT 6

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US-10-032-717-5
; Sequence 5, Application US/10032717
; Patent No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre K. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sing
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032,717
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2003
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis (truncated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2001)
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: 1218-1
US-10-032-717-5
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Query Match 55.3%; Score 2003; DB 12; Length 2003;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2003; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1981 CCAGTAGATGAGACATATGAAGC 2003

RESULT 7

US-10-032-717-23
; Sequence 23, Application US/10032717
; Patent No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flanagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032,717
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 2013
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis (mutated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2013)
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: LKWS.R1218-1
US-10-032-717-23

Query Match 54.9%; Score 1987.4; DB 12; Length 2013;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2004; Conservative 0; Mismatches 6; Indels 3; Gaps 1;

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DB 1621 GTGGTAAAGGACCCAGGACATACAGGAGGGGATTTTATTAAGTATATAGAAAGTACTGGT 1680
QY 1678 TCTGTAGAACCTTTATTTCTAGCTCGATATGGCTAGCATTTAGAAAAGCAGGGAATAT 1737
DB 1681 TCTGTAGAACCTTTATTTCTAGCTCGATATGGCTAGCATTTAGAAAAGCAGGGAATAT 1740
QY 1738 CGTGTAGACTGAGATATGCTACTGATGACAGATATTTGATGATGTAAGACGATCTCAG 1797
DB 1741 CGTGTAGACTGAGATATGCTACTGATGACAGATATTTGATGATGTAAGACGATCTCAG 1800
QY 1798 ATTGAGTGCAGGACCAACAAATGAACCCAGGTGAGGATCTGACATCTTAAACCTTTTAAAGTT 1857
DB 1801 ATTGAGTGCAGGACCAACAAATGAACCCAGGTGAGGATCTGACATCTTAAACCTTTTAAAGTT 1860
QY 1858 GCAGATGCTATCAACCAATTAATTTAGCAACAGATAGTTTGGTACGATTTGAACATAT 1917
DB 1861 GCAGATGCTATCAACCAATTAATTTAGCAACAGATAGTTTGGTACGATTTGAACATAT 1920
QY 1918 TTAGTGCAGACCTTAATTTCAACATTTCTGTTATAGTTTACGTTGACCGAATCGAATTC 1977
DB 1921 TTAGTGCAGACCTTAATTTCAACATTTCTGTTATAGTTTACGTTGACCGAATCGAATTC 1980
QY 1978 ATCCAGTAGATGAGACATATGAAGCGGAACAA 2010
DB 1981 ATCCAGTAGATGAGACATATGAAGCGGAATAA 2013

RESULT 8

US-10-032-717-11
; Sequence 11, Application US/10032717
; Patent No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan

QY 1369 GATATTATAGCGAGTCAAGAGATTCCGAAATTAGAAATTAACCTCCAGAACTTCAGATCAA 1428
DB 1381 GATATTATAGCGAGTCAAGAGATTCCGAAATTAGAAATTAACCTCCAGAACTTCAGATCAA 1440
QY 1429 CCAAAATTATGAGTCATATAGCCATAGATTAATGTCATATCAACAGTATTCCCGGACGGGT 1488
DB 1441 CCAAAATTATGAGTCATATAGCCATAGATTAATGTCATATCAACAGTATTCCCGGACGGGT 1500
QY 1489 AACATACCGGATAGTACCTGTAATTTCTTGGACACATCGAAGTGCAGATTTTAAACAAT 1548
DB 1501 AACATACCGGATAGTACCTGTAATTTCTTGGACACATCGAAGTGCAGATTTTAAACAAT 1560
QY 1549 ACAATATATTCAGATAAAATCACTCAAAATTCGCGCGGTAAATGTTGGATTAATTTACCG 1608
DB 1561 ACAATATATTCAGATAAAATCACTCAAAATTCGCGCGGTAAATGTTGGATTAATTTACCG 1620
QY 1609 TTTGTTCCAGTGTAAAGGACACAGGACATACAGAGGGGATTTTATACAGTATAATAGA 1668
DB 1621 TTTGTTCCAGTGTAAAGGACACAGGACATACAGAGGGGATTTTATACAGTATAATAGA 1680
QY 1669 AGTACTGGTCTGTAGGAACCTTATTTCTAGCTCGATATGGCTAGCATTTAGAAAAAGCA 1728
DB 1681 AGTACTGGTCTGTAGGAACCTTATTTCTAGCTCGATATGGCTAGCATTTAGAAAAAGCA 1740
QY 1729 GCGAAATATCGTGTAGGATGAGTATGCTACTGATGCAGATTTGTCATGTAAC 1788
DB 1741 GCGAAATATCGTGTAGGATGAGTATGCTACTGATGCAGATTTGTCATGTAAC 1800
QY 1789 GATGCTCAGATTGAGTGCAGAAACCAATGAACCCAGTGCAGGATCTGACATCTTAAACT 1848
DB 1801 GATGCTCAGATTGAGTGCAGAAACCAATGAACCCAGTGCAGGATCTGACATCTTAAACT 1860
QY 1849 TTTAAAGTTGAGTGCAGATGCTATCAACAACTTAAATTTAGCAAGATTTGCTAGCATTTG 1908
DB 1861 TTTAAAGTTGAGTGCAGATGCTATCAACAACTTAAATTTAGCAAGATTTGCTAGCATTTG 1920
QY 1909 AATCAATATTTAGTGCAGACCTTAATTCACATTAATCTGGTATAGTTAGTTGACCGA 1968
DB 1921 AATCAATATTTAGTGCAGACCTTAATTCACATTAATCTGGTATAGTTAGTTGACCGA 1980
QY 1969 ATCGAATTCATCCAGTAGATGAGACATATGAGCGGAACAA 2010
DB 1981 ATCGAATTCATCCAGTAGATGAGACATATGAGCGGAATAA 2022

RESULT 10

US-10-032-717-39
; Sequence 39, Application US/10032717
; Patent No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flanagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins with
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032,717
; PRIORITY FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIORITY FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 2022
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis (mutated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2022)
; NAME/KEY: misc_feature

; LOCATION: (0)...(0)
; OTHER INFORMATION: LRNS.N1218-1
US-10-032-717-39

Query Match 54.9%; Score 1986.4; DB 12; Length 2022;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 2009; Conservative 0; Mismatches 1; Indels 12; Gaps 1;

QY 1 ATCAGTCCAAATTAATCAAAATGAATATGAATTAATAGATGCGACACCTTCTACTTCTGTA 60
DB 1 ATCAGTCCAAATTAATCAAAATGAATATGAATTAATAGATGCGACACCTTCTACTTCTGTA 60
QY 61 TCCAAATGATTTAAACAGATACCCCTTTTGGCAATGAGCAAAATGCGCTACAAAATATG 120
DB 61 TCCAAATGATTTAAACAGATACCCCTTTTGGCAATGAGCAAAATGCGCTACAAAATATG 120
QY 121 GATTATAAGATTTATTAATAATGCTGCGGGAAATGCTAGTGAATACCTGGTTCACCT 180
DB 121 GATTATAAGATTTATTAATAATGCTGCGGGAAATGCTAGTGAATACCTGGTTCACCT 180
QY 181 GAAGTACTTGTAGCGGACAAAGATGAGCTAAGCGCGCAATGATATAGTAGTAAATTA 240
DB 181 GAAGTACTTGTAGCGGACAAAGATGAGCTAAGCGCGCAATGATATAGTAGTAAATTA 240
QY 241 CTATCAGGTTTAGGGTCCCATTTGTTGGCCGATAGTGAATTTTATCTCAACTTATT 300
DB 241 CTATCAGGTTTAGGGTCCCATTTGTTGGCCGATAGTGAATTTTATCTCAACTTATT 300
QY 301 GATATTCTGTGGCTTCAGGGGAAAGAGTCAATGGGAAATTTTATGAAACAGTAGAA 360
DB 301 GATATTCTGTGGCTTCAGGGGAAAGAGTCAATGGGAAATTTTATGAAACAGTAGAA 360
QY 361 GAACCTCATTAATCAAAATAATAGCAGAAATATCAAGGAAATAAAGCGCTTCGGAAATTAGAA 420
DB 361 GAACCTCATTAATCAAAATAATAGCAGAAATATCAAGGAAATAAAGCGCTTCGGAAATTAGAA 420
QY 421 GGATTAAGTAAATTAATCAAAATTAATCTAATCTGCGCTTTGAAGAAATGGGAAAGAAATCCA 480
DB 421 GGATTAAGTAAATTAATCAAAATTAATCTAATCTGCGCTTTGAAGAAATGGGAAAGAAATCCA 480
QY 481 -----AATGGTTCAAGAGCCTTACGAGATGCGGAAATCGATTTGAATCTCTG 528
DB 481 TTAAGAAATCTTAATGGTTCAAGAGCCTTACGAGATGCGGAAATCGATTTGAATCTCTG 540
QY 529 GATAGTTTATTTACGCAATATATGCGCATCTTTTAGAGTGACAAATTTTGAAGTACCATTTC 588
DB 541 GATAGTTTATTTACGCAATATATGCGCATCTTTTAGAGTGACAAATTTTGAAGTACCATTTC 600
QY 589 CTTACTGTATATGCAATGGCAGCCAACTTCAATTTACTGTTATTAAGGACGCGTCAATTT 648
DB 601 CTTACTGTATATGCAATGGCAGCCAACTTCAATTTACTGTTATTAAGGACGCGTCAATTT 660
QY 649 TTTGGAGAGAAATGGGATGGTCAACAACTACTATTAATACTATTAATGATGCTCAATG 708
DB 661 TTTGGAGAGAAATGGGATGGTCAACAACTACTATTAATACTATTAATGATGCTCAATG 720
QY 709 AAATTTACTGCAAGATTTCTGATCACTGTGTAAAGTGTATGAAACTGTTTAGCAAAA 768
DB 721 AAATTTACTGCAAGATTTCTGATCACTGTGTAAAGTGTATGAAACTGTTTAGCAAAA 780
QY 769 TTAAGAGGACGAGCGCTAAACAACTGGGTTGACTATAACAAATTCCTGAGAGAAATGACA 828
DB 781 TTAAGAGGACGAGCGCTAAACAACTGGGTTGACTATAACAAATTCCTGAGAGAAATGACA 840
QY 829 CTGGCGGTTTATAGATGTTGTCATTAATTTCCCAAAATTTATGACACGACGTAACCAATG 888
DB 841 CTGGCGGTTTATAGATGTTGTCATTAATTTCCCAAAATTTATGACACGACGTAACCAATG 900
QY 889 GAAACGAAAGCACTTAACAGAGGAGTATATACAGATCCACTGGCGGCTTAACCGTG 948
DB 901 GAAACGAAAGCACTTAACAGAGGAGTATATACAGATCCACTGGCGGCTTAACCGTG 960
QY 949 TCTTCAATTTGTTCTGTTGATGACAAAGCAACCTTCTTTTGGAGTATAGAAATCATCCGTT 1008

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Db 961 TCCTCAATGGTCTCGTGTGACAAAGCACCTTCTTCGGAGTGATGAATCATCCGTT 1020
QY 1009 ATTCGACACCCCATGATTTGATTTATATTAACGGGACTCAAGTGTATACAAATCAAGA 1068
Db 1021 ATTCGACACCCCATGATTTGATTTATATTAACGGGACTCAAGTGTATACAAATCAAGA 1080
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Db 1081 AGCAATTTCTCCGCTCGCTATATTAAGACATTTGGGCTGTCTATCAATAAGCTTACCATCGT 1140
QY 1129 GTCAAGTAGGGGTAGTAACTTTCACAAATGATGGAACTAATCAAAATCTACACAGCACT 1188
Db 1141 GTCAAGTAGGGGTAGTAACTTTCACAAATGATGGAACTAATCAAAATCTACACAGCACT 1200
QY 1189 AGTACCTTTGATTTTACGAATATGATATTTTCAAGACTCTATCAAGGATGCGATGCTC 1248
Db 1201 AGTACCTTTGATTTTACGAATATGATATTTTCAAGACTCTATCAAGGATGCGATGCTC 1260
QY 1249 CTTGATATTTGTTTACCCCTGGTTTACGTATATATTTTGGAAATGCCAAGAGTCCGAGTTT 1308
Db 1261 CTTGATATTTGTTTACCCCTGGTTTACGTATATATTTTGGAAATGCCAAGAGTCCGAGTTT 1320
QY 1309 TTCAATGTTAAACCAATTTGAATAATACCAAGAAAGCGTTTAAAGTATATATTTCCAAAT 1368
Db 1321 TTCAATGTTAAACCAATTTGAATAATACCAAGAAAGCGTTTAAAGTATATATTTCCAAAT 1380
QY 1369 GATATTTATAGGAGTACAAAGATTTCCGAATTTAGATTTTACCTCCAGAACTTCAGATCAA 1428
Db 1381 GATATTTATAGGAGTACAAAGATTTCCGAATTTAGATTTTACCTCCAGAACTTCAGATCAA 1440
QY 1429 CCAATATTTAGTTCATATAGCATAGATTTTGTCTATATCAAGATTTTCCCGCGACGGT 1488
Db 1441 CCAATATTTAGTTCATATAGCATAGATTTTGTCTATATCAAGATTTTCCCGCGACGGT 1500
QY 1489 AACACTACCGGATTTAGTACCTGTATTTTCTTGGACACATCCGAAGTGCAGATTTTAAACAAAT 1548
Db 1501 AACACTACCGGATTTAGTACCTGTATTTTCTTGGACACATCCGAAGTGCAGATTTTAAACAAAT 1560
QY 1549 ACAATATATTCAGATAAAATCACTCAAAATTCGGCCGTTAAATTTGGGATAATTTACG 1608
Db 1561 ACAATATATTCAGATAAAATCACTCAAAATTCGGCCGTTAAATTTGGGATAATTTACG 1620
QY 1609 TTTGTTCCAGTGGTAAAGGACCGAGCATACAGAGGGGATTTTACGTATATATAGA 1668
Db 1621 TTTGTTCCAGTGGTAAAGGACCGAGCATACAGAGGGGATTTTACGTATATATAGA 1680
QY 1669 AGTACTGTTCTGTAGGAACCTTATTTCTAGCTCGATATGGCTAGCATTTAGAAAAGCA 1728
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QY 1729 GGGAAATATCGTGTAAAGCTGAGATATGCTACTGATGAGATATTTGATTTGATGTAATAC 1789
Db 1741 GGGAAATATCGTGTAAAGCTGAGATATGCTACTGATGAGATATTTGATTTGATGTAATAC 1800
QY 1789 GATGCTCAGATTCAGATCCGAAACCAATGACCCAGGTGAGGATCTGACATCTAAACT 1848
Db 1801 GATGCTCAGATTCAGATCCGAAACCAATGACCCAGGTGAGGATCTGACATCTAAACT 1860
QY 1849 TTTAAAGTTGAGATGCTATACAAACATTTAAATTTAGCAACAGATAGTTGCTAGCATTTG 1908
Db 1861 TTTAAAGTTGAGATGCTATACAAACATTTAAATTTAGCAACAGATAGTTGCTAGCATTTG 1920
QY 1909 AAACATAATTTAGGTGAAGACCTTAATCAACATTTATCTGGTATAGTTTACGTTGACCGA 1968
Db 1921 AAACATAATTTAGGTGAAGACCTTAATCAACATTTATCTGGTATAGTTTACGTTGACCGA 1980
QY 1969 ATCGAATTCATCCAGTAGATGAGACATATGAAAGGGAACAA 2010
Db 1981 ATCGAATTCATCCAGTAGATGAGACATATGAAAGGGAACAA 2022
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RESULT 11

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US-10-032-717-43
; Sequence 43, Application US/10032717
; Patent No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
; Pesticidal Activity Against Coleopterans
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032,717
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 2013
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis (mutated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2013)
; NAME/KEY: misc.feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: LRMS.R1218-1
US-10-032-717-43
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Query Match 54.8%; Score 1985.8; DB 12; Length 2013;

Best Local Similarity 99.5%; Pred. No. 0;

Matches 2003; Conservative 0; Mismatches 7; Indels 3; Gaps 1;

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QY 1 ATGAGTCCAAATATCAAAATGAATATGAATATATAGATGCGACACCTTCTTACTTCTGTA 60
Db 1 ATGAGTCCAAATATCAAAATGAATATGAATATATAGATGCGACACCTTCTTACTTCTGTA 60
QY 61 TCCAAATGATTTCAAGATACCCCTTTTGGCAATGAGCGCAACAAATGCGCTACAAAATATG 120
Db 61 TCCAAATGATTTCAAGATACCCCTTTTGGCAATGAGCGCAACAAATGCGCTACAAAATATG 120
QY 121 GATTTATAAGATTTATTAATAATGCTCTCGCGGAAATCTAGTAGTAATACCTTGGTTTCACT 180
Db 121 GATTTATAAGATTTATTAATAATGCTCTCGCGGAAATCTAGTAGTAATACCTTGGTTTCACT 180
QY 181 GAAGTACTTGTAGCGGACAAAGATGCAAGCTAAGGCCGCAATTTGATATAGTAGGTAATAA 240
Db 181 GAAGTACTTGTAGCGGACAAAGATGCAAGCTAAGGCCGCAATTTGATATAGTAGGTAATAA 240
QY 241 CTATCAGGTTTAGGGGTCCTCATTTGTTGGCCGATAGTAGTCTTTATACCTTAACTTATT 300
Db 241 CTATCAGGTTTAGGGGTCCTCATTTGTTGGCCGATAGTAGTCTTTATACCTTAACTTATT 300
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QY 361 GAACTCTATTATCAAAAATAGCAGATATGCAAGGAATTAAGCGCTTTTCGGAATTAGAA 420
Db 361 GAACTCTATTATCAAAAATAGCAGATATGCAAGGAATTAAGCGCTTTTCGGAATTAGAA 420
QY 421 GGATTAGTAAATTAATCAATTAATATCTAATCTGGCTTGAAGATGGGAAGAAATCC- 479
Db 421 GGATTAGTAAATTAATCAATTAATATCTAATCTGGCTTGAAGATGGGAAGAAATCC- 480
QY 480 --AATGGTTCAAGGCTTACGAGATGTCGAAATCGATTTGAAATCTCGATAGTTTA 537
Db 481 TTAAGAAATGCTTAGAGCCTTACGAGATGTCGAAATCGATTTGAAATCTCGATAGTTTA 540
QY 538 TTTACGCAATATATGCCATCTTTTAGAGTGAACAAATTTTGAAGTACCAATTCCTTACTGTA 597
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Db 541 TTTAGCAATATATAGCCATCTTTTAGAGTGAACAATTTTGAAGTACCAATCTCTTACTGTA 600
QY 598 TATGCAATGCGAGCAACCTTCAITTAATCTGTTATTAAGAGCGGTCATATTTTGGAGAA 657
Db 601 TATGCAATGCGAGCAACCTTCAITTAATCTGTTATTAAGAGCGGTCATATTTTGGAGAA 660
QY 658 GAATGGGATGGTCAACACTATCTATTAATAA CTATTATGATCGTCAAACTTACT 717
Db 661 GAATGGGATGGTCAACACTATCTATTAATAA CTATTATGATCGTCAAACTTACT 720
QY 718 GCAGATATTCTGATCACTGTGTAAGTGTATGAACTGGTTTGTAGCAAAATTAAGGC 777
Db 721 GCAGATATTCTGATCACTGTGTAAGTGTATGAACTGGTTTGTAGCAAAATTAAGGC 780
QY 778 ACAGCGCTAAACAATGGGTTGACTATAA CCAATTCGGTATAGAGAAATGACACTGGCGGTT 837
Db 781 ACAGCGCTAAACAATGGGTTGACTATAA CCAATTCGGTATAGAGAAATGACACTGGCGGTT 840
QY 838 TTAGATGTTGTTGATATTCCCAATTTATGACA CACGCAAGTACCCAATGGAAACGAAA 897
Db 841 TTAGATGTTGTTGATATTCCCAATTTATGACA CACGCAAGTACCCAATGGAAACGAAA 900
QY 898 GCACAACTAACAGGGAAGTATATACAGATCCACTGGCGGGGTAAACGTGCTTCAATT 957
Db 901 GCACAACTAACAGGGAAGTATATACAGATCCACTGGCGGGGTAAACGTGCTTCAATT 960
QY 958 GGTTCCTGTTATGACAAAGCACCTTCTTTCGGAGTATAGAACTCATCGTTATTTCGACCA 1017
Db 961 GGTTCCTGTTATGACAAAGCACCTTCTTTCGGAGTATAGAACTCATCGTTATTTCGACCA 1020
QY 1018 CCCATGTTATTTGATTTATAA CCGGACTCACAGTGTATACAAATCAAGAAGCAATTTCT 1077
Db 1021 CCCATGTTATTTGATTTATAA CCGGACTCACAGTGTATACAAATCAAGAAGCAATTTCT 1080
QY 1078 TCCGCTCGCTATATAGACAACTGGCTGTGTCATCAATATAGCTTACCATCTGTGCTAGG 1137
Db 1081 TCCGCTCGCTATATAGACAACTGGCTGTGTCATCAATATAGCTTACCATCTGTGCTAGG 1140
QY 1138 GTPAGTAATCTTCAACAAATGTATGAACTAATCAAAATCTACACAGCACTAGTACCTTT 1197
Db 1141 GTPAGTAATCTTCAACAAATGTATGAACTAATCAAAATCTACACAGCACTAGTACCTTT 1200
QY 1198 GATTTTCAAGATTTATGATTTTCAAGA CTCTATCAAAAGTATGAGTACTCTTGTATAT 1257
Db 1201 GATTTTCAAGATTTATGATTTTCAAGA CTCTATCAAAAGTATGAGTACTCTTGTATAT 1260
QY 1258 GTTTACCTGTTATACGTATATATTTTGGAA TGCAGAGTCCAGATGTTTTCATGGTA 1317
Db 1261 GTTTACCTGTTATACGTATATATTTTGGAA TGCAGAGTCCAGATGTTTTCATGGTA 1320
QY 1318 AACCAATTTGAATTAATACCAAGAAAGCGTTAAAGTATATTAATCCAGTTTCCAAAGATATTATA 1377
Db 1321 AACCAATTTGAATTAATACCAAGAAAGCGTTAAAGTATATTAATCCAGTTTCCAAAGATATTATA 1380
QY 1378 GCGAGTACAAGAGATTCGGAATTTAGAA TTAACCTCCAGAACTTCAGATCAACCAAAATAT 1437
Db 1381 GCGAGTACAAGAGATTCGGAATTTAGAA TTAACCTCCAGAACTTCAGATCAACCAAAATAT 1440
QY 1438 GAGTCATATAGCCATAGATTTATGTCATAT CACAAGTATTCGCGGAGCGGTAACTATCC 1497
Db 1441 GAGTCATATAGCCATAGATTTATGTCATAT CACAAGTATTCGCGGAGCGGTAACTATCC 1500
QY 1498 GGATTAAGTACCTGTTATTTCTTGGACACAT CCGAAGTGCAGATTTAAACAATACAAATATAT 1557
Db 1501 GGATTAAGTACCTGTTATTTCTTGGACACAT CCGAAGTGCAGATTTAAACAATACAAATATAT 1560
QY 1558 TCAGATAAATCACTCAAAATTCGCGCGGTTTAAAT GTTTGGGATTAATTTACGTTTGTTCGA 1617
Db 1561 TCAGATAAATCACTCAAAATTCGCGCGGTTTAAAT GTTTGGGATTAATTTACGTTTGTTCGA 1620
QY 1618 GTGGTAAAGGACACAGACATACAGAGGGGATTTATTA CAGTATTAATAGAGTACTGGT 1677
Db 1621 GTGGTAAAGGACACAGACATACAGAGGGGATTTATTA CAGTATTAATAGAGTACTGGT 1680

QY 1678 TCTGTAGGAACCTTATTTCTAGCTCGATATGCGCTAGCATTTAGAAAAGCAGGGAATAT 1737
Db 1681 TCTGTAGGAACCTTATTTCTAGCTCGATATGCGCTAGCATTTAGAAAAGCAGGGAATAT 1740
QY 1738 CGTGTAAAGTCTGAGATATGCTACTGATGAGATATTTGTATTTGATGTAATGTAACGATGCTCAG 1797
Db 1741 CGTGTAAAGTCTGAGATATGCTACTGATGAGATATTTGTATTTGATGTAATGTAACGATGCTCAG 1800
QY 1798 ATTCAAGTCCCAAAAACAATGAACCCAGGTCAGGATCTGACATCTAAACTTTTAAAGTT 1857
Db 1801 ATTCAAGTCCCAAAAACAATGAACCCAGGTCAGGATCTGACATCTAAACTTTTAAAGTT 1860
QY 1858 GCAGATGCTTATCAACACTTAAATTTAGCAACAGATAGTTCGCTAGCATTTAGAAACATAAT 1917
Db 1861 GCAGATGCTTATCAACACTTAAATTTAGCAACAGATAGTTCGCTAGCATTTAGAAACATAAT 1920
QY 1918 TTAGGTGAAGACCTTAATTTCAACATTTATCTGTTATAGTTTACGTTGACCGAATCGAATTC 1977
Db 1921 TTAGGTGAAGACCTTAATTTCAACATTTATCTGTTATAGTTTACGTTGACCGAATCGAATTC 1980
QY 1978 ATCCCAAGTATGAGACATATGAGCGGAACAA 2010
Db 1981 ATCCCAAGTATGAGACATATGAGCGGAATAA 2013

RESULT 12

US-10-032-717-19
; Sequence 19, Application US/10032717
; Patent No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Xiang Feng
; APPLICANT: Nicholas B. Duck
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins with
; Pesticidal Activity Against Coleopterans
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032,717
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; TYPE: DNA
; LENGTH: 1860
; ORGANISM: Bacillus thuringiensis (truncated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (10)...(1860)
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: 49PVD
US-10-032-717-19

Query Match 51.0%; Score 1848.4; DB 12; Length 1860;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1849; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 142 ATGCTCGCGGAAATGCTAGTGAATACCTGCTTCACTTCACTGTAAGTACTCTTTAGCGGACAA 201
Db 10 ATGCTCGCGGAAATGCTAGTGAATACCTGCTTCACTTCACTGTAAGTACTCTTTAGCGGACAA 69
QY 202 GATGCACTTAAGCCCGCAATTTGATAGTAGTAAATTAATCACTTACAGTTTAGGGGTCCCA 261
Db 70 GATGCACTTAAGCCCGCAATTTGATAGTAGTAAATTAATCACTTACAGTTTAGGGGTCCCA 129
QY 262 TTGTTGGCCGATAGTACTTTTATATCTTATATCACTTATTTGATATTTCTGTGGCCTTCAGGG 321
Db 130 TTGTTGGCCGATAGTACTTTTATATCTTATATCACTTATTTGATATTTCTGTGGCCTTCAGGG 189

QY 322 GAAAGAGTCAATGGGAATTTTATGGAACAAGTAGAAGAACTCATTAATCAAAAAATA 381
DB 190 GAAAGAGTCAATGGGAATTTTATGGAACAAGTAGAAGAACTCATTAATCAAAAAATA 249
QY 382 GCAGATATGCAAGAAATAAGCGCTTTCCGGAATTTAGGAAGATTAGGTAATAATACCAA 441
DB 250 GCAGATATGCAAGAAATAAGCGCTTTCCGGAATTTAGGAAGATTAGGTAATAATACCAA 309
QY 442 TTATATCTAATCGCTTGAAGATGGAAGAAATCAAAATGGTTCAAGAGCCCTTACGA 501
DB 310 TTATATCTAATCGCTTGAAGATGGAAGAAATCAAAATGGTTCAAGAGCCCTTACGA 369
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QY 562 AGAGTGACAAATTTTGAAGTACCAATCTCTACTGATATGCAATGGCAGCCCACTTCAT 621
DB 430 AGAGTGACAAATTTTGAAGTACCAATCTCTACTGATATGCAATGGCAGCCCACTTCAT 489
QY 622 TTACTGTTATTAAGGACGCGTCAATTTTGGAGAGGATGGGATGGTCAACACTACT 681
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QY 682 ATTAATAACTATTATGATCGTCAAAATGAAACTTACTGCAAGAAATTTCTGATCAGTGTGTA 741
DB 550 ATTAATAACTATTATGATCGTCAAAATGAAACTTACTGCAAGAAATTTCTGATCAGTGTGTA 609
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DB 670 TATAACCAATTCGTTAGAGAAATGACATCGCGGTTTATGATGTTGTCATTTATTCCTCA 729
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QY 922 ACAGATCACTGGGCGCGGTAAACGCTGCTTCAATGTTGTTCTGTTATGACAAAGCACT 981
DB 790 ACAGATCACTGGGCGCGGTAAACGCTGCTTCAATGTTGTTCTGTTATGACAAAGCACT 849
QY 982 TCTTTCCGAGTGATAGATCATCGTTATTCGACCAACCCCATGTTATTTGATTTATATAACG 1041
DB 850 TCTTTCCGAGTGATAGATCATCGTTATTCGACCAACCCCATGTTATTTGATTTATATAACG 909
QY 1042 GGACTCAAGTGATATACAAATCAAGAAGCAATTTCTTCGCTCGCTATATAAGACATTTGG 1101
DB 910 GGACTCAAGTGATATACAAATCAAGAAGCAATTTCTTCGCTCGCTATATAAGACATTTGG 969
QY 1102 GCTGTTATCAAAATAGCTACATCGTGTAGTAGGGGTAGTAATCTTCAACAAATGAT 1161
DB 970 GCTGTTATCAAAATAGCTACATCGTGTAGTAGGGGTAGTAATCTTCAACAAATGAT 1029
QY 1162 GGAATATCAAAATCTACAGCACTAGTACCTTTGATTTTACCAATATGATATTTAC 1221
DB 1030 GGAATATCAAAATCTACAGCACTAGTACCTTTGATTTTACCAATATGATATTTAC 1089
QY 1222 AAGACTCTATCAAGGATGCACTCTCTTGATATGTTTACCTGGTTATACGTATATA 1281
DB 1090 AAGACTCTATCAAGGATGCACTCTCTTGATATGTTTACCTGGTTATACGTATATA 1149
QY 1282 TTTTTTGGAAATGCCAGAAAGTCCAGTTTTTCATGGTAAACCAATGCAATTAATACCAAG 1341
DB 1150 TTTTTTGGAAATGCCAGAAAGTCCAGTTTTTCATGGTAAACCAATGCAATTAATACCAAG 1209
QY 1342 ACGTTAAAGTATATCCAGTTTCCAAAGATATTTAGCGAGTACAAAGATTTCCGAATTA 1401
DB 1210 ACGTTAAAGTATATCCAGTTTCCAAAGATATTTAGCGAGTACAAAGATTTCCGAATTA 1269

QY 1402 GAATTAACCTCCAGAACTTCAGATCAACCAAAATTTATGAGTCATATAGCCATAGATTATGT 1461
DB 1270 GAATTAACCTCCAGAACTTCAGATCAACCAAAATTTATGAGTCATATAGCCATAGATTATGT 1329
QY 1462 CATATCAAGATATTCCCGGCAAGGGTAAACACTACCGGATTTAGCTGATTTTCTTGG 1521
DB 1330 CATATCAAGATATTCCCGGCAAGGGTAAACACTACCGGATTTAGCTGATTTTCTTGG 1389
QY 1522 ACATATCGAAGTGCAGATTTTAAACAATAATATATTCAGATAAAATCACTCAAAATTCGG 1581
DB 1390 ACATATCGAAGTGCAGATTTTAAACAATAATATATTCAGATAAAATCACTCAAAATTCGG 1449
QY 1582 GCCGTTAAATTTGGGATAATTTACCGTTTGTTCAGTGGTAAAGGACCGAGGACATACA 1641
DB 1450 GCCGTTAAATTTGGGATAATTTACCGTTTGTTCAGTGGTAAAGGACCGAGGACATACA 1509
QY 1642 GGAGGGGATTTATACAGTATATAGAGTACTGGTTCTGTAGGAACCTTATTTCTAGCT 1701
DB 1510 GGAGGGGATTTATTTACAGTATATAGAGTACTGGTTCTGTAGGAACCTTATTTCTAGCT 1569
QY 1702 CGATATGGCCTTAGCATTTAGAAAGGAGGGAATATATCGTGTAAAGCTGAGATATGCTACT 1761
DB 1570 CGATATGGCCTTAGCATTTAGAAAGGAGGGAATATATCGTGTAAAGCTGAGATATGCTACT 1629
QY 1762 GATGAGATATTTGATTTGATGTAACGATGCTCAGATTCAGATGCCAAAACAAATGAAC 1821
DB 1630 GATGAGATATTTGATTTGATGTAACGATGCTCAGATTCAGATGCCAAAACAAATGAAC 1689
QY 1822 CCAGTGAGGATCTGACATCTAAACCTTTTAAAGTTCAGATGCTATCAACAATTAAT 1881
DB 1690 CCAGTGAGGATCTGACATCTAAACCTTTTAAAGTTCAGATGCTATCAACAATTAAT 1749
QY 1882 TTACCAACAGATGCTCGTAGCATTCGAACATAATTTAGTGTGAAGACCTTAATTCACA 1941
DB 1750 TTACCAACAGATGCTCGTAGCATTCGAACATAATTTAGTGTGAAGACCTTAATTCACA 1809
QY 1942 TTATCTGTTATGTTTACGTTGACCGAATCGAATTCATCCAGTAGATGA 1991
DB 1810 TTATCTGTTATGTTTACGTTGACCGAATCGAATTCATCCAGTAGATTA 1859

RESULT 13

US-10-032-717-33
; Sequence 33, Application US/10032717
; Patent No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1 Proteins With
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032,717
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 1854
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis (mutated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1854)
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: LKMS.R49PVD
US-10-032-717-33

RESULT 15
US-10-032-717-45
; Sequence 45: Application US/10032717
; Patent No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1 Proteins With
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032,717
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 1854
; TYPE: DNA
; ORGANISM: *Bacillus thuringiensis* (mutated).
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1854)
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: LRMS.R49PVD
US-10-032-717-45

Query Match 50.4%; Score 1825.8; DB 12; Length 1854;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1843; Conservative 0; Mismatches 7; Indels 3; Gaps 1;
QY 142 ATGTCGCGGGAATGCTAGTGAATACCTGGTTCACCTGAAGTACTTGTAGCGGACAA 201
DB 1 ATGTCGCGGGAATGCTAGTGAATACCTGGTTCACCTGAAGTACTTGTAGCGGACAA 60
QY 202 GATGCAAGTAAAGCGGCAATGATAGTAGTAAATTAATATACAGGTTTGGGGTCCCA 261
DB 61 GATGCAAGTAAAGCGGCAATGATAGTAGTAAATTAATATACAGGTTTGGGGTCCCA 120
QY 262 TTTGTTGGCCGATAGTACTTATATACCTCACTTATGATTTCTGTGGCCTTCAGGG 321
DB 121 TTTGTTGGCCGATAGTACTTATATACCTCACTTATGATTTCTGTGGCCTTCAGGG 180
QY 322 GAAAGAGTCAATGGGAAATTTTATGGAAACAAGTAGAAGAACTCATTAATCAAAAATA 381
DB 181 GAAAGAGTCAATGGGAAATTTTATGGAAACAAGTAGAAGAACTCATTAATCAAAAATA 240
QY 382 GCAGATATGCAAGGAATAAAGCGCTTTCGGAAATTAGAGGATAGGTAAATAATTACCA 441
DB 241 GCAGATATGCAAGGAATAAAGCGCTTTCGGAAATTAGAGGATAGGTAAATAATTACCA 300
QY 442 TATATCTAATCTCGCTTGAAGATGGGAAGAAATCC----AAATGGTTCAAGAGCTTA 498
DB 301 TATATCTAATCTCGCTTGAAGATGGGAAGAAATCCATTAAGAATGTCTAGAGCCTTA 360
QY 499 CGAGATGTCGGAATCGATTTGAAATCCCTGGATAGTTTATTTAGGCNATATATGCCATCT 558
DB 361 CGAGATGTCGGAATCGATTTGAAATCCCTGGATAGTTTATTTAGGCNATATATGCCATCT 420
QY 559 TTTAGAGTGCAAAATTTGAAGTACCATTCTTACTGTATATGCAATGGCAGCCCACTT 618
DB 421 TTTAGAGTGCAAAATTTGAAGTACCATTCTTACTGTATATGCAATGGCAGCCCACTT 480
QY 619 CATTTACTGTATTAAGGACCGCTCAATTTTGGAGAGAAATGGGGATGGTCAACAAT 678
DB 481 CATTTACTGTATTAAGGACCGCTCAATTTTGGAGAGAAATGGGGATGGTCAACAAT 540

QY 679 ACTATTATAAATCTATTATGATCGTCAAAATGAAACTTACTGCGAATATTCTGATCACTGT 738
DB 541 ACTATTATAAATCTATTATGATCGTCAAAATGAAACTTACTGCGAATATTCTGATCACTGT 600
QY 739 GTAAAGTGGTATGAAACTGTTTGTAGCAAAATTTAAAGGACGACGCGCTAAACAATGGTT 798
DB 601 GTAAAGTGGTATGAAACTGTTTGTAGCAAAATTTAAAGGACGACGCGCTAAACAATGGTT 660
QY 799 GACTATAACCAATTCGTTAGAGAAATGACATCGGCGGTTTGTAGATGTTGTGATTTATTC 858
DB 661 GACTATAACCAATTCGTTAGAGAAATGACATCGGCGGTTTGTAGATGTTGTGATTTATTC 720
QY 859 CCAAAATTTATGACACGACGCTACCAATGGAACCAAAAGCAAACTAAACAAGGAAGTA 918
DB 721 CCAAAATTTATGACACGACGCTACCAATGGAACCAAAAGCAAACTAAACAAGGAAGTA 780
QY 919 TATACAGATCCACTGGCGCGGTAAACGTTCTTCAATTTGGTTTCTGGTATGACAAAGCA 978
DB 781 TATACAGATCCACTGGCGCGGTAAACGTTCTTCAATTTGGTTTCTGGTATGACAAAGCA 840
QY 979 CTTTCTTTCGGAGTATAGAAATCATCCGTTATTCGACCAACCCCATGTTTGTATTTATTA 1038
DB 841 CTTTCTTTCGGAGTATAGAAATCATCCGTTATTCGACCAACCCCATGTTTGTATTTATA 900
QY 1039 ACGGGAATCAGAGTGTATACAAATCAAGAAGCAATTTCTTCCGCTCGCTATATAAGCAT 1098
DB 901 ACGGGAATCAGAGTGTATACAAATCAAGAAGCAATTTCTTCCGCTCGCTATATAAGCAT 960
QY 1099 TGGGCTGGTCAATCAATAAGCTACCATCGTGTAGTGGGGTAGTAACTCTTCAACAAATG 1158
DB 961 TGGGCTGGTCAATCAATAAGCTACCATCGTGTAGTGGGGTAGTAACTCTTCAACAAATG 1020
QY 1159 TATGGAATCAATAAATCTACAGCACTAGTACCTTTGATTTTACGAATTTATGATTT 1218
DB 1021 TATGGAATCAATAAATCTACAGCACTAGTACCTTTGATTTTACGAATTTATGATTT 1080
QY 1219 TACAAGACTCTATCAAGGATGACGACTCTTGTATTTTACCTGGTTATAGCTAT 1278
DB 1081 TACAAGACTCTATCAAGGATGACGACTCTTGTATTTTACCTGGTTATAGCTAT 1140
QY 1279 ATATTTTGGAAATGCCAGAGTCGAGTTTTTTCATGGTAAACCAATTTGAATAATACAGA 1338
DB 1141 ATATTTTGGAAATGCCAGAGTCGAGTTTTTTCATGGTAAACCAATTTGAATAATACAGA 1200
QY 1339 AAGACGTTAAAGTATTAATCCAGTTTCCAAAGATATTTATAGCGAGTACAAGAGATTCGGA 1398
DB 1201 AAGACGTTAAAGTATTAATCCAGTTTCCAAAGATATTTATAGCGAGTACAAGAGATTCGGA 1260
QY 1399 TTAGAAATTAACCTCCAGAAATTTTTCAGATCAACCAAAATTTAGTTCATATAGCCATAGATTA 1458
DB 1261 TTAGAAATTAACCTCCAGAAATTTTTCAGATCAACCAAAATTTAGTTCATATAGCCATAGATTA 1320
QY 1459 TGTATATCAAGTATTTCCCGCGAGGGTAAACACTACCGGATTAGTACTGTATTTTCT 1518
DB 1321 TGTATATCAAGTATTTCCCGCGAGGGTAAACACTACCGGATTAGTACTGTATTTTCT 1380
QY 1519 TGAACACATCGAAGTGCAGATTTTAAACAATACAATATATTTCAAGATAAATCATCAAAAT 1578
DB 1381 TGAACACATCGAAGTGCAGATTTTAAACAATACAATATATTTCAAGATAAATCATCAAAAT 1440
QY 1579 CCGGCGGTTAAATGTTGGGATAATTTTCCGTTTGTTCAGTGGTAAAGGACCGACAT 1638
DB 1441 CCGGCGGTTAAATGTTGGGATAATTTTCCGTTTGTTCAGTGGTAAAGGACCGACAT 1500
QY 1639 ACAGAGGGGATTTTATTAAGTATTAAGAGTACTGGTTCTGTAGGAACCTTTATTTCTA 1698
DB 1501 ACAGAGGGGATTTTATTAAGTATTAAGAGTACTGGTTCTGTAGGAACCTTTATTTCTA 1560
QY 1699 GCTCGATATGGCCTAGCATTTAGAAAAGCAGGGAATATTCGTTAGACTGAGATATGCT 1758
DB 1561 GCTCGATATGGCCTAGCATTTAGAAAAGCAGGGAATATTCGTTAGACTGAGATATGCT 1620

QY 1759 ACTGATGCAGATATTGTATTGCTATTAACGATGCTCAGATTCAGATCCCAAAACAAATG 1818
|||||
Db 1821 ACTGATGCAGATATTGTATTGCTATTAACGATGCTCAGATTCAGATCCCAAAACAAATG 1680
|||||
QY 1819 AACCCAGGTGAGGATCTGACATCTAAAACTTTTAAAGTTGCAGATGCTTATCACAACATTA 1878
|||||
Db 1681 AACCCAGGTGAGGATCTGACATCTAAAACTTTTAAAGTTGCAGATGCTTATCACAACATTA 1740
|||||
QY 1879 AATTTAGCAACAGATAGTTTCGCTAGCATTTGAAACATATTTTAGGTGAAGACCTTAATTCA 1938
|||||
Db 1741 AATTTAGCAACAGATAGTTTCGCTAGCATTTGAAACATATTTTAGGTGAAGACCTTAATTCA 1800
|||||
QY 1939 ACATTATCTGGTATAGTTTACGTTGACCCGAATCGAATTCATCCCAAGTAGATGA 1991
|||||
Db 1801 ACATTATCTGGTATAGTTTACGTTGACCCGAATCGAATTCATCCCAAGTAGATGA 1853
|||||

Search completed: January 7, 2003, 05:12:35
Job time : 226 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 05:11:04 ; Search time 45 Seconds

(without alignments)
2576.403 Million cell updates/sec

Title: US-10-032-717-2

Perfect score: 6332

Sequence: 1 MSPNNQNEYIIDATPSTV.....MSETEGTFYIESVELIVDVE 1206

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3066	48.4	1160	1 I40589	parasporal crystal
2	2595.5	41.0	1157	1 S49247	parasporal crystal
3	2440	38.5	1154	2 S39536	parasporal crystal
4	2348	37.1	1138	2 A48944	parasporal crystal
5	2340	37.0	1228	2 S00873	parasporal crystal
6	2174.5	34.3	1189	2 S00944	parasporal crystal
7	2150.5	34.0	1156	2 S19306	parasporal crystal
8	2145	33.9	1176	2 A48970	parasporal crystal
9	2115.5	33.4	1172	2 S32689	parasporal crystal
10	2078.5	32.8	1165	2 S11446	parasporal crystal
11	2073.5	32.7	1176	2 JT0241	parasporal crystal
12	2070.5	32.7	1176	2 JC2219	parasporal crystal
13	2069	32.7	1166	2 S32645	parasporal crystal
14	2065	32.6	1160	2 S32647	parasporal crystal
15	2063.5	32.6	1176	2 S02215	parasporal crystal
16	2062.5	32.6	1176	2 A22617	parasporal crystal
17	2058	32.5	1181	2 A41052	parasporal crystal
18	2053	32.4	1155	2 JD0002	parasporal crystal
19	2048.5	32.4	1171	2 I40572	parasporal crystal
20	2045	32.3	1155	2 S02134	parasporal crystal
21	2042	32.2	1155	2 A26513	parasporal crystal
22	2034.5	32.1	1156	2 A29125	parasporal crystal
23	2034.5	32.1	1171	2 A37829	parasporal crystal
24	2027	32.0	1177	2 A49785	parasporal crystal
25	2025	32.0	1155	2 I39838	parasporal crystal
26	2023.5	32.0	1178	1 USBSXH	parasporal crystal
27	2020	31.9	1174	2 A42459	parasporal crystal
28	2005	31.7	1174	2 S32649	parasporal crystal
29	1995.5	31.5	1156	2 A29838	parasporal crystal

30 1830 28.9 1136 1 USBS81 parasporal crystal
31 1792 28.3 1180 2 I39870 parasporal crystal
32 1787 28.2 1180 2 A26858 parasporal crystal
33 1655 26.1 934 2 A22798 parasporal crystal
34 1533.5 24.2 823 2 S04181 parasporal crystal
35 1514 23.9 719 2 I40590 cryv465 protein - insecticidal prote
36 1511 23.9 719 2 I39815 parasporal crystal
37 1502 23.7 719 2 S25383 insecticidal prote
38 1496 23.6 719 2 I39814 parasporal crystal
39 1241 19.6 659 2 S10228 parasporal crystal
40 1208 19.1 652 2 I39811 parasporal crystal
41 1194.5 18.9 652 2 A27323 parasporal crystal
42 1194 18.9 655 2 JC7140 paratoxin - Bacillu
43 1128 17.8 934 2 B29838 parasporal crystal
44 1105 17.5 649 1 JH0261 parasporal crystal
45 962 15.2 618 2 S11445 parasporal crystal

ALIGNMENTS

RESULT 1

I40589

parasporal crystal protein cry8Cal - Bacillus thuringiensis

N;Alternate names: parasporal crystal protein cryiii

C;Species: Bacillus thuringiensis

C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 01-Dec-2000

C;Accession: I40589

R;Sato, R.; Takeuchi, K.; Ogiwara, K.; Minami, M.; Kaji, Y.; Suzuki, N.; Hori, H.; Asa

Curr. Microbiol. 28, 15-19, 1994

A;Title: Cloning, heterologous expression, and localization of a novel crystal protein

A;Reference number: I40589; MUID:94100786; PMID:7764305

A;Accession: I40589

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-1160 <RES>

A;Cross-references: EMBL:U04366; NID:G532523; PIDN:AAA21119.1; PID:G532524

C;Superfamily: parasporal crystal protein

C;Keywords: delta-endotoxin

Query Match 48.4%; Score 3066; DB 2; Length 1160;
Best Local Similarity 50.3%; Pred. No. 5.4e-169;
Matches 632; Conservative 180; Mismatches 298; Indels 146; Gaps 23;

QY 1 MSPNNQNEYIIDATPSTVSNDNSRYPFANETPALQNNMDYKDYKWSAGNASEYPCSP 60

DB 1 MSPNNQNEYIIDALSPTSVSDNSIRYPLANDQTNTLQNNYKDYKNTSTWELSRNP 60

QY 61 EVLVSGQDAAKAIDIVGKLLGLGVFPVGPVIVSLYTLQIDILMPGCKSQWEIFMQVE 120

DB 61 GTFTSAQDAVGTGIDIVSTIISGLGIPVLGEVFSILGSLGLLPSPNNVNVQIFMNRVE 120

QY 121 ELNQKTAEVARNKAUSELGLGNNTQLYUTALEEHEENPNSGRALRDVNRREILDSLF 180

DB 121 ELIDQKILDSVRSRAIADLANSAIVEYQVALEDWRKNPHSTRSAALVRFEGNAEAIL 180

QY 181 TQMPSPRVNFEVPFTVTYVMAANLHLLKDKASIFGEWGWSTTTTNNYDQMKLTA 240

DB 181 RTNMGSSQNTYETPLPTTQAASLHLLVNRDVIYIGKEWGPQNDIDILFYKEQVSYTA 240

QY 241 EYSDHCVKMYETGLAKLKGTSAKQWVDYNOFREMTLAVLDVVVALFPNYDTRTPMETKA 300

DB 241 RYSDHCQWYNAGLNKLGRTGAKQWVDYNNFRRENNVMVLDLVALFPNYDIARYPLETNA 300

QY 301 QLTREVTYDPLGAV---NVSSIGSWD---KAPSGVIESSVIRPHVFDYITGLTVYT 353

DB 301 ELTREIFTDPGVSVYTGQSSTLSWYDMPAALPESFTLE-NLLRKDPFTLLQEIIRMYT 359

QY 354 QSRSSISARVIRWAGHOISYHRVSRGNSNQMYGTGNQLHS-----TSTFDFTNYDIY 407

DB 360 SFRQNGTIEYINWGGQRLLT-----LSYIGSSFNKISYGLVLAGAEDIIPVGQNDIY 410

QY 408 KTLKSKDALLDIVPG-YTYVIFFMPEVEFFMVNQLNTRKTLKYNPVSVDIIASTRDSE 466

Db 906 GNLELVFVGPISGESLEREQDRNKAENLGRKRAIEDRVYLAQAQANHLFVYDQOOL 965
Qy 967 NPDVEITDLTAADLIQSIPIVYVEMFPEIPGMNTYKFTETDLRQQAWSLYDORNAIPN 1026
Db 966 NPEIGLABINEASNLVESISGVYSDTLQIQINYEITELSDRLQQAASYLYTSRNVQN 1025
Qy 1027 GDFRNLGNWATPGVFEVQCOINHSTSVLVPWDEQVSQFTVQPNQRYLVRTARKEGVG 1086
Db 1026 GDFNSGLSDSWNTTMDASVQODGNHFLVLSHWDAAQVSQQLRVNPNCKVYLVRTARKVGG 1085
Qy 1087 NGYVSIIRGGNCTETLTFSASDYDNGMYNTQVSTNGYNTNNAQTQASTNGYNNNM 1146
Db 1086 DGYVIRGARHQETLTINACDYVNGY----- 1114
Qy 1147 YNTQASNTNGYNTSVYNDQTIYTKVTPIFYTDQMIEMSETEGTFVIESVELI 1202
Db 1115 -----VNDNS-----YITEVVFYPTKHWVSESGSFYIDSIEFI 1153

RESULT 3
S39536
parasporal crystal protein cry39a1 - Bacillus thuringiensis
N;Alternate names: delta-endotoxin-related protein; parasporal crystal protein cryX
C;Species: Bacillus thuringiensis
C;Date: 07-Oct-1994 #sequence_revision 01-Dec-1995 #text_change 01-Dec-2000
C;Accession: S39536
R;Shevelev, A.B.; Svarinsky, M.A.; Karasin, A.I.; Kogan, Y.N.; Chestukhina, G.G.; Stepan
PEBS Lett. 336, 79-82, 1993
A;Title: Primary structure of the cryX, the novel delta-endotoxin-related gene from Bac
A;Reference number: S39536; MUID:94085596; PMID:8262221
A;Accession: S39536
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1154 <SHE>
A;Cross-references: EMBL:X75019
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin

Query Match 38.5%; Score 2440; DB 2; Length 1154;
Best Local Similarity 44.0%; Pred. No. 8.6e-133;
Matches 534; Conservative 177; Mismatches 357; Indels 146; Gaps 25;

Qy 42 KYDLKMSAGNASHYFGSPVLSVQDAAKAAIDIVGKLKSLGVPFVGPVIVSLYQLID 101
Db 30 KYDLKMSAGNASHYFGSPVLSVQDAAKAAIDIVGKLKSLGVPFVGPVIVSLYQLID 101
Qy 102 ILWPSGKSQWEIPEQVEELINQIAEVARNKALSELEGNGNYQLYLTALKEWENPN 161
Db 87 FLWPSDQAVWEAFIEQVEELINQIAEVARNKALSELEGNGNYQLYLTALKEWENPN 146
Qy 162 GSRALDRVRNFEILDSLTQYMPSP-----RVNPEVEFLTVYAMAANHLHLKLDASIP 217
Db 147 GVRA-NLVLRFEILHALFVSSMSPFGSGPSQRFQOQLLVYQAANHLHLADAKEY 205
Qy 218 GEWGWSTTTNNYDRMKL-TAEDSHCVKWTETGLAKLGTSAKQWVDYNOFRREMT 276
Db 206 GARWGLRESQIGLYFNELOTRDYTHNCVAYNGLAGLGRGSAESWLKYHQFRREAT 265
Qy 277 LAVLDVVALFENYDTRTYPMETKQLITEVYTDPLGAVNVSS-----IGSWD-KAPS 328
Db 266 LMAVDLALFPYNNTRYPIAVNPQLTRVYDPLGVPSSESSLFPELRCLRWQETSAMT 325
Qy 329 FGVISSVIRPPHFDYDTGLTVVTSRIS-SARYIRHMAHQIYXHVRSRGSN--LQQ 385
Db 326 FSNLENALISSPHLFDTNLNLMTYGSFVHLTNQIGVHSHVTSLLASGPTVLRR 385
Qy 386 MYGTNQLHSTSTDFNTNYDIYKTLK-----DAVLLDIV-----YPGTYIFFGMP 433
Db 386 NYGSTTSI--VNYFSENDRDVQINTRSHTGFGQNAFLFGITRAQFYPGGTY----- 436
Qy 434 VEFPMVQNLNTRKTLKYNFVSKDIIAETRSELELPETSDQPNYESYHRLCHITS-- 491
Db 437 ----SVTQRNALTCEQNYNSID-----ELPSLDPNETPSYHRLSHITSYL 480

Qy 492 -----IPATGNTTGLVPFVSWTHRSADLNNTIYSDKITQIOPAVKWDNLFPVVPVVKPGH 546
Db 481 HRVLTIDGINIYSGNLPTVYVTHRDVLTNTITADRITQPLVASFEIPAGTIVVGRGPF 540
Qy 547 TGGDLLQVNRSTGSGVGLFLARYGLALEKAKYRVLRYA--TDADIVLHVNDQAI---Q 601
Db 541 TGGDIL---RRTG-VGTFGTIRVTTAPLQYRIRFRFASTTNLFIGIRVGRQVNYFD 596
Qy 602 MPKTMNPGEDLTSTPKVADAITLNLATDSSL-----ALKENLGEDPNSTLSGIYVDRI 657
Db 597 FGRTMNRGDELRYSFATREFTTDFNFRQPOELISVFANAFSAQOE-----VYFDRI 648
Qy 658 EPIFVDETYEABOLEAAKAVNALFNTKDGRLPGVTDYEVNOAANLVECLSDDLVENE 717
Db 649 EIIIPVNPAREAKEDEAAKAVASLFRTRDGLQVNVKQVQDOAANLVSCLSDQCYD 708
Qy 718 KRLFLDAVRAKRLSEARNLLQDPDFQEIENG--ENGWTAETGIEVIEGDAALFKGYRLRP 775
Db 709 KMLLEAVRAAKRLSRERLLQDPDFNTINSTENGKASGVNTISGGPPFKGRALQLA 768
Qy 776 GAREIDTETVYLYOKVSEGVLPKPYTRYLRGLRPGVSGSOGLEIFTIRHQTNRIVKQVDD 835
Db 769 SAR-----ENPTYIYQKVDASELKPTRYRSDGPFVKSQDLEIDLIIHHKVKHLVKNVDPN 824
Qy 836 LLPDVPSPNSDGSINRCSEOKYVNSRLEVEN-----RSGEAHEFSIPIDTGEIDYVEN 888
Db 825 LVSTYDPPDSCSGINRCQEQQWNAQLTEHHHPMDCEAAQTHFESYIDTGLNLSVD 884
Qy 889 AGIWWGPKITDPEGYATLGNLELVSEGLSGDALERLQREEQWQKIOWTRRRETDRIYM 948
Db 885 QGIWAIKVRTTDGATLGNLELVSEGLSGDALERLQREEQWQKIOWTRRRETDRIYM 944
Qy 949 ASKQAVDLVADYQDQQLNPDVEITDLTAQDLIQSIPIVYVEMFPEIPGMNTYKFTETLT 1008
Db 945 DAKOSINHLFVDYQDQQLNPDVEITDLTAQDLIQSIPIVYVEMFPEIPGMNTYKFTETLT 1004
Qy 1009 DRLOQANSLYDORNAIPNGDFRNLGNLNNWATPGVEVQCOINHSTSVLVPWDEQVSQOFTV 1068
Db 1005 NRLQQAASYLYTSRNVQNGDFNGLDSWNAITAGASVQDGNTHFLVLSHWDAAQVSQPRV 1064
Qy 1069 QPNQRYLVRTARKEGVNGVYSIRDCGNQOTETLTFSASDYDNGMYNTQVSTNGYNTN 1128
Db 1065 QPNCKYLVRTARKEGVNGVYSIRDCGNQOTETLTFSASDYDNGMYNTQVSTNGYNTN 1113
Qy 1129 NAYNTQASTNGYNNMNTQASTNGYNTSVYNDQTIYTKVTPIFYTDQMIEMSETEGTFV 1188
Db 1114 -----DNT-YLTKEVIFYSHTEHMMVEVN 1136
Qy 1189 ETEGTFVIESVELI 1202
Db 1137 ETEGAFHIDSIEFV 1150

RESULT 4
A48944
parasporal crystal protein cry7Aa1 - Bacillus thuringiensis
N;Alternate names: parasporal crystal protein cryIIIC
C;Species: Bacillus thuringiensis
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 01-Dec-2000
C;Accession: A48944
R;Lambert, B.; Hofte, H.; Amny, K.; Jansens, S.; Soetaert, P.; Peferoen, M.
Appl. Environ. Microbiol. 58, 2536-2542, 1992
A;Title: Novel Bacillus thuringiensis insecticidal crystal protein with a silent activ
A;Reference number: A48944; MUID:92384571; PMID:1514800
A;Contents: ETS137J
A;Accession: A48944
A;Status: preliminary
A;Molecule type: DNA; protein
A;Residues: 1-1138 <LAW>
A;Cross-references: GB:M64478; NID:gl42760; PIDN:AAA22351.1; PID:gl42761
A;Note: sequence extracted from NCBI backbone (NCBIN:112092, NCBIP:112093)
C;Superfamily: parasporal crystal protein

C:Keywords: delta-endotoxin

Query Match 37.1%; Score 2348; DB 2; Length 1138;
Best Local Similarity 41.7%; Pred. No. 1.8e-127;
Matches 512; Conservative 211; Mismatches 385; Indels 120

Qy	1	MSPNNQNEYELIDATPSTSVNSDSNRYPFANEPTNALQNMDYKDYLMKSGAGNASYFPGSP	60
Db	1	MNLNLDGYE-----DSNRTLNSLNTPTOKALSPSLKNNNYQDLSITERE-----QP	49
Qy	61	EVLVSGODAAKAAIDIVGKLLSLGVFPVGPVIVSLYLTOLIIDILWPSEKSOWEIFMEQVE	120
Db	50	EALASGNTAINTVVSVTGATLSALGVPCASFIYFYLUKIAGLWLPENGKI-WDEFMTVE	108
Qy	121	ELINOKIAEYARNKALSELGLGNNYOYLITALEEWEENPNGSRALDRVRNRFELDSLF	180
Db	109	ALIDOKIEEYVRNKAIELDGLSALDKYKALADMWLGKQDDPEAILSVATEPRIIDSLF	168
Qy	181	TOYMPSPRVNTFVFPFLTYVTYVMAANLHLLLLKDAISFGEWGHSTYTTINNYDROMKLT	240
Db	169	EFSPMPFKVGTGYEIPLLTYVAQANLHALLRSTLTDYDKWGTQNNI BENYNRQKKRIS	228
Qy	241	EYSDHCWKVETGLAKLKGTSAKQVDVYNQFRZEMTLAVLDVVALFPNTDTRYPMETKA	300
Db	229	EYSDHCTKYNSGLSLNGSTGYEOWINYNFRREMILMALDLVAVFPFHPDPRYSNETST	288
Qy	301	QLTREVTYDPLGAVNVSISGSWYDKAPSGFVIESSVIRPPIHVFYITGLTVYTSQSISIS	360
Db	289	QLTREVTYDVPV-SLSISN----PDIGSPFSQMENTAIRTPHLVDVLDLYEIVTSKYKAPS	343
Qy	361	ARY----IRHWAGHOISYHRVSRGNSLQO---MYGTQNQLHSTSTFDTNYDIYKTLISKDAV	415
Db	344	HEIQPDLFYSAHKVSPKK-SEQSNLLTYGTGIYKTSYVSSGAYSFHGNDIYKTLAAPS	402
Qy	416	LLDVIYPGYTYIFFGMEVEFFFMVNLNTRKTLKYNPVSKDIIASTRSELELPPETSD	475
Db	403	---VYVP-YTQ-NYGVQVEFYGVKGHVHYRGDKYD-----LTYSDIQDLPD--G	447
Qy	476	QPNVTESTHRLCHTYSI-----PATGNTTGLVPVPSWTHRSADLNNTIYSDKITQIPAVKC	531
Db	448	EPIHEKTYHRLCHATAIFKSTPDDNAT--IPIPSWTHRSAEYNNRIYPNKITKI PAVOM	505
Qy	532	WDNLFPFVVKPGCHTGCDLLOYNRSYTGVTGLFARYGLAEKAGKYRVRLRYATD--A	589
Db	506	YKLDDBPSTVVKGPFTGCDLVK-RGSTGYIGDI-KATVNSPLSQ--KYRVRYRYAINVSG	561
Qy	590	DIVLHVNDAQIQMPE-----TMNPGSBLSTKTFPKVADAITTLNLTADSSIALKHLNIGED	643
Db	562	QFNVYINDKITLQTKFQNTVETIGEGKDLTVGSGFYEYSTTIQFPDHPKITLHLSDL	621
Qy	644	PNSTLSGIVYDRIEFTFVDETYEAEODLEAAKANVALFTNTKDGRLPGVDTYEVNQAA	703
Db	622	NNSSF----YVDSIEFTFVDVYNAEKEKLEKAKAVNTLFTEGRNALQKDVTDYKYVDQS	677
Qy	704	NLVECLSDLYPNKEKRLIFDAVREAKELSEARNLLQDPDFQELNG--ENGWTASTGIEVI	761
Db	678	ILVDCISGDLYPNEKRELONLVKAKLSYRNLLDPTFDSINSSEENGWYGSNGIVIG	737
Qy	762	EGDALFKRGYRLRLPGAREIDTETVPTYLYOKVEBGLVKYTRYRLRGFVSGSGLBIFT	821
Db	738	NGDFVFKGNLYIFSGTNN--DTQ-YPTVLYOKIDESKLKEYTRYKLKGFIESSQDLBAYVI	794
Qy	822	RHQTNRIVQNVDPDLLPDVSPVNSDGSINRSEOKYNSRLEVENRS-----GEAHEFS	875
Db	795	RYDAKHRTLVDSDNLLPDILPENTCGFPNRCAAQYLDENPSPCECSMQDGLSDSHSFS	854
Qy	876	IPIDTGIDYNNENAGIWWGFKITDPEGYATLGNLELVEEGLPSGDALERLQREEQWKI Q	935
Db	855	LNIDTGSINHNENLGIWVLFKISLEGYAKFGNLEVIDGPVIGEARLVKRQETWRNK	914
Qy	936	MTRRREETDRRYMASKQAVDRSLYADYQDQQLNPVDEITDLTAADLIQSIPTVYNNEMFPE	995
Db	915	LAQLTETTOALYTRAKOALDNLFANAODSHLRKQDVTFAEIAAARKIYOSIREAYMSWLSV	974

Qy	996	IPGMNYTKFTTELTRDLRQQAWSLYDORNAIPNGDFPGLSNNNATPGVEVQOINHTSVLVI	10555
Dd	975	VPGNVHPHFTELSGRVQRAPQLDYVRNVVRNGRFPLNGLSDMIVTSDDVKVQBEENGNNVLVL	10364
Qy	1056	PNWDEQVSQQCFVTQPVRORYVLRVTAKEGSGVGNGYYSIRDGGNOTETLTFFSASDYDTNGMY	11155
Dd	1035	NNWDAQVQLWNKLYQDRGVILHWTARKIGIGSEYITIIDEECHTDQLAFTACE	10875
Qy	1116	NTOVSNTNGYNTNNAYNTQASSTNGSYNNANNMTYNTQASNTNGYNTNSVVNDGTGYITKTVT	11755
Dd	1088	--EIDASNAF-----	11055
Qy	1176	FIPYTDQMWTLEMSSETEGTFYIERSVELIV	1203
Dd	1106	FPDTEKVHIEIGETEGIFLVESIELFL	1133

RESULT 5

S00873

A:Parasporal crystal protein cryvBa1 - Bacillus thuringiensis subsp. thuringie
 A:Alternate names: parasporal crystal protein cryvA4
 C:Species: Bacillus thuringiensis subsp. thuringiensis
 C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 01-Dec-2000
 C:Accession: S00873

R:Brizard, B.L.; Whiteley, H.R.
 Nucleic Acids Res. 16, 2723-2724, 1988

A>Title: Nucleotide sequence of an additional crystal protein gene cloned f
 A:Reference number: S00873; UID:88203216; PMID:3362680
 A:Molecule type: DNA
 A:Residues: 1-1228 <BRI>
 A:Cross-references: EMBL:X06711; NID:g40264; PIDN:CAA29898.1; PID:g580949
 C:Genetics:

Query Match	37.0%;	Score 2340;	DB 2;	Length 1228;
Best Local Similarity	42.1%;	Pred. No. 5.8e-127;		
Matches 533:	Conservative 193;	Mismatches 435;	Indels 106;	Gaps

Qy	1	MSPNNQYEYIIDATPTSPVSNSDNRPFFANEPFNALQNMDYKDYLKMSAGNASYEPGSP	60
Db	1	MTSNKRNENEIINA-----VSNHSAQ-----MDLLPDARIEDSLCIAEGNID-----P	44
Qy	61	EVLVSGQDAAKAADIVCKLLSLGLGVFPVGPVIVSLYLTQLIDLLWPSEKSKOWEIPMEQVE	120
Db	45	FVSAS--TVQTGINIAGRILGVLVGVPFAGQLASFYSLVGLGELWPRG-RDQWEIFLEHVE	100
Qy	121	ELINKIAEYARNKALSELEGIGNNYLYLTALBEEENPNGSRALLRDVNRNFEILDLSLF	180
Db	101	QLINQOITENARNATALRLOGUSFRAYQOOSLEDWENRDDARTSVLTQTYALMLDF	160
Qy	181	TQYMPSEVTVTFVPLTVYAMAANLHLLLLKQASIFGEWGWSTTTTNNYIDROMKLLTA	240
Db	161	LNAMPPLPAIRNOEVLPMVYAAQANLHLLLRASLFGSEFGLTSQBIQRYERQVERTR	220
Qy	241	EYSDHCVKWYETGLAKGTSAKOWDYNOFREMVLAVLDVVALPNYDTRYTPMETKA	300
Db	221	DYSDCYCEWYNTGLSLRGTNAAASVWRVYNOFRERDLTGLVLDLVALPFSYDTRTYPINTSA	280
Qy	301	QLTRVRYTDPUGA--VNVSSIGSWY-DKASFGVIESVVRPHVDPYDINGLTVYVTSQRS	357
Db	281	QLTRVRYTDALGATGVNWSH--WNYNNAASFSAIEAALRSHLLDLFLBQLTIFGSASSR	339
Qy	358	ISSARYIRHWAGHQISYHRSVRSNGNLQOMYGTQNHLSTSTPFTNYDIYKTLISKDAVLL	417
Db	340	WSNTRHMYTWGHTIQSRPICGGLTSTHGATWTSINPV--TLFASRDVYRTSSYAGVLL	398
Qy	418	DIVVPGYTYIPFGMPEVEFFVMVNLN-NTRKTLKYNPVSKDIIASTRDSLELPPEPSSQ	476

Db 399 ---WGIVLEPHGVETVAFNFTPNQINSDRGNTANYSQPYESGLQKDSSELPETTER 455
Qy 477 PNYESYSHRLCHITSIPTATNTGLVPFVSWTHRSADLNTTIYSKTIQIPAVKWDNLP 536
Db 456 PNYESYSHRLSHIGILOSRYN---VPYISWTHRSADRTNTIGPNRIQIPMVKASELPQ 512
Qy 537 FVPVVGKPGHGTGDLQVNRSTGSGVTLFLARYGLALEKAGKYRVLRYATDADIVLHVN 596
Db 513 GTTVRGSGFGTGDILR-RTNKGFGPIRVTVNGPLTQ---RYRIGFRYASTVDPDFVS 568
Qy 597 DA-----QIQMPKTNPGEDITSKTFKADATITLNLATDSSLAKHNL-GEDEPNTLSG 650
Db 569 RGGTVNFRRLTNWSDGLKYGNP-VRAFTPTFTTQIODIIRTSIQGLSGN---G 623
Qy 651 IVYVDRIEFPVDETYAEQDLAAKAVNALFTNTKD-GLRPGVTDYEVNQAANLVECL 709
Db 624 EVIDIKISIIPTATFEAYDLERAQEAVALFTWNPRLKTDVTDHIDOVSNLVAEL 683
Qy 710 SDDLYPNKRLFLDVAAREAKLSEARNLLQDPDFQIN-----GE 749
Db 684 SDEFCLDEKRELLKVKYAKLSDERNLLQDPNFTSINKQPDFISTNEQSNFTSIHQSE 743
Qy 750 NGWTASTGIEVIEGDLAKGKYRLPGAREIDTETPTVLYQKVEGVLPKPTVRLRGP 809
Db 744 HGWNGSENITIQEGNDVFKENYVTLPGT---FNECYPTLYQKIGESKAYTRYQLRGY 800
Qy 810 VGSSQGLEIFTIRHQTNRIVKNVP--DDLTP--DVSPVNSDGSINRCSEQKYNSRLVE 865
Db 801 IEDSQDLIYLIRYNAKHETLDVPTGESLWPLSVESPIGRCEPNRCAPHFEPWNPDLCS 860
Qy 866 NRSGE-----AHFESIPIDTGEIDYNENAGIWWGPKIDPEGYATLGNLELVEEGLSGD 920
Db 861 CRDGEKCAHSHHFSLDIDVGCTDLHENLGVVVFVKIQEGHARLGNLEPFEKPLLGE 920
Qy 921 ALERLORZQWQKQMTRRREBTDRLRYMASQAVDLVADYQDQQLNPDVEITDLTAQD 980
Db 921 ALSRVKAEKWRDKREKLOLETKRYVTEAKEAVDALFVDSQYDRLOADTNGIMHAADK 980
Qy 981 LIQSPVYVNMFPBIPGMNYTKFTLDRLOQMSLVLDORNAIPNGDPNGLSNWATP 1040
Db 981 LVHRIEAYLSELVPIGVNABIFELSGHITALSIDARVNVKNGDFNGLTCCWNVK 1040
Qy 1041 GVEVQOQNHSTVLVLPNNDEQVSQOFTVQPNQRYVLRVATKEGVNGVSVIRDCGNQTE 1100
Db 1041 HVDVQOHSRSDLVPEAEAVSQAVCPGCGYILRVATYKEGYEGCVTHIEENTD 1100
Qy 1101 TLTSASDYDNGMYNTQVSNVTNGNTNAYNTQASSTNGYNNMYTQASNTNGYNTN 1160
Db 1101 ELKP--KNREBEVYPTDTGTCDNYTAHQGTAGCADACNSRNAGYEDAYEDVDTASVNYK 1158
Qy 1161 SVYNDQ-----GYITKTVPFTVPTQDMWIMSETEGTFFI 1196
Db 1159 PTYBEETTVDRDNHCEYDRGVNYPVPAGYVTKLEYFPEETDVTWIEIGETEGKIV 1218
Qy 1197 ESVELIV 1203
Db 1219 DSVELL 1225

RESULT 6
S00944
parasporal crystal protein cry1Ca1 - Bacillus thuringiensis (strain entomocidus 60.5)
C:Species: Bacillus thuringiensis
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 01-Dec-2000
C:Accession: S00944
R:Honee, G.; van der Salm, T.; Visser, B.
Nucleic Acids Res. 16, 6240, 1988
A:Title: Nucleotide sequence of crystal protein gene isolated from B. thuringiensis subs
A:Reference number: S00944; MUID:88289380; PMID:3399402
A:Accession: S00944
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-1189 <HON>

A:Cross-references: EMBL:X07518; NID:g40293; PIDN:CAA30396.1; PID:g40294
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin
Query Match 34.3%; Score 2174.5; DB 2; Length 1189;
Best Local Similarity 40.0%; Pred. No. 2.1e-117;
Matches 504; Conservative 189; Mismatches 437; Indels 129; Gaps 31;
Qy 1 MSPNNQNEYIIDATPSTSVSNDNRYPFANEPTNLQNMDYKDYLKMSAGNASEYPSGP 60
Db 1 MEENQNC-----IPNCLSNPE----- 19
Qy 61 EVLVSGQ--DAAKAIDIVGKLASGLGVFPVGPITVSYLTQIDILMPSEKSOEIMFEQ 118
Db 20 EVLADGERISNGNSIDISLSLVQFLVSNFV-PCGGFLVGLIDFVWGVGPSQMDAFLVQ 78
Qy 119 VEEILNQIAIYARNAKALSEGLEGNRYQLYLTALFEWENPGNSRALRDVNRFEILD 178
Db 79 IEQLINERIAAFARNAAIANLEGIGNNFYVEAFKEWEDPNPNPRTTRVIDRFLDGL 138
Qy 179 LFTQYMPSPRTNPEVPEPLTVYMAANLHLLLLKDAISFGEGWGSTTTINNYIDROMKL 238
Db 139 LLEKDIFSRISGFEVPLSVYQAANLHLALRDSVIFGRWGLTTINNVNENLIRH 198
Qy 239 TAEYSDHCVKWYETGLAKLGTSAKQWVDYNQFRREMTLAVLDVVALFPNPDYTRTYPMET 298
Db 199 IDEYADHCANTYRGLNLPKSTYQDMITYNLRERDLTLVLDIAAFPNDNRYPIQP 258
Qy 299 KAQTRVYTDPLGAVNVSSIGSWYKAPSGVIESVIRPHVFDXITGLTVTVTQSRSI 358
Db 259 VGQLTREYVTDPL--INFNPOLQSVQALPTFNVMESSIRPNPLFDILNNLTITFTDFSV 316
Qy 359 SSARYIRHAGHQLSYHRVSRGSLNQMYGTQNLHSTSTFDFTNYDIYKLSKDAV-LL 417
Db 317 GRNFI---WGHRRVSISSIGGNITSPYIGREANQEPSPFT-NGPVFTLSNPTLRL 372
Qy 418 DIVPGYTYIPFGMEPEVEFFMVNQLNTRTKLKNPVSKOIIASTRSELELPETSQDP 477
Db 373 QQPWAPFNLRGVEGEF-----STPTNSFTYRG-----RGTVDSLTELPEDSNP 420
Qy 478 NYEYSYHRLCHITSIPTATN---TTGLVPFVSWTHRSADLNTTIYSKTIQIPAVKWDN 534
Db 421 PREGYSHRLCHATFVQSRGTPPLTGV--VFSWTDRAATLTNTIDPERINQIPLVKGRV 478
Qy 535 LPFPVVKPGHGTGDLQVNRSTGSGVTLFLARYGLALEKAGKYRVLRYAT--DADIV 592
Db 479 WGGTSVITGPGFTGDLRRN---TFGDVSVLQVNSPITQRYRLFRVASSRDARVI 534
Qy 593 LHVDA-----QIQMP--KTNVNGEDLTSKTFKADATITLNLATDSSLAKHNLGE 642
Db 535 VLTGAASVGVGGQSVNMPKQKTMGEINLTSRTFRTDFSNPFSFRANPDII--GISE 591
Qy 643 DP-----NSTLSGIVVDRIEIPVDETYAEQDLAAKAVNALFTNTKD-GLRPGVTDY 697
Db 592 QPLFGAGSISSGELYIDKIEIILADATFEASDLERAQKAVNALFTSNQIGLKTVDY 651
Qy 698 EVNQAANLVECLSDLYPNKRLFLDVAAREAKLSEARNLLQDPDFQIN--GENGWAS 755
Db 652 HIDQVSNLVDCLSDFECLDEKREKSEKVKHAKLSDERLNLQDPNFRGINQPDGWRGS 711
Qy 756 TGIIEVIGDALFKGRYLRLPGAREIDTETPTVLYQKVEGVLPKPTVRYLRGFGVSSQG 815
Db 712 TDITIQGGDDVFKENYVTLPGT--VD-ECYPTLYQKIDESKLAAYTFELRGYIEDSQD 768
Qy 816 LEITFIRHQTNRIVKNVPDD-----LLPDVSPVNSDGSINRCSEQKYNSRLVENRSGE- 870
Db 769 LEIYLIRYNAKHETVNVPGTGLPQASQSPIGKCGEPNRCAPHLEWNPDLDCS CRDGEK 828
Qy 871 ----AHFESIPIDTGEIDYNENAGIWWGPKIDPEGYATLGNLELVEEGLSGDALERLQ 926
Db 829 CAHSHHFTLDIDVGCTDLNEDLGVWVIFKIQDQGHARLGNLEPFEKPLLGEALARK 888
Qy 927 REEQWQKQMTRRREBTDRLRYMASQAVDLVADYQDQQLNPDVEITDLTAQDLIQSIP 986

Db 889 RAEKWRDREKLEQLETNIVYKEAKESVDALFVNSQYDRLOQVDTNAMIHAADKRVHRIR 948
QY 987 YVYNEFPEIPGNNYTKFTLTDRLOQANSYLDQORNAIPNGDFRNGLSNWNATPGVEV-Q 1045
Db 949 EAYLPESLVIPIGNAIAFELEGRIITFAYSLSYDARNVIRKNGDFNGLLWNVKGHVDVEE 1008
QY 1046 QINHTSVLIPNWDQVSOFTVQPNQRYVLRVTAKGEGVNGVSIRODGNQOTETLTFS 1105
Db 1009 QNNHRSVLVPEWAEVSOEVRVCPGRIILRTAYKEGEGECVTHIEIEDNTDELKFS 1068
QY 1106 ASDYDNGMYNTQVSNNGYNTNAY-NTQASSTNGYN---ANN-----MYN----- 1148
Db 1069 -NCVEBEVPPNNTVTCNNYTGTOBEYEGYTSRNQGYDEAYGNNPSPADYASVYEKSY 1127
QY 1149 TOASNTNGYNTSVNDOT---GYLTQVTFIPIYTDQWMIEMSETEGTPIESVELIV 1203
Db 1128 TDGRRENPCESNRNGYGDYPLPAGYVTKDLEYFPETDKWIEIGETGTPVDSVELLL 1186
RESULT 7
S19306
parasporal crystal protein cry9Aa1 - Bacillus thuringiensis
N:Alternate names: delta-endotoxin; insecticidal crystal protein; parasporal crystal pro
C:Species: Bacillus thuringiensis
C:Date: 04-Dec-1992 #sequence revision 04-Dec-1992 #text_change 01-Dec-2000
C:Accession: S19306; S23588; A44847; S14602; S14837
R:Smulevitch, S.V.; Osterman, A.L.; Shevelev, A.B.; Kaluger, S.V.; Karasin, A.I.; Kadyro
FBS Lett. 293, 25-28, 1991
A:Title: Nucleotide sequence of a novel delta-endotoxin gene cryIg of Bacillus thuringie
A:Reference number: S19306; MUID:92070568; PMID:1660003
A:Accession: S19306
A:Molecule type: DNA
A:Residues: 1-1156 <SMU>
A:Cross-references: EMBL:X58120; NID:9870929; PIDN:CAA41122.1; PID:940271
A:Experimental source: subsp. galleriae
A:Accession: S23588
A:Molecule type: protein
A:Residues: 24-34 <SMUI>
A:Experimental source: subsp. galleriae
R:Gleave, A.P.; Hedges, R.J.; Broadwell, A.H.
J. Gen. Microbiol. 138, 55-62, 1992
A:Title: Identification of an insecticidal crystal protein from Bacillus thuringiensis D
A:Reference number: A44847; MUID:92211329; PMID:1556556
A:Accession: A44847
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1151 <GLE>
A:Cross-references: EMBL:X58534; NID:948879; PIDN:CAA41425.1; PID:948880
A:Experimental source: isolate DSIR517
A:Note: sequence extracted from NCBI backbone (NCBIN:92865, NCBIP:92867)
C:Genetics:
A:Gene: cryIg
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin
Query Match 34.0%; Score 2150.5; DB 2; Length 1156;
Best Local Similarity 40.0%; Pred. No. 4.8e-116;
Matches 500; Conservative 203; Mismatches 396; Indels 151; Gaps 28;
QY 5 NONEYBIIIDATSTSVNSNRNPFANEP-----TNALQNMIDKDYLRKMSAGNASEYGP 58
Db 2 NQNGHGIIGASNGCCASDDVAKYPLANNPYSSALNLSNCSNLSILNWINIIG----- 53
QY 59 SPEVLVSGDAAKAAIDIVGKLLSGLVGPVGPVLSYLTQLI-DILWPSEKSKQWEIFME 117
Db 54 -----DAKEAVSIGTIVLSLTAPSLTGLISIVYDLIGKVLGGSGGQISDLSIC 104
QY 118 QVEELINQIAEYARNKALSELGLGNNYQLYLTALAEEMENPNNGSKALRDVNRREILD 177
Db 105 DILLSIIDLRVSQSLVNDGIADFNGLVLLRYNLEADLSWKNKFNNSASA-BELTRFIAD 163
QY 178 SLFTQYMPFSFRVT-----NPEVPFLTVYAMAANLHLLLLKDAISIFGEMG-WSTTTI 228

Db 164 SEFDRLITRGSLTNGSGSLARQNAQILLPLSPASAAFFHLLLRDLATRYGTNNGLYNATPF 223
QY 229 NNYDYROMKLTREYSDHCVKVYETGLAKL--KGTSAKQWVDYNQFRREMTLAVLDVVALP 286
Db 224 INYQKLELIELYTDYCVHMYNRGNELRQRTSATAWLEFHYRREMTLAVLDIVASP 283
QY 287 PNYDRTYVMEKTAOLTRBYVTDPLGAVNVSSI--GSWYD--KAPSFVIESSVIRPPHV 342
Db 284 SLSDITNPIETDFQLSRVITYDPIGFVHRSLSRGESWFSVNRANFSOLENAIPNRPFS 343
QY 343 FDIITGLTVYTSRSI---SSARYIRHWAGHOISYHRVSRGSLNQOMYGTNTQNLHSTSTP 359
Db 344 W-FLNNMIISTGSLTLPVSPSTDRARVMYG---SRDRIS-PANSQFITEILISQHTTATQ 358
QY 400 DFTNVDIYKLSKDAVLLDIVPGTYTFFGMEPEVEFFMNVQNLNTRKTLKNFVSKDII 459
Db 399 TILGRNIFRVDISOACNLNDTTY-----GYNRAVFYHDASEGQRS-----VYEGY 444
QY 460 AST-----RDSLELPPETSDQPNYESYSHRLCHITSIPATG-----NTTGLVPVP 505
Db 445 RTTGIDNPRVQNTLYLPGENSIDIPTEDYTHLS--TTINLTGGLRQVASHRRSLVMY 502
QY 506 SWTHRSADLNTIYDKITQIPAVKCMNDLPFVVPVKGPGHTGGDLLQVNRSTGSGVTLP 565
Db 503 GWTHKSLARNNTINPRITQIPLTKVDTRGTGVSVDGFIGGALLQ-RTDHGSLGVL- 560
QY 566 LARYGLALEKAGKYRVLRYATDAIVLHVND----QIQMPKTMNPGEDLSKTFKQVAD 621
Db 561 --RVQFPLHLRQYRIRVYASTNIRLSVNGSFGTISQNLPTMRLGEDRYGSPAIRB 618
QY 622 AITTLNLTADSSIALKLNHGEDPNSTLSGIVVVDRIEPIPDVETYEABODLEAAKAVNA 681
Db 619 FVTSRTPASPD---QIRLTIEP-SFIRQEVYVDRIEPIPNPTREKEDLEAAKAVAS 674
QY 682 LFTNTKQGLRPGVTDYEVNQAANLYECLSDLLYPNEKLLPDAVREAKLSBARNLLQDP 741
Db 675 LFTRTDGLQVNVKDYQVDAQANLVSLCSDEQYGYDKWLEAVRAAKLSERNLLQDP 734
QY 742 DROEING--ENGWASTAGIEVIEGDLAKGRVLRILPGAREIDETETPTLYLOKVEGVUK 799
Db 735 DFTNTNSTEENGWAKSNGVTISEGPFYKGRALASAR---ENYPTIYQKVDASELK 790
QY 800 PYTRVLRGFGVSSQGLEIFTIRHOTNRIVKNVPPDLLPDPVSPVNSDGSINCSQKQYN 859
Db 791 PYTRVLDGFWKSSQDLEIDLHKKHVLKXVNPVNLVSDTYPDDSCSGINRCQEQQWN 850
QY 860 SLEVEN-----RSGEAPEFSIPDTGEIDYNNENAGIWWGFKITDPEGYATLGNLELV 912
Db 851 AQLETEHHHPMDCCAAQTHEPFSYIDTGLNSVYDQGIWAFKVRITTDGYATLGNLELV 910
QY 913 EEPGLSGDALERLOREOQWKIOMTERRRETDRTYMAKQAVDRLYADYQDQOLNPDVEI 972
Db 911 EVGPLSGSLERERQDNTKWSAELGRKGAETDRVYQDAKQSNHLLFVDYQDQOLNPEIGM 970
QY 973 TDLTAQQLIQSIPIVYVYNNEMFPEIPGMNYTKFTLTDRLOQANSYLDQORNAIPNGDFRNG 1032
Db 971 ADIMDAQNLVASISDVYSDAVLQIPGINVEIYTELNRLOQASLYLTSRNAVQNGDFRNG 1030
QY 1033 LSNWNATPGVEVQQINHYSVLVPIPNWDBQVSQOFTVQPNQRYVLRVTARKEGVNGYVSI 1092
Db 1031 LDSMNATAGASVQDQGNTHFLVLSHWDQAQVSQFQVQPNCKYVLRVTAEBKVGGDGYVTI 1090
QY 1093 RQGGNOTETLTFSADSDYDNGMYNTQVSNNGYNTNAYNTQASSTNGYNNANNMYNTQAS 1152
Db 1091 RDAHHTTETLTFFNACDYDINGTYVT----- 1115
QY 1153 NTNGYNTSVYNDQGYITKVTPIFYTDQWMIEMSETEGTPIESVELI 1202
Db 1116 -----DNT-YLTKEVVFPEPETHMMVVEVNEGAFHDSIEPV 1152
RESULT 8

Db	678	LLQDRNFRSINGQLDRGWRGSTDIITIQGGDDVFKENIVVTLPCTFD----	ECYPTPLYQKID	734	
Qy	795	EGVLKPYTRYLRGFGVSSQGLBEIFIRHOTNRIVKVNPDLLPDSVPNSDGS	-----	849	
Db	735	ESKLUKSYTRYELRGYIEDSQDLBIYLIRYNKAHEIVNVPG--TGSWLPS	SIENSIPCGE	792	
Qy	850	-NRCSEQKYNLSRLEVENRSGE-----	AHEFSIPDITGEIDYNNENAGI	VWGFKITDPEGY	903
Db	793	PNRCAPHLEWNPNLDCSRGCEKCAHSHHFSLDIDVGCTDLNEDLG	VWVIFKIKTQDGH	852	
Qy	904	ATLGNLEIVTEGPGSLGDALRERLORESOQWKIQMTRRREFTDRRYAS	KASQAVDLRYADYQD	963	
Db	853	ARLGNLFLEKEKPLGALGARVRAEKKWRDKEKLEWETNI	VYKSAKESVDALFVNSQY	912	
Qy	964	QOLNPDPVEITDLTAAQDLIOSIPVYNEMPEPEPGNNYTKFTELTDR	LQOQASLYDORNA	102	
Db	913	DRLQADTNIAWIIHAADKRVHRIREAYVPELPSVIPGVNAGIFELEGR	IFATSYSLYDARNV	972	

	QY	I P G D F E N G L S N W A T P G V E V - Q I N H S T S V L I P N W D E Q V S O Q F T V Q P N Q R V L T V T A R K 1 0 8 2
		----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- -----
	D b	I K N G D F A N G L L C W N L K G H D V B E E Q N N H R S V L V P P E A E A V S O E V R V C P G R G Y I L R V T A Y K 1 0 3 2

```

QY   1083  EGNGVGVYSIRKGGNQIEILFFS-----ASDY-----DTNGMYNTQVSNTN 1123
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db    1033  EGYGEGCVTHIIEDNTDELKFSVCBEEVYPNNVTCTNDYATQEYGGAY---TSRNH 1089
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::

QY   1124  GYTNNAVNTQAOSTNGVNANNMNTQASNTNGYNTSVYNDQT----GYTKTVTFIPY 1179
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db    1090  GYGKSYESNSVDQAYASVVEEKADTGRDRNHCSNRGYGDYTPLPAGYVTKLEYFPE 1149
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::

QY   1180  TDQMWMSETEGTFTYESVELIV 1203
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db    1150  TDKVWEIGETEGTFIVDSVELLL 1173
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::

RESULT 9
S32689
Parasporal crystal protein crytHal - Bacillus thuringiensis
C:Species: Bacillus thuringiensis
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C:Accession: S32689
R:Lambert, B.
submitted to the EMBL Data Library, April 1993

A:Reference number: S32645
A:Accession: S32689
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1172 <LAW>
A:Cross-references: EMBL:Z2513; NID:g296086; PIDN:CAA80236.1; PID:g296087
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match          33.4%; Score 2115, 5; DB 2; Length 1172;
Best Local Similarity 39.3%; Pred.No. 5.2e-114;
Matches 496; Conservative 186; Mismatches 421; Indels 159; Gaps 37;

QY   4     NNQXEYII DATPTSVSNDSNRYPFANEPTALQNNDKYDKLKMSAGNASAYPGSPVL 63
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db    5     NNQOY-----VPYNCLSNPEN-----EILDIESLSR----- 32

QY   64     VSGDQAKAAIDIVGKLLSLGLGVFPVGPIVSLYTQLIIDILWPSSGEKQWEIFMQVEILI 123
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db    33     -SREQVAEISLGITRRFLLES!-----LFGASFQFALFDIIWGVIGPDQWNLFIAQIEQLI 86
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::

QY   124     NOKTAEVARNKALSELGIGNNYLYLTALEEWEENPNGPSALFDVNRPFILSLFTQY 183
      :||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db    87     DQRTEAHVRNQAIISRLGELGDSYVYTESLEFWESAPNNEALOQDVNRFRSNTDNALITA 146
      :||::|||::|||::|||::|||::|||::|||::|||::|||::|||::

QY   184     MPSFRVTNFVPPFTVYAMAANHLHLLKKDAS IFGESEWGSTTTNNKYDRQMKLTAEYS 243
      :||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db    147     IPIREOGFEIPLUSVYQAOANHLSLRDADV FQGRWLDTVTVVNNHNKLINLIWTYS 206
      :||::|||::|||::|||::|||::|||::|||::|||::|||::|||::

QY   244     DHCVKVTETGLAKLKGTS AKOWVDYNOFRREMTILAVLDVVALFPNYDTRTYPMETKAQLT 303
      :||::|||::|||::|||::|||::|||::|||::|||::|||::|||::

```

RESIT. T. 0

REC-001 3
932689

parasporal crystal protein cry1Ha1 - *Bacillus thuringiensis*

C:Species: *Bacillus thuringiensis*

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000

C;Accession: S32689

R; Lambert, B.
submitted to the FBI Data Bureau: May 17 1963

Submitted to the EMBL Data Library, April 1993
 Accession number: S32645

A;REFERENCE NUMBER: S32643
A:Accession: S32689

A:Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1172 <LAM>

A;Cross-references: EMBL:Z22513; NID:g296086; PIDN:CAA80236.1; PID:g296087

C;Superfamily: parasporal crystal protein

C;Keywords: delta-endotoxin

Quincy Match 33 48. 80000 0115 E. PB 3. 1 month 1173.

Query Match 33.4%; score 2113.3; DB 2; length 1172;
Best Local Similarity 39.3%; Pred No 5 2e-114.

Matches 496; Conservative 186; Mismatches 421; Indels 159; Gaps

QY 4 NNQNEYBIIDATPSTSVSNDNSNRYPFANEPTNALQNMDYKDYLKMSAGNASEYPGSPEVL 63

Category	Sub-category	Value
A	1	10
	2	20
	3	30
	4	40
B	1	10
	2	20
	3	30
	4	40
C	1	10
	2	20
	3	30
	4	40
D	1	10
	2	20
	3	30
	4	40
E	1	10
	2	20
	3	30
	4	40
F	1	10
	2	20
	3	30
	4	40
G	1	10
	2	20
	3	30
	4	40
H	1	10
	2	20
	3	30
	4	40
I	1	10
	2	20
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J	1	10
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	3	30
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K	1	10
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	3	30
	4	40
L	1	10
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M	1	10
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N	1	10
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O	1	10
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P	1	10
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Q	1	10
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	3	30
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R	1	10
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	3	30
	4	40
S	1	10
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V	1	10
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X	1	10
	2	20
	3	30
	4	40
Y	1	10
	2	20
	3	30
	4	40
Z	1	10
	2	20
	3	30
	4	40

db 5 NNQNY-----VPYNCLSNPEN-----EILDIESLSSR----- 32

Q: 64 YES000AAAINDVWYI SCLGUREICBIVSL YTOI IDTI WBSCEKSOPIEWEQVEELT 123

QY	04	05	06	07	08	09	10	11	12	13																																							
04	V	S	Q	A	R	A	D	I	V	A	N	T	S	F	V	G	F	I	V	A	T	I	Q	I	D	I	D	I	B	F	S	O	E	K	S	Q	W	E	I	F	M	E	Q	V	E	E	L	I	123

Db 33 -SREOVAEISGLTRFLES-----LPGASFGFALFDIIWGVIGPDOWNFLACIEOLI 86

.....

Qy 124 NOKIAFYARNKALSELEGLGNYYQLYLTALEEENPGSRALRDVNRFEILDLSFTQY 183

[illegible]

Db 87 DQRIEAHVRNQAI SRLEGLGDSYEVYIESLREWEASPNNEALQQDVNRFRSNTDNALITA 146

Q: 104 MDCBZTHNPPBZDEI TWYAMAA NI HI I I YKASCTECPBPCINOCSTTWT NATUNVDBOMWT TAPBVS 242

QY 104 MFSKVINFEVFETIVATATANTHDDNDASIFGEWGSIIINNIDRQNTIAEIS 243

147 TPTI:REOGFEETPTI:SVWVQAANT:HI:SLI:PDVAVEGQRWGI:DTVTWNNHYNRI:INI:NTYS 206

[illegible]

QY 244 DHCVKWYETGLAKLKGTSAKQWVDYNQFRREMTLAVLDVVALFPNYDTRTPMETKAQLT 303

Db 207 DHCAQNFNRLDNFGVVSAR---YLDFOREVTISVLIDIVALPNYDIRTYPISTQSOQLT 262
QY 304 REYVTPPLGAVNVSSIGSWTDKAPSFVIESSVIRPHVFDYITGLTVYVTSRSISARY 363
Db 263 REIYTPGVA-----EPGASLANIQLNIREPLHMDFLRLVIYT---GVQSGIY 308
QY 364 IRWAGHOISYHRVSR--GSNLO-QMYCT-----NONLHSTSTDFNTVNDIYKTLSD 413
Db 309 --HWAGHIEISRTGNLSSNQPLGYTAASADRAFNNHSET-----IYRTLS-- 357
QY 414 AVLLDI---VYPGYTYIFPGMEVEFPFVWQNLNTRKLYKNPVSKDIIASTRDSSELELP 470
Db 358 APIYSVSGGISPNRTRVEG---VRFLIARDNNLDSLPFLYRK-----EGTLDSPTELP 408
QY 471 PETSDQPNYESYHRLCHI-----TSIPATGNTTGLVPSFVSWTHRSADLNNTIYSDKITOI 526
Db 409 PEDESTPPYIGYHRLCHAFARSPVILEPSNFARLVPFVSWTHRSASPTNEVSPSRTQI 468
QY 527 PAVKCDNLPFPVAVKPGHGTGDLLOYNR-STGSGVTGLFLARYGLALEKAGKRVRLRY 585
Db 469 PWYKAHTLASCASVIGKPGTGGDITRNINILGDLGLRVTVYVYVGRLPQ---SYIYRLRY 525
QY 586 ATDAD---IVLVHNDQ--TOMPKTMNPGEDLTSTKTFKADAITTLNLTATDSSLALKHNL 640
Db 526 ASVANGSGVFRHLPPQPSYGISFPRTMTGDTLSRSPALTTFTPTILT-----RA 576
QY 641 GEDPNSTLSGIYVVDRIEFTPVDETYEABQDLEAKAVALFNATKX-DGLRPGVTDYEV 699
Db 577 QEEFNLTIPRGVYDRIEFYFVDATFAGYDLERAQAVNALEFTSTNQRGLKTDITDIHI 636
QY 700 NOANLVECLSDDLYPNEKELLFDVAREAKRLSEARNLLODPOEING--ENGWASTAG 757
Db 637 DQVSNLVECLSDDEFLDEKELSEKVKHAKRLSDGRNLLQORNFISINGLLDRGWRGSTD 696
QY 758 IEVIEGDALFKGRYLRLPGAREIDTPTYLYKQVEEGLPKYTRYRLRGFVSGSOGLE 817
Db 697 ITIQSGDDVFKENKVTLPGTFD--ECYPTYLYKIDESKLYATRYOLRGYIEDSDLE 753
QY 818 IFTIRQTNRIKVNVP---DOLLPOVSPVNS---DGSINRSCQKYVNSRLSEVENRSE-- 870
Db 754 IYLIRNAKHEIVNVPGTGSLWP--LSVENSIGPCGESNRCAPHLWNPNDLDCSRDGEKC 812
QY 871 ---AHBFSPIDTGEIDYNNAGIWWGFKITDPGAYATLGNLELVEGSLSGDALERLQR 927
Db 813 AHSHHFSLDIDVGCTDLNEDLGWVIFKIKTDQGHARIGNLEPLEEKPLVGEALARVKR 872
QY 928 EEOWKIQMTRREEDRRYMAKQAVDRLYADYQDQOLNPDVEITDLTAQDLIQSIPI 987
Db 873 AEKKWRDKRKLFEFTNIYVYKEAKESVDALFVNSQYDKLADTNIAIHAADKRVHIRE 932
QY 988 VYNEMPEPISGMNYYKFTELTDRLQOAWSLYDORNAIPNGDFRNLGNNAWATPGVEV-QQ 1046
Db 933 AYLPELSVIFGVNADIFEELEGRIFTAYSIDARNVTKNGDFNGLLCWVKVGHVDVEEQ 992
QY 1047 INHTSVLIVNWBDOVSQOFTVOPNORVLYRKYARKEGVNGVYSIRDDGNOTETLTFSS- 1105
Db 993 NNHRSVLVPEWAEVSEVRCVCGYIILRVYAKGYGEGCVTHIEIDNDELKFSN 1052
QY 1106 -----ASDYDTN--GMINTQVSNNTNGYNTNAYNTQASSTNGYNNANNMTNQ 1150
Db 1053 CVBEEVPSNTVTCNDYTAQNEEYGTYSRNOGY--DEAVESNSSVPANY--ASVYEEK 1108
QY 1151 ASWTNGYNTSV-----YNDQT-----GYIKTVTFIPTYQMIEMSETGTFYIESVEL 1201
Db 1109 A-YTDRRENSCEFNRGYRDYTPLPAGYVYVKELEYFFGTAKVWIEIGETGTFIVDSVEL 1167
QY 1202 IV 1203
Db 1168 LL 1169

RESULT 10

S11446
parasporal crystal cry1dai - Bacillus thuringiensis
N:Alternate names: parasporal crystal protein cry1D
C:Species: Bacillus thuringiensis
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 01-Dec-2000
C:Accession: S11446
R:Hoefte, H.; Soetaert, P.; Janssens, S.; Peferoen, M.
Nucleic Acids Res. 18, 5545, 1990
A:Title: Nucleotide sequence and deduced amino acid sequence of a new Lepidoptera-specific
A:Reference number: S11446; MUID:91016842; PMID:2216728
A:Accession: S11446
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1165 <HOB>
A:Cross-references: EMBL:X54160; NID:940279; PIDN:CAA38099.1; PID:g40280
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin
Query Match 32.8%; Score 2078.5; DB 2; Length 1165;
Best Local Similarity 39.4%; Pred. No. 7, 1e-112;
Matches 499; Conservative 175; Mismatches 426; Indels 165; Gaps 33;
QY 1 MSPNNQVEYIIDATSTSVSDNSNRYPPFANEPTNALQNDYKDKYKMSAGNASEYVPGSP 6C
Db 1 MEINNQNC-----VPYNCL-----SNPKETILGE 25
QY 61 EVLVSGQDAKAADIVGKLLSGLVYVPGPIVLSLTOLIDILWPSGEKSQWEIFMEQVE 120
Db 26 ERLETGNTVADISLGLINFLYSNF-VPGGGFVIG-----LLELWGFIPGSQWDIFLAQIE 80
QY 121 ELINQIAEYARKKALSELGLNNTYQLYLTALKEEENPNGRALDRVNRREILDSLF 180
Db 81 QLISQRIEFANQALSRLEGSLNLYKVYVAFSDMEKDPALREEMRIQDNANSL 140
QY 181 TOTMPSFRVNTPEVPLTVYMAANLHLLKLDASIFGEWGSTTTINNYDROKMLTA 240
Db 141 ITAIPLEFRQNVYVALLSVVQAANLHLGILRDSVFGERWGYDTATINNRYSDLTSLIH 200
QY 241 EYSDHCWKVYELAKLKGTSKQWQVYQVQVREMTLAVLDVVALPNVDYTRYPMETKA 300
Db 201 VYTNHCVDYTNQGLRLEGRFLSDMIVNFRFRQLFTISVLIDIVAFPPNYDIRTYPIQTAT 260
QY 301 QLTRYVYTD-PLGAVNVSSIGSWYDKAPSGFVIESVIRPHVFDYITGLTVYVTSRSIS 359
Db 261 QLTRYVYLDLPFINENLSPAASY---PTFSAEASAIIRSPHLVDPLNSFTIYTD-----S 312
QY 360 SARYIRHWAGHOISYHRVSRGSLN--QMYGNQNLHSTSTDFNT-NDIYKTLKSDAVL 416
Db 313 LARY-AYWGHVLSNFRGTGTTNLRSPLYGREGNTERPVTITASPSVPIFTLS----- 366
QY 417 LDIVYPGTYI-----PFGVPEVEFPFVWQNLNTRKLYKNPVSKDIIASTR--DSE 466
Db 367 -----YITGLDMSNPVAGIEGVEP-----QNTISRIYKSGPIDSF 403
QY 467 LELPETSQPNYESYHRLCHITSIPATGNTTGLVPSFVSWTHRSADLNNTIYSDKITOI 526
Db 404 SELPPQDASVSPAIGYSHRLCHATFLERISGPRIAGTVFSWTHRSASPTNEVSPSRTQI 463
QY 527 PAVKCDNLPFPVAVKPGHGTGDLLOYNRSTGSGVTLFLARYGLALEKAGKRVRLRYA 586
Db 464 PWYKAHTLASCASVIGKPGTGGDILTRN-SMGLCTGLAVTFTGRLPQ---SYIYFRYA 519
QY 587 TDADIVLVHNDQ-----TOMPKTMNPGEDLTSTKTFKADAITTLNLTATDSSLALKHNLG 641
Db 520 SVANRSCTFRYQPSYGISFPKTMADAGEPLTSRSP-----AHTTLFTPTTFSRA-----Q 570
QY 642 EDPNSTLSGIYVVDRIEFTPVDETYEABQDLEAKAVALFNATKX-DGLRPGVTDYEVN 700
Db 571 EEPDLVQSGVIDRIEFYFVATFASVYDLERAQVNALEFTSTNQLGLKTDVTDYHID 630
QY 701 QANLVECLSDDLYPNEKELLFDVAREAKRLSEARNLLODPOEIN--GENGWASTAGI 758
Db 631 QVSNLVACLSDBEFLDEKELSEKVKHAKRLSDERNLLODPPNFRGINRQPDRCWRGSTD 690

RESULT 12
JC2219
parasporal crystal protein cryIAa - Bacillus thuringiensis
C:Species: Bacillus thuringiensis
C:Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 01-Dec-2000
C:Accession: JC2219
R:Udayasuriyan, V.; Nakamura, A.; Mori, H.; Masaki, H.; Uozumi, T.
Biosci. Biotechnol. Biochem. 58, 830-835, 1994
A:Title: Cloning of a new cryIA(a) gene from Bacillus thuringiensis strain FU-2-7 and an
A:Reference number: JC2219; MUID:94289859; PMID:7764972
A:Accession: JC2219
A:Molecule type: DNA
A:Residues: 1-1176 <UDA>
A:Cross-references: DDBJ:D17518; NID:G506190; PIDN:BAA04468.1; PID:G535781
C:Genetics:
A:Gene: cryIA(a)
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 32.7%; Score 2070.5; DB 2; Length 1176;
Best Local Similarity 39.5%; Pred. No. 2.1e-111;
Matches 492; Conservative 176; Mismatches 440; Indels 137; Gaps 33;

QY 23 DSNRYFANE--PTNALQNDYKDYLMKSNAGNASEYPGSEVLVSGQDAKAA---IDIV 77
DB 2 DNN--PNINECIPYCNLSN-----PEVEVLGGERIETGYTPIDIS 39

QY 78 GKLLSLGLVPPFVGVIVSLYTLQIDILWPSEKQWEIFMEQVEELINOKIAEYARNKALS 137
DB 40 LSLTQFLLESEF-PGAGFVLGLVDIIWIFGPGQDAFLVQIQLINQRIEFAFNQALIS 98

QY 138 ELEGNNYQLYLTALAEWEENPGSRALDRVNRREIFLDSLTQYMPSPRVNFEVPEFL 197
DB 99 RLEGSLNLYIYAESPWEADPTNPALREMRIQFNQDMSALTTPALPLAVQNYQVPL 158

QY 198 TVYMAANLHLLKDAISFEGEWGHSTTINNYDROKMLTAEYSDHCVKVTETGLAKL 257
DB 159 SVYVQANLHLVLRDVSFVGQWGFDAATINSRYNDLTGLIGNYTDYAVRVNTGLERV 218

QY 258 KGTSAKQWYDYNQFREMTLAVLDVVALFPNYDTRYVPMETKALREVYTDPLGAVNVVS 317
DB 219 WGFSDSDWRYNQFRELTLVLDIVALFSYDUSRYRPIRTVSQLTREIYNP---VLEN 275

QY 318 STGSWYDKAPSGVIBSSVIRPVPDYITGLTVYTSQSRSSISSARYIRHWAGHQISYHRV 377
DB 276 FDGSEFRGAQR---IQON-IRQPHLMDILNISIITYDVH-----RGFNYSQGHQITASPV 326

QY 378 --SRGSNLQOMYGTNQNLHSTSTFDFTNVDIYKLSKDAVLDDIVPGYTYIPFG----- 430
DB 327 GFSGPEFAPPLFGNAGNAAPPVLVSLTGLGIFRTLSS-----PLVRRITLGGPNN 377

QY 431 ----MPEVEFFMVNQLNTRKTLKYNPVSKDIIASTROSELELPPETSQDPNYESYSHR 485
DB 378 QELFVLDDGTEFEFASLTWLPSTI-YRQ-----RGTVSLDVIPPQDMSVPPRAGFSHR 430

QY 486 LCHITSIPATGNT--TGLVPFVSWTHRSADLNNIYSDKITQIPAVKCDNLPFVFWVGK 543
DB 431 LSHVTMLSQAGAVYTLRAPTFSQWRSKSAEFNIIIPSSQITQIPLKSTNLGSGTSVVGK 490

QY 544 PCHTGGDLLOYRSTGVSUTFLARYGLALEKAKRVRLRYATDADIVLHN-DA----- 598
DB 491 PFTGGDILR-RTSPGQISTL---RVNITAPLSQRYRVIRYASTTNLFQHTSIDGRPIN 546

QY 599 QIQPKTMNPGDLTSKTFKVAADAITLNLATDSSL---ALKHNGEDPNSTLGIWVV 654
DB 547 QGNFATWSSGNLQSGSRFTVGFTHPFNSGSSVFTLSAHVFNNGNE-----VVI 598

QY 655 DRIEIPVDETYEAEODLEAKKAVNALFTNTKD-GLRFGVTDYEVNQANLVECLSDDL 713
DB 599 DRIEFPVAEVTAEAYDLERAKQAVNELTSSNQIGLKTDDVDYHDQVSNLVECLSDDF 658

QY 714 YNEKRLFLDFAVREAKRLSEARNLQDDPQFQING--ENGWTASTGIEVIEGDLPKGY 771

DB 659 CLDEKQELSEKVKHAKRLSDERNLQDPNFRGINRQLDRGWRGSTDITIQGGDDVPKENY 718
QY 772 LRIPGAREIDTETYPYLYQKVEEGLVPYRVRLAGFVSSQGLFIFTRHQTNRIVKN 831
DB 719 VTULGTFD---ECYPILYQKIDESKLYATRYQLRGYIEDSODLEIYLIRYNAKHETVN 775
QY 832 VPDD-----LLPDVSPVNSDGSINRSEQKYVNSRLSEVENRSGE-----AHEFSIPIDTGE 882
DB 776 VPQTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFSLDIDVGC 835
QY 883 IDYENAGIIVGFKITDPGYATLGNLELVSEGPLSGDALERLQREEQQKIQMTRRREE 942
DB 836 TDLNEDLGVVIFKIKTODGHARLGNLEPLBKPLVGEALARKAEKRWDRKRELEWE 895
QY 943 TDRRYWASQAVDRLVADYQDQNLNPDVEITDLTAQODLIQSIPIYVYVNMFPPIGNYIT 1002
DB 896 TNIVYKEAKESVDALFVNSQYDQLOQADTNIAHAAKRVHSIREAYLPSELSVIPGVNAA 955
QY 1003 KFTETLDRLQOAWSLYDQRNAIPNGDFRNGLSNMNATPGVEV--QQINHTSVLVIPNWDEQ 1061
DB 956 IPEELGRISTAFSLYDARNVIKNGDFNNGLSQWNVKGVHDVEEQNNQSVLVVPEWEAE 1015
QY 1062 VSOQFTVQPNQRYLVLTARKGNGVGYVSIIRDGGNQTETLTFSS-----AS 1107
DB 1016 VSGEVRVCPGCGYILRTAYKEGEGCGVTHIEIENNTDELKPSNCVBEIYPNNTVTCN 1075
QY 1108 DYDTN-----GMVNTQVSNYNTVNTNATQASSTNGYNNMNTQASNTNGYNTNSV 1162
DB 1076 DYTVOEEYGGAY---TSNRGY--NEAPSVADYASVYEEKSY--TDGRRNCPCEFRNG 1128
QY 1163 YNDQT---GYITKTVPFIPYTDQWMIEMSETEGTFYIESVELIV 1203
DB 1129 YRDYPLPVGYVYKLEYPETDKWVIEGEGEGTFIVDSVELLL 1173

RESULT 13
S32645
parasporal crystal protein cryIgal - Bacillus thuringiensis
C:Species: Bacillus thuringiensis
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C:Accession: S32645
R:Lambert, B.
submitted to the EMBL Data Library, April 1993
A:Reference number: S32645
A:Accession: S32645
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1166 <LAM>
A:Cross-references: EMBL:Z22510; NID:G295861; PIDN:CAA80233.1; PID:G295862
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 32.7%; Score 2069; DB 2; Length 1166;
Best Local Similarity 38.4%; Pred. No. 2.5e-111;
Matches 481; Conservative 193; Mismatches 415; Indels 164; Gaps 32;

QY 22 NDSNYPFANEPTNALQNDYKDYLMKSNAGNASEYPGSEVLVSGQDAKAAIDIVGKLL 81
DB 4 SQONQY---IPYCNLNPSEBIF-----NARNSNFGLVSVQS 37

QY 82 SGL-----GVFPVGPVIVSLYTLQIDILWPSEKQWEIFMEQVEELINOKIAEYARNK 134
DB 38 SGLTRFLLEAAVPEAGFALGLP---DIWGLGVDDQHSFLRQIQLRQIETELERNR 93

QY 135 ALSELEGNNYQLYLTALAEWEENPGSRALDRVNRREIFLDSLTQYMPSPRVNFEV 194
DB 94 ATAIIITGLSSSNLYVEALREWENPNPNPASQERVTRTFRLLTDDAIVTGLPLAIRNLEV 153

QY 195 PLYTVYMAANLHLLKDAISFEGEWGHSTTINNYDROKMLTAEYSDHCVKVTETGL 254
DB 154 VNLSYTOAANLHLLSLRDVAVYFGRWGLTQANIEDLYTRLTSNIQEYSDHCAWYNOGL 213

QY 255 AKLKGTSAKQWYDYNQFREMTLAVLDVVALFPNYDTRYVPMETKALREVYTDPLGAV 314

Db 214 NEIGGISRR-----YLDFODLTISVLDIVALFPNPDYDIRTYPTQSLTRBIYTPSVVAG 269
QY 315 NVSSIGSWYDKAPSGVLESSVIRPPHVDYITGLTVTQTSRISYIRHWAGHQISY 374
Db 270 NI-----NFGLSANVLRAPHLMDFDIRVIVT-----NSVRSTPYWAGHEVIS 313
QY 375 HRVSRGSLQ--QMYGTNQLHSTSTDFNYD-----IYKTLSDKADVLL 417
Db 314 RRTGOGGNEIRFPGLYGAANAEPVPIRPTGFTDQRQWYRARSRVVSRSSGGDFSLV 373
QY 418 DIVVPGYIYIFGHEPEVEFFWVQNLNTRKLYKYNPVSQDIASRDSLELHPPTSQOP 477
Db 374 DAV--GFLTIP-----SAVSIYRNGFGFTDID-----EPIEGTDP- 409
QY 478 NYEYSRHLCHITSIPATG--NTTGLVPVSWTHRSADLNNTIYSDKITQIPAVKCDNL 535
Db 410 -FTGYSRHLCHVGFGLASSPFIQYARAPISFNTHRSATLNTIAPDVITQIPLVKAFNLH 468
QY 536 PFVPVVKPGHGTGDLLOYNRSTGSGVTLFLARYGLALEKAGKYRVRLYA--TDADIVL 593
Db 469 SGATVKGPGTGGDLA-RINVGSGDM--RVNITAPLSQRYVRIRYASTTDLQPYT 524
QY 594 EVNDAQOM-----PKTMNGBDLTSKTPKVAADAITLNLATSSALKKNLGEDPNSTLSG 650
Db 525 NINGTTINIGFSSSTMSGDDLOVGRFVAGFTPTPTSDANSTFTICAGFGSPNNE--- 581
QY 651 IVVYDRLEFIPVDEYAEQLEAKKAVNALFTNTKD-GLRPGVTDYEVNQANLVECL 709
Db 582 -VYIDRLEFPAEVTTFEAYDLEKAKAVNALFTSSNQIGLKTVDTHIDKVNLSVCL 640
QY 710 SDDLVPNEKRLFLDAVRAKELSEARNLQDPDFQBIN--GENGWASTGTGIEVIEGDALF 767
Db 641 SDEFCLDEKRESEKVKHAKLSDEBNLQDPNFPNGINRQPDGRGSGTDTIQGDDVP 700
QY 768 KGRVLRIPGAREIDTETPTLYXQKVEGVLKPYTRYLRGLRGVSGSGLEIFTIRHOTNR 827
Db 701 KENYVTLPGTDP--GCYPTLYXQKIDSKLVKRYTRYLQGVIEDSQLEIYLIRYNAKH 757
QY 828 IVKNVDD-----LLPDVSPVNSDGSINRSEKQYVNSLEVENRSGE-----AHEFSIPTI 878
Db 758 ETNVNPGTGLWPLSAQSPIGKCGEFPNRCAPHLEWNPDLDCSRNGEKAHSHHFLSDI 817
QY 879 DTGSDIDYENAGIWWGFKITPEGVATLGNLELVEEGLSDGALERLQREKQOWKIOMTR 938
Db 818 DVGCTDLNEDLGWVIFKIKTQDGHARGNLNLEFLEKPLGLENLARVKAERKWDKZEK 877
QY 939 RRETDRRYMAKQAVDRLYADYDQOQLNPVIEITDLTAADLIQSIPIVYNEMPEPIPG 998
Db 878 LELETNIIVYKEAKESVDALFVNSQYDQLQADTNIAHAAADKRVHSIREAYLPELSVPFG 937
QY 999 MNYTKFTLTDLQOAKSLYDORNALPNGDFENGLSNNAATPGVEV-QQINHTSVLVIPI 1057
Db 938 YNAAFEELEGRIIFAFSLYDARNYKNGDFNGLSCWNVKGVHVDVBEQNHRSLVAVPE 997
QY 1058 WDEQVSOQFTQPNORYVLRVYARKEGVNGVYSIRDCGNOTETLTFSS-----1105
Db 998 WEAEVSEQRVCPGRGYILRTAYKEGGEGCVTHBENNTDELKFNCEVEEYVPNT 1057
QY 1106 --ASDYDTN-----GMVNTQVSNNTNGYNTNAYNTQASSTNGYNNANNYN-----TOASNT 1154
Db 1058 VTCNDYNTANQEYKAY--TSHNRGY--DEAYGNPNVPADYTP--VYEKAYTDGRRE 1110
QY 1155 NGYNTNSVYNDQT-----GYIKTKVTFPIYTDQMWJEMSETETGTFYIESVELIV 1203
Db 1111 NPCESNRGYGDYTPLPAGYVYKLEYFPETDKWVIEIGETGTFIVESVELIL 1163

RESULT 14

S32647

parasporal crystal protein cry1db1 - Bacillus thuringiensis

C;Species: Bacillus thuringiensis

C;Date: 20-Feb-1995 #sequence #revision 20-Feb-1995 #text_change 01-Dec-2000

C;Accession: S32647
R;Lambert, B.
submitted to the EMBL Data Library, April 1993
A;Reference number: S32645
A;Accession: S32647
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1160 <LAMB>
A;Cross-references: EMBL:Z22511; NID:g295863; PIDN:CAA80234.1; PID:g295864
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin

Query Match 32.6%; Score 2065; DB 2; Length 1160;
Best Local Similarity 39.3%; Pred. No. 4.2e-111;
Matches 480; Conservative 190; Mismatches 456; Indels 126; Gaps 28;

QY 33 PTNALQNDYKDYKMSAGNASEYPGSPVULVSGDAAKAAIDIVGKLLSLGVFPVGPPI 92
Db 11 PYNCLSN---PDAILLDA-----ERLETGNTVADISLGLINFLYSNP-VPGGGPI 56
QY 93 VSLYTLQIDILWPGEKSQWEIEMQVEELINOKIAEYARNKALSELEGNGNYOLYLTA 152
Db 57 VG-----LLELWGFVSGSQWEIFLAQLEQLISQRIEFARNQALSRLEGLSNYIYET 112
QY 153 LEEWEPNGSRALRVNRFELDLSFTQYMPSRVTNFEVPELTVYMAANLHLLK 212
Db 113 FRAMEKOPSALREEMRTQFNVNSALIAAIPLLRVNYEVALLSVTVQAANLHLSVL 172
QY 213 DASIFGSENGWSTTTINNYDROMKLTABYSDHCVKMYETGLAKLKTSAKOWVDYNOFR 272
Db 173 DVSVYQGWGDPATVNSRYSDLTRELHVVYTDHCVTDYNDGLKNLEGSRLSDWVYVNRFR 232
QY 273 REMTLAVLDVVALFPNDTRYPMETKAQLTREVYTD-PLGAVNVSSIGSVYDKAPSGV 331
Db 233 RRLTISVLIDIIAFPNVDIEAYPIQTASQLTREVYDLFPVNETLSPASTY---PTSA 288
QY 332 IESSVIRPPHVDYITGLTVTQTSRISYIRHWAGHQISYHRVSRGSL--QOMYGT 389
Db 289 AESAIIRSPHLVDLNGFTIYTD--SLASYAY---WGHVLVNSFTGTNTLRSPLYGR 343
QY 390 NQNLHSTSTPFT--NYDIYKTLSDKADVLLDIVPGYTVIFF-----GMPEVERFPM 438
Db 344 EGNTERPVTISASPSVPIFRTLS-----YFTGLNNPNVAGIEGVF-- 385
QY 439 VNQLNTRKTLKYNPVSKDIIASIR--DSELELPETSQDNVESYSHRLCHITSIPATG 496
Db 386 -----QNTISRSIYRKSGPIDSFSELPQDVSVSPAIGSYHRLCHATSLEIS 433
QY 497 NTTGLVPVSWTHRSADLNNTIYSDKITQIPAVKCDNLFPVVPVVKPGHGTGDLLOYNR 556
Db 434 GPRTAGTVFWSWTHRSASPINEVSPSRITQIPWKAHTLASGASVIKPGFTGGDILTRN- 492
QY 557 STGSVGLTLFLARYGLALEKAGKYRVRLYATDADIULHVNDAQ-----IQMPKTNWGED 611
Db 493 SMGDLGALRVFTTGRLPQ--SYIRFRYASVANRSGTFRYSQPPSYGISFPKTMDEGEA 549
QY 612 LTKTEKVAADITLNLATSSALKKNLGEDPNSTLSGIYVVDRIEPIPVDETVEAQQD 671
Db 550 LTTSSP-----AHTLTFTPTFSRA-----QEEFDLYIQSGVYIDRIEPIPVDAFESIN 600
QY 672 LEAKAKVNALFTNTKD-GLRPGVTDYEVNQANLVECLSDDLVPNEKRLFLDAVREAKR 730
Db 601 LERAKVNALFTSTNQLGLKTDVTHIDQVSNLVECLSDPECLDEKRESEKVKHAKR 660
QY 731 LSEARNLQDPPQBIN--GENGWASTGTGIEVIEGDALFKGRYLRLLPGAREIDTETPTY 788
Db 661 LSDERNLQDPPNFRGINRQPDGRGSGTDTIQGDDVFKENYVTLTGTFD---ECYPTY 717
QY 789 LYQKVEGVLKPYTRYLRGLRGVSGSGLEIFTIRHOTNRIVKNVDD-----LLPDVSPVN 844
Db 718 LYQKIDSKLKAITYQLRGYIEDSQLEIYLIRYNAKHIEIVNVPNGTSLWPLSVQSPIG 777
QY 845 SDGSINRSEKQYVNSRLEVENRSGE-----AHEFSIPTGTGIDYENAGIWWGFKITD 899

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Db 778 KCPEPNRCAPHLEWNPDLDCSCREDEKCAHSHHFLSDIDVGCTDLNEDLGWVIFIKT 837
Qy 900 PEGVATIGNLELVEEGLSGDALERLQREEQWIKQTRREEDTDYRMASKQAVDRLYA 959
Db 838 QDGHARLGNLEFLVEGLVGEALARKVRAEKWKDRKLELENTIIVYKEAKESVDALFV 897
Qy 960 DYDQOQLNPVEITDLTAAODLIQSIPIVYNEMFPEIPGMYTFTLTDLRLOQAWSLYD 1019
Db 898 NSQYDQLOADNTNMIHAAKRVHSIREAYLPESLVIPGVNAGIPELEGEIFTAYSLYD 957
Qy 1020 ORNAIPNGDFRNGLSNNWATPGVEV-QQINHTSVLVIPNWDQVSQFTVQPNQRYVLV 1078
Db 958 ARNVKNGDFNGLSCWNVKGVHVDVEQNNHRSVLVPEWEAEVSQEVVCPGGRGYILRV 1017
Qy 1079 TARKEGVNGVSRIDGNGTETLTFSASDYDTNGMYNTQVSTNGYNTNAYNTQASST 1138
Db 1018 TAYKEGEGECVTIHEVDNNTDELKF--SNCEKEQVPGNTVACNDKXKHGANACSSRN 1075
Qy 1139 NGYNNANMYNT-----QASNTNGYNTNSVYNDQ-----TGVIKTVTFIPYTD 1181
Db 1076 RGYDESYESNSSIPADYAPVVEEAYTDGQGNCFEPRGHTPLPAGVYTAELFFPETD 1135
Qy 1182 QMNIEMSETEGTFVIBSEVLIV 1203
Db 1136 TVWVEIGETEGTFIVDSVELLL 1157

RESULT 15
S02215
parasporal crystal protein cryA - Bacillus thuringiensis (strain entomocidus)
C:Species: Bacillus thuringiensis
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 01-Dec-2000
C:Accession: S02215
R:Masson, L.; Marcotte, P.; Prefontaine, G.; Brousseau, R.
Nucleic Acids Res. 17, 446, 1989
A:Title: Nucleotide sequence of a gene cloned from Bacillus thuringiensis subspecies ent
A:Reference number: S02215; MUID:89098405; PMID:2911478
A:Accession: S02215
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-1176 <MAS>
A:Cross-references: EMBL:X13535; NID:g40266; PIDN:CAA31886.1; PID:g40267
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 32.6%; Score 2063.5; DB 2; Length 1176;
Best Local Similarity 39.5%; Pred. No. 5.3e-111;
Matches 492; Conservative 175; Mismatches 441; Indels 137; Gaps 33;

Qy 23 DSNRYPEANE--PTNALQNMDBYKDYLMKMSAGNASEYFGSPVLYSGODAAKAA---IDIV 77
Db 2 DNN--FNINECIPNCLSN-----PEVEVLGGERTGTGTPIDIS 39
Qy 78 GKLLSGLVGPFVGVIVSLYLTQILDLMPSGEKSQWEIFMEQVEBELINQKIAEYARNKALS 137
Db 40 LSLTQFLLSSEFV-PGAGFVLGLVDIIWGIFGPSQWADAPPVQIEQLINQRIEFPARNQAIS 98
Qy 138 ELSEGLNNYQLYLTALBEWENPNGRSALRDVRNRPFLDSLTQYQWPSFRVTFVFPFL 197
Db 99 RLEGLSLYQIYAESFREWEDPTNPALREEMRIQFNDMNSALTATPALLAVQNYQVPLL 158
Qy 198 TVYAMAANLHLLKADASIFGEEWGWSTTTNNYVDROMKLTAEYSDBHCKWYETGLAKL 257
Db 159 SVVYQAANLHLSVLDRVSVFGQRMGFDAAATINSRYNDLTRLIGNYTDYAVRWYNTGLERV 218
Qy 258 KGTSAKOWDYNQPRREMTLAVLDWALFPNYDTRTPMETKAQLTREVYTDPLGAVNVVS 317
Db 219 WGPDSRDWRYNQPRRELTLDIVLAFNSYDSRRPIRVTSQLTREIYNP---VLEN 275
Qy 318 SIGSWYDKAPSGFVIESVIRPPHFVYITGLTVYTSQSSISARYIRHWAGHQAISYHRV 377
Db 276 FDGSGFRGMAQR---IQGN-IRQPHLMDILNSITITVDVH-----RGFNYSGHQITASPV 326
```

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Qy 378 --SRGSNLQOMYGTQNLHSTSTFTDFTNYDIYKTLGSKDAVLLDIVPGYTYIEFG----- 430
Db 327 GFSGPFAFLPFGNAGNAAPPVLVSLTGIGIFRLSS-----PLYRRIILGSGPNN 377
Qy 431 -----MPEVEFFMVNOLNNRTRKLYKNPVSKOIIASTRDESELEPPETSDQPNYSYSHR 465
Db 378 QELFVLDTGTEFSPASLTNNLPSTI-YRQ-----RGTVDSLDVIPEQDNSVPPRAGFSHR 430
Qy 486 LCHITSIPATGNT--TGLVPVFSWTHRSADLNTIYSDKITQIPAVKCDWNLFPVPVVK 543
Db 431 LSHVTWLSQAQAVVYTLRAPTFWQHSRAEFNNIIPSSQITQIPLTKSTNLSGSGTSVVK 450
Qy 544 PGHTGDLQYNRSTGSVGTFLFARYGLALEKAGKRVLRVATDADIVLHVN-DA----- 558
Db 491 PGFTGDLIR-RTSPQISTL---RVNITAPLSQRVVRIRVASTTNLQPHSTIDGRPIN 546
Qy 599 QIQMPTKMPGDELTSKTPKVAADAITTLNATDSSL-----ALKHNIGEDPNSTLSGIVV 654
Db 547 QGNFSAITMSSGSLQSGSFRTVGTFTFPNFSNGSVPTLSAHVFNSGNE-----VYI 598
Qy 655 DRIEIPVDETYEAEODLEAAKAVNALPTNTKD-GLRPGVTDYEVNQAAANLVECLSDDL 713
Db 599 DRIEFVPAEVTFEARYDLERAAQKAVNELFTSSNQIGLKTDTVDYTHIDQVSNLYECLSD 658
Qy 714 YPNEKLLLPDAVREAKRLGEARNLLQDPDFOEING--ENGWTAFTASTGIEVIEGDLPKGRY 771
Db 659 CLDEKQELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITIQGGDDVFKENY 718
Qy 772 LRUPGAREIDTETPTLYLYQKVEEVLKPYTRYLRGRFVSGSQGLRIFTRHQTNRIVKN 831
Db 719 VTLGTFD--ECYPTVLYQKIDESKLKAYTRYQLRGYIEDSQDLSEILYLRVNAKHETVN 775
Qy 832 VPDD-----LLPDPVSPVNSDGSINRCSEQKVNRLRLEVRNRSGE-----AHFSPIDTGE 882
Db 776 VPGTGLWPLSAQSPGKCEPRNCAPHLEWNPDLDCSCRDGKCAHSHHFLSDIDVGC 835
Qy 883 IDYNEAGIIVWVGPKITDPEGYATLGNLELVEEGLSGDALERLQREEQWIKQIOWTRREE 942
Db 836 TDNEDLGWVWVIFKITYDGHARLGNLEFLVEEKLPLVGEALARKVRAEKWKDRKREKLEWE 895
Qy 943 TDRRYMASKQAVDRLYADYQDQQLNPDEITDLTAAQDLIQSIPIVYNEMFPEIPGMYT 1002
Db 896 TNIVYKEAKESVDALFVNSQYDQLQADTNIAIHAADKRVHSIREAYLPESLVIPGVNAA 955
Qy 1003 KFTELDRLOQAWSLYDORNAIENGDFRNGLSNNWATPGVEV-QQINHTSVLVIPNWDQ 1061
Db 956 IFBELEGRIPTAFSLYDARNVINKGDFNGLSCWNVKGVHVDVEEQNNORSVLVVPWEAE 1015
Qy 1062 VSOQFTVQPNORYLVRVARTARKEGVNGVGYYSIRDGNOTETLTFES-----AS 1107
Db 1016 VSQEVRCVCGRGYILAVTAYKEGVEGCVTHIEENTDELKFCNVCBEELIYNNVTTCN 1075
Qy 1108 DYDTN-----GMVNTQVSTNGYNTNAYNTQASSTNGYNNANMYNTQASNTNGYNTNSV 1162
Db 1076 DYTWNQEEVGAY--TSNRNGY--NEAPSVPADYASVYEEKSY--TDGRENPCFENRG 1128
Qy 1163 YNDQT-----GYITKTVTFIPYTDQMIEMSETEGTFVIBSEVLIV 1203
Db 1129 YRDYTLPLPGVYTVKELEYPPETDKWIEIGETEGTFIVDSVELLL 1173

Search completed: January 7, 2003, 05:17:29
Job time : 51 secs
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 05:16:28 ; Search time 43 Seconds
(without alignments)
531.524 Million cell updates/sec

Title: US-10-032-717-2
Perfect score: 6332
Sequence: 1 MSPNNQNEVEIIDATPSTSV.....MSTETGTFYIESVELIVDVS 1206

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117078 seqs, 18951520 residues

Total number of hits satisfying chosen parameters: 117078

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6332	100.0	1206	12	US-10-032-717-2
2	5673	89.6	1210	12	US-10-032-717-4
3	3511	55.4	669	12	US-10-032-717-10
4	3511	55.4	669	12	US-10-032-717-16
5	3502	55.3	667	12	US-10-032-717-6
6	3499	55.3	673	12	US-10-032-717-12
7	3499	55.3	673	12	US-10-032-717-22
8	3499	55.3	670	12	US-10-032-717-40
9	3485.5	55.0	670	12	US-10-032-717-24
10	3485.5	55.0	670	12	US-10-032-717-44
11	3229	51.0	616	12	US-10-032-717-20
12	3217	50.8	620	12	US-10-032-717-30
13	3217	50.8	620	12	US-10-032-717-32
14	3217	50.8	620	12	US-10-032-717-42
15	3203.5	50.6	617	12	US-10-032-717-34
16	3203.5	50.6	617	12	US-10-032-717-46
17	2852	45.0	673	12	US-10-032-717-18
18	2821	44.6	667	12	US-10-032-717-8
19	2335	36.9	1186	10	US-09-826-660-23

20	2208	34.9	1163	10	US-09-756-526A-2	Sequence 2, Appli
21	2181.5	34.5	1316	9	US-10-120-544A-4	Sequence 4, Appli
22	2151.5	34.0	1163	10	US-09-826-660-21	Sequence 21, Appl
23	2116.5	33.4	1386	9	US-10-120-544A-6	Sequence 6, Appli
24	2061	32.5	1177	10	US-09-873-873-26	Sequence 26, Appl
25	2061	32.5	1177	10	US-09-873-873-28	Sequence 28, Appl
26	2053	32.4	1155	10	US-09-756-643-2	Sequence 2, Appli
27	2053	32.4	1177	10	US-09-873-873-10	Sequence 10, Appl
28	2053	32.4	1177	10	US-09-873-873-12	Sequence 12, Appl
29	2053	32.4	1177	10	US-09-873-873-14	Sequence 14, Appl
30	2050	32.4	1193	10	US-09-873-873-30	Sequence 30, Appl
31	2042	32.2	1177	10	US-09-873-873-34	Sequence 34, Appl
32	2028.5	32.0	1332	9	US-10-120-544A-18	Sequence 2, Appli
33	2023.5	32.0	1178	10	US-09-851-194-2	Sequence 6, Appli
34	2020	31.9	1174	10	US-09-826-660-6	Sequence 15, Appl
35	2007.5	31.7	1156	10	US-09-826-660-15	Sequence 20, Appl
36	2006.5	31.7	1344	9	US-10-120-544A-20	Sequence 2, Appli
37	1992	31.5	1148	10	US-09-826-660-2	Sequence 4, Appli
38	1827.5	28.9	1109	10	US-09-756-526A-4	Sequence 25, Appl
39	1274	20.1	643	10	US-09-826-660-25	Sequence 2, Appli
40	1194.5	18.9	644	10	US-09-943-692-2	Sequence 27, Appl
41	1079	17.0	655	10	US-09-826-660-27	Sequence 11, Appl
42	1070	16.9	547	10	US-09-826-660-11	Sequence 4, Appli
43	931	14.7	605	10	US-09-826-660-4	Sequence 6, Appli
44	687	10.8	1257	10	US-09-738-363-6	Sequence 4, Appli
45	672	10.6	333	10	US-09-851-194-4	

ALIGNMENTS

RESULT 1
US-10-032-717-2
; Sequence 2, Application US/10032717
; Patent No. US0020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032,717
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1206
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-032-717-2

Query Match	100.0%	Score 6332;	DB 12;	Length 1206;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1206;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MSPNNQNEVEIIDATPSTSVSNDSPNPPANETNALQNNNDYKDKLMSAGNASEYPGSP	60	
Db	1	MSPNNQNEVEIIDATPSTSVSNDSPNPPANETNALQNNNDYKDKLMSAGNASEYPGSP	60	
QY	61	EVLVSGDAAKAIDIVGKLLSGLVFPVGPVIVSLVLTQLIDILWPGEKSKQWIFMEQVE	120	
Db	61	EVLVSGDAAKAIDIVGKLLSGLVFPVGPVIVSLVLTQLIDILWPGEKSKQWIFMEQVE	120	
QY	121	ELINQIAEYARNKALSELEGLGNNTALQNTALEEENPNSRALDVRNRFEILDSLF	180	
Db	121	ELINQIAEYARNKALSELEGLGNNTALQNTALEEENPNSRALDVRNRFEILDSLF	180	

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181  TQMPFRVTNFEVPLTVYMAANLHLLKDAISFGEEGWSSTTTNNYYDQMKLTA 240
181  TQMPFRVTNFEVPLTVYMAANLHLLKDAISFGEEGWSSTTTNNYYDQMKLTA 240
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241  EYSDHCWKYETGLAKLKTSAQWVDYNOFREMVLAVLDVVALPNYDTRTPMETKA 300
301  QLTREVYTDPLGAVNVSSIGSWDKAPSGVIESVIRPPHVDYITGLTVYTSRSISS 360
301  QLTREVYTDPLGAVNVSSIGSWDKAPSGVIESVIRPPHVDYITGLTVYTSRSISS 360
361  ARYIRHWAGHQISYHRVSRGSLNQMYGTNQNLHSTSTFTDFTNYDIYKTLSDKDAVLLDIV 420
361  ARYIRHWAGHQISYHRVSRGSLNQMYGTNQNLHSTSTFTDFTNYDIYKTLSDKDAVLLDIV 420
421  YPGYTIFFGMPVEVEFPMVNLNTRTKLKNPVSKDIIASTRDSLELPPETSDQPNYE 480
421  YPGYTIFFGMPVEVEFPMVNLNTRTKLKNPVSKDIIASTRDSLELPPETSDQPNYE 480
481  SYSHRLCHITSIPATGNTTGLVPVFSWTHRSADLNNTIYSDKITQIPAVKWNLPVVPV 540
481  SYSHRLCHITSIPATGNTTGLVPVFSWTHRSADLNNTIYSDKITQIPAVKWNLPVVPV 540
541  VKPGHGTGGDLLOYNRSTSGVGLFLARYGLALEKAGKYRRLRYATDADIVLVNDAQI 600
541  VKPGHGTGGDLLOYNRSTSGVGLFLARYGLALEKAGKYRRLRYATDADIVLVNDAQI 600
601  QMPKTNWPGEDLTSKTPKVADATITLMLATDSSLALKHNGEDPNSTLSGIVYVDRIEPI 660
601  QMPKTNWPGEDLTSKTPKVADATITLMLATDSSLALKHNGEDPNSTLSGIVYVDRIEPI 660
661  PVDETVEAEODLEAAKAVNALFNTKDGRLPGVTDVEVQAANLVECLSDDLVPNEKRL 720
661  PVDETVEAEODLEAAKAVNALFNTKDGRLPGVTDVEVQAANLVECLSDDLVPNEKRL 720
721  LFDVAEREAKLSEARNLLODPDFQIEINGENGWTAISTGIEVIEGDALFKGRLYLPAGAREI 780
721  LFDVAEREAKLSEARNLLODPDFQIEINGENGWTAISTGIEVIEGDALFKGRLYLPAGAREI 780
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781  DTETPTLYLYKVEEGLKPYTRYRLRGFVSSQGLBIFIRHQTNRIVKRVNPDLLPDV 840
841  SPVNSDGSINRCSEOKVNSRLEVENRSGAHEPSIPIDTGEIDYENAGIWWGFKITDP 900
841  SPVNSDGSINRCSEOKVNSRLEVENRSGAHEPSIPIDTGEIDYENAGIWWGFKITDP 900
901  EGYATLGNLLEVEGPLSGDALERLQREOQWKIOMTRREETDRRYMASKQAVDRLYAD 960
901  EGYATLGNLLEVEGPLSGDALERLQREOQWKIOMTRREETDRRYMASKQAVDRLYAD 960
961  YQOQNLNPDVEITDLTAQDLIOSIPVYVNMFPPEIFGMNYTKETELTDRLQOAWSLYDQ 1020
961  YQOQNLNPDVEITDLTAQDLIOSIPVYVNMFPPEIFGMNYTKETELTDRLQOAWSLYDQ 1020
1021  RNAIPNGDFRNLGNMNAATPCVEVQOQINHTSVLVPNWDEQVSOQFTVQPNORVVLAVTA 1080
1021  RNAIPNGDFRNLGNMNAATPCVEVQOQINHTSVLVPNWDEQVSOQFTVQPNORVVLAVTA 1080
1081  RKEGVNGVYVSRDGGNOTETLTPSASDYDNTGMYNTQVSNNTNGYNTNNAYNTOASSTNG 1140
1081  RKEGVNGVYVSRDGGNOTETLTPSASDYDNTGMYNTQVSNNTNGYNTNNAYNTOASSTNG 1140
1141  YNANNMYNTQASNTNGYNTSVNDQGYITKTVPPTPYTDOMKIEMSETEGTYIESVE 1200
1141  YNANNMYNTQASNTNGYNTSVNDQGYITKTVPPTPYTDOMKIEMSETEGTYIESVE 1200
1201  LIYDVE 1206
1201  LIYDVE 1206
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RESULT 2
US-10-032-717-4
; Sequence 4, Application US/10032717
; Patent No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1 Proteins With
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032,717
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1210
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-032-717-4

Query Match      89.6%; Score 5673; DB 12; Length 1210;
Best Local Similarity 89.2%; Pred. No. 0;
Matches 1095; Conservative 33; Mismatches 61; Indels 38; Gaps 7;

QY 1 MSPNNQNEYIIDATPSTSVSNDNRYPFANEPTNALQNDYKDKLMSAGNASBYPGSP 60
DB 1 MSPNNQNEYIIDATPSTSVSNDNRYPFANEPTNALQNDYKDKLMSAGNASBYPGSP 60
QY 61 EVLVSGQDAAKAAIDIVGKLSGLGVFPVGPVLSVLTQILIDILMPSGKSKQWEIFMEQVE 120
DB 61 EVLVSGQDAAKAAIDIVGKLSGLGVFPVGPVLSVLTQILIDILMPSGKSKQWEIFMEQVE 120
QY 121 ELINQKIAYARNKALSELEGNNYQVLTALBEEWENPNSRRLDRVNRPEIILDSLF 160
DB 121 ELINQKIAYARNKALSELEGNNYQVLTALBEEWENPNSRRLDRVNRPEIILDSLF 160
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DB 181 TQMPFRVTNFEVPLTVYMAANLHLLKDAISFGEEGWSSTTTNNYYDQMKLTA 240
QY 241 EYSDHCWKYETGLAKLKTSAQWVDYNOFREMVLAVLDVVALPNYDTRTPMETKA 300
DB 241 EYSDHCWKYETGLAKLKTSAQWVDYNOFREMVLAVLDVVALPNYDTRTPMETKA 300
QY 301 QLTREVYTDPLGAVNVSSIGSWDKAPSGVIESVIRPPHVDYITGLTVYTSRSISS 360
DB 301 QLTREVYTDPLGAVNVSSIGSWDKAPSGVIESVIRPPHVDYITGLTVYTSRSISS 360
QY 361 ARYIRHWAGHQISYHRVSRGSLNQMYGTNQNLHSTSTFTDFTNYDIYKTLSDKDAVLLDIV 420
DB 361 ARYIRHWAGHQISYHRVSRGSLNQMYGTNQNLHSTSTFTDFTNYDIYKTLSDKDAVLLDIV 420
QY 421 YPGYTIFFGMPVEVEFPMVNLNTRTKLKNPVSKDIIASTRDSLELPPETSDQPNYE 480
DB 421 YPGYTIFFGMPVEVEFPMVNLNTRTKLKNPVSKDIIASTRDSLELPPETSDQPNYE 480
QY 481 SYSHRLCHITSIPATGNTTGLVPVFSWTHRSADLNNTIYSDKITQIPAVKWNLPVVPV 538
DB 481 SYSHRLCHITSIPATGNTTGLVPVFSWTHRSADLNNTIYSDKITQIPAVKWNLPVVPV 538
539 ----PVVKGPGHGTGGDLLOYNRSTSGVGLFLARYGLALEKAGKYRRLRYATDADIVL 593
541 GPNNTVVSGPFTGGGIKVRN-----GVIIISHMVKISDINKEYSMRIRYASANNTEP 595
594 HVNDAQIQM-----PKTNMNGEDLTSKTPKVADATITLMLATDSSLALKHNGEDPNSTLS 649
596 YINPSEENVKSHAQKTNRGEALTYNKFNYA-TLPPIKFTT-----TEPPTITLG 643
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QY 650 GI-----VVDRIEIPVDTEYEAEQDLBAKKAVALNFTNTKDLRPGVTDYEV 699
DB 644 AIPEAEPLGIEAVIDRIEIPVDTEYEAEQDLBAKKAVALNFTNTKDLRPGVTDYEV 703
QY 700 NOANLVCELSDDLYPEKRLLPDAVREAKRLSARNLLQDPDPFOEINGENGTASTGIE 759
DB 704 NOANLVCELSDDLYPEKRLLPDAVREAKRLSARNLLQDPDPFOEINGENGTASTGIE 763
QY 760 VIEGDALFKRYLRLPGAREIDTETPTLYLQKVEEGLVLPYTYRGRFVSSQGLEIF 819
DB 764 VIEGDALFKRYLRLPGAREIDTETPTLYLQKVEEGLVLPYTYRGRFVSSQGLEIF 823
QY 820 TIRHQTNRIVKRVNPDLLPVSFVNSDGSINRCSEQKYVNSRLEVENRSGEAHFSIPID 879
DB 824 TIRHQTNRIVKRVNPDLLPVSFVNSDGSINRCSEQKYVNSRLEVENRSGEAHFSIPID 883
QY 880 TGEIDVYENAGIIVGFKITDPEGYATILGNLELVEBGLSGDALRERQEQWIKIOMTRR 939
DB 884 TGEIDVYENAGIIVGFKITDPEGYATILGNLELVEBGLSGDALRERQEQWIKIOMTRR 943
QY 940 REETDRYMAKQAVDRLYADYQDQQLNPVIEITDLTAAQDLIOSIPVYNEMPEIPGM 999
DB 944 REETDRYMAKQAVDRLYADYQDQQLNPVIEITDLTAAQDLIOSIPVYNEMPEIPGM 1003
QY 1000 NYTKFTLTDLRQAWSLYDQRNAIPNGDFRNLGNNAATPGVEVQOINHTSVLVIPIWD 1059
DB 1004 NYTKFTLTDLRQAWSLYDQRNAIPNGDFRNLGNNAATPGVEVQOINHTSVLVIPIWD 1063
QY 1060 EQVSQOFTVQPNQRYLVRVARTKEGVNGYVSIIDGNGQTETLTFPSADSDYDNGMYNQV 1119
DB 1064 EQVSQOFTVQPNQRYLVRVARTKEGVNGYVSIIDGNGQTETLTFPSADSDYDNGMYNQV 1123
QY 1120 SNTNGYNNAYNTQASSTNGYNNANNAYNTQASNTNGYNNVNDQGYITKVTPIPY 1179
DB 1124 SNTNGYNNAYNTQASSTNGYNNANNAYNTQASNTNGYNNVNDQGYITKVTPIPY 1183
QY 1180 TDQWMIEMSETEGFFYIESVELIVDVE 1206
DB 1184 TDQWMIEMSETEGFFYIESVELIVDVE 1210

RESULT 3
US-10-032-717-10
; Sequence 10, Application US/10032717
; Patent No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
; FILE REFERENCE: 35718/237005
; CURRENT FILING DATE: 2001-10-23
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Maize optimized Cry1218-1
US-10-032-717-10

Query Match 55.4%; Score 3511; DB 12; Length 669;
Best Local Similarity 100.0%; Pred. No. 5.6e-239;
Matches 669; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MSPNNONEVEIIDATPSTSVSNDNRYNPFANEPTNALQNMDYKDYLKMSAGNASSEYRGSP 60
DB 1 MSPNNONEVEIIDATPSTSVSNDNRYNPFANEPTNALQNMDYKDYLKMSAGNASSEYRGSP 60
QY 61 EVLVSGQDAAKAAIDIVGKLLSGLVFPFVGVPIVSLYTLQILIDILWPSGEKQOWEIFMEQVE 120
DB 61 EVLVSGQDAAKAAIDIVGKLLSGLVFPFVGVPIVSLYTLQILIDILWPSGEKQOWEIFMEQVE 120
QY 121 ELINQKIAEYARKKALSELEGLGNNTQLYLTALBEEHENPNSGRALRDVNRREIFDLSLF 180
DB 121 ELINQKIAEYARKKALSELEGLGNNTQLYLTALBEEHENPNSGRALRDVNRREIFDLSLF 180
QY 181 TQMPSPFRVTNPFVPLTVYMAAANLHLLLDKASIFGEEWGWSTTTINNYDROMKLTATA 240
DB 181 TQMPSPFRVTNPFVPLTVYMAAANLHLLLDKASIFGEEWGWSTTTINNYDROMKLTATA 240
QY 241 EYSDHCVKMYETGLAKLKGTSKQWVDYNOQFREMTLAVLDVVALFPNYDTRTYPMETKA 300
DB 241 EYSDHCVKMYETGLAKLKGTSKQWVDYNOQFREMTLAVLDVVALFPNYDTRTYPMETKA 300
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QY 361 ARYIRHWAGHOISYHRVSRGSLNQMYGTNQLHSTSTDFNTYDIYKTLSDKAVLLDIV 420
DB 361 ARYIRHWAGHOISYHRVSRGSLNQMYGTNQLHSTSTDFNTYDIYKTLSDKAVLLDIV 420
QY 421 YPGYTYIFFGMEPEVFFMVNQLNNTKTLKYNPVSVDIIASTRSDSELELPPESTDQPNYE 480
DB 421 YPGYTYIFFGMEPEVFFMVNQLNNTKTLKYNPVSVDIIASTRSDSELELPPESTDQPNYE 480
QY 481 SYSHRLCHITSIPATGTYTGLVFPVSWTHRSADLNNTIYSDKITOIPAVKCDNLPVPV 540
DB 481 SYSHRLCHITSIPATGTYTGLVFPVSWTHRSADLNNTIYSDKITOIPAVKCDNLPVPV 540
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DB 541 VKGPGHGTGDLQYNRSTGSGVTLFLARYGLALEKAGKYRVRLYRATDADIVLHVNDQAI 600
QY 601 QMPKTNVPGEDLTSTKTFKVADAITTLNLTATDSSSLAKHNLGDEPNSTLSGIVVVDRIEFTI 660
DB 601 QMPKTNVPGEDLTSTKTFKVADAITTLNLTATDSSSLAKHNLGDEPNSTLSGIVVVDRIEFTI 660
QY 661 PVDETYEAE 669
DB 661 PVDETYEAE 669

RESULT 4
US-10-032-717-16
; Sequence 16, Application US/10032717
; Patent No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
; FILE REFERENCE: 35718/237005
; CURRENT FILING DATE: 2001-10-23
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 669
; TYPE: PRT
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ORGANISM: Bacillus thuringiensis (truncated)
US-10-032-717-16

Query Match 55.4%; Score 3511; DB 12; Length 669;
Best Local Similarity 100.0%; Pred. No. 5.6e-239; Indels 0; Gaps 0;
Matches 669; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPNNQNEVEIIDATPSTSVSNDNRYPPANEPTNALQNDYKDYKMSAGNASEYPGSP 60
DB 1 MSPNNQNEVEIIDATPSTSVSNDNRYPPANEPTNALQNDYKDYKMSAGNASEYPGSP 60

QY 61 EVLVSGODAAKAAIDIVGKLLSGLVGVPFVGSIVSLYQLIDILWPSEKQWEIFMEQVE 120
DB 61 EVLVSGODAAKAAIDIVGKLLSGLVGVPFVGSIVSLYQLIDILWPSEKQWEIFMEQVE 120

QY 121 ELINQKIAEYARNKALSELEGLGNNYQLYLTALBEEWENPNSGALRDVNRFEILDSLF 180
DB 121 ELINQKIAEYARNKALSELEGLGNNYQLYLTALBEEWENPNSGALRDVNRFEILDSLF 180

QY 181 TOYMPSPRVTFNFEVFPFLTVYMAAANLHLLKDAISIFGEENGWSTTTINNYDQMKLTA 240
DB 181 TOYMPSPRVTFNFEVFPFLTVYMAAANLHLLKDAISIFGEENGWSTTTINNYDQMKLTA 240

QY 241 EYSDHCVKYETGLAKLGTSAKQWVDYNOFRREMTLAVLDVVALFPNYDTRTYPMETKA 300
DB 241 EYSDHCVKYETGLAKLGTSAKQWVDYNOFRREMTLAVLDVVALFPNYDTRTYPMETKA 300

QY 301 QLTREVYTDPLGAVNVSSIGSWYDKAPSGVIESVIRPPHVFYITGLTVYTSRIS 360
DB 301 QLTREVYTDPLGAVNVSSIGSWYDKAPSGVIESVIRPPHVFYITGLTVYTSRIS 360

QY 361 ARYIRHWAGHQISYHRVSRGSLNQMGYNQNLHSTSTFDTNNDIYKTLKDAVLDDIV 420
DB 361 ARYIRHWAGHQISYHRVSRGSLNQMGYNQNLHSTSTFDTNNDIYKTLKDAVLDDIV 420

QY 421 YPGYTIFFGMEPEVEFFMVNQLNTRKTLKYNPVSQDIIASTRDSELELPETSDQNYE 480
DB 421 YPGYTIFFGMEPEVEFFMVNQLNTRKTLKYNPVSQDIIASTRDSELELPETSDQNYE 480

QY 481 SYSHRLCHITSIPATGNTTGLVPFVSWTHRSADLNNTIYSDKITQIPAVKCDNLPPVPV 540
DB 481 SYSHRLCHITSIPATGNTTGLVPFVSWTHRSADLNNTIYSDKITQIPAVKCDNLPPVPV 540

QY 541 VKGPGHTGGDLLQNRSTGSGVTLFLARYGLALEKAGKRYRLRYATDADIVLVNDAQI 600
DB 541 VKGPGHTGGDLLQNRSTGSGVTLFLARYGLALEKAGKRYRLRYATDADIVLVNDAQI 600

QY 601 QMPKTMNPGEDLTSKTPKVAADITTLNLTADSSSLAKHNLGDPNSTLSGIVYVDRIEPI 660
DB 601 QMPKTMNPGEDLTSKTPKVAADITTLNLTADSSSLAKHNLGDPNSTLSGIVYVDRIEPI 660

QY 661 PVDETYEAE 669
DB 661 PVDETYEAE 669

RESULT 5
US-10-032-717-6
; Sequence 6, Application US/10032717
; Patent No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1e1 Proteins With
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032.717
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838

PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis (truncated)
US-10-032-717-6

Query Match 55.3%; Score 3502; DB 12; Length 667;
Best Local Similarity 100.0%; Pred. No. 2.4e-238; Indels 0; Gaps 0;
Matches 667; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPNNQNEVEIIDATPSTSVSNDNRYPPANEPTNALQNDYKDYKMSAGNASEYPGSP 60
DB 1 MSPNNQNEVEIIDATPSTSVSNDNRYPPANEPTNALQNDYKDYKMSAGNASEYPGSP 60

QY 61 EVLVSGODAAKAAIDIVGKLLSGLVGVPFVGSIVSLYQLIDILWPSEKQWEIFMEQVE 120
DB 61 EVLVSGODAAKAAIDIVGKLLSGLVGVPFVGSIVSLYQLIDILWPSEKQWEIFMEQVE 120

QY 121 ELINQKIAEYARNKALSELEGLGNNYQLYLTALBEEWENPNSGALRDVNRFEILDSLF 180
DB 121 ELINQKIAEYARNKALSELEGLGNNYQLYLTALBEEWENPNSGALRDVNRFEILDSLF 180

QY 181 TOYMPSPRVTFNFEVFPFLTVYMAAANLHLLKDAISIFGEENGWSTTTINNYDQMKLTA 240
DB 181 TOYMPSPRVTFNFEVFPFLTVYMAAANLHLLKDAISIFGEENGWSTTTINNYDQMKLTA 240

QY 241 EYSDHCVKYETGLAKLGTSAKQWVDYNOFRREMTLAVLDVVALFPNYDTRTYPMETKA 300
DB 241 EYSDHCVKYETGLAKLGTSAKQWVDYNOFRREMTLAVLDVVALFPNYDTRTYPMETKA 300

QY 301 QLTREVYTDPLGAVNVSSIGSWYDKAPSGVIESVIRPPHVFYITGLTVYTSRIS 360
DB 301 QLTREVYTDPLGAVNVSSIGSWYDKAPSGVIESVIRPPHVFYITGLTVYTSRIS 360

QY 361 ARYIRHWAGHQISYHRVSRGSLNQMGYNQNLHSTSTFDTNNDIYKTLKDAVLDDIV 420
DB 361 ARYIRHWAGHQISYHRVSRGSLNQMGYNQNLHSTSTFDTNNDIYKTLKDAVLDDIV 420

QY 421 YPGYTIFFGMEPEVEFFMVNQLNTRKTLKYNPVSQDIIASTRDSELELPETSDQNYE 480
DB 421 YPGYTIFFGMEPEVEFFMVNQLNTRKTLKYNPVSQDIIASTRDSELELPETSDQNYE 480

QY 481 SYSHRLCHITSIPATGNTTGLVPFVSWTHRSADLNNTIYSDKITQIPAVKCDNLPPVPV 540
DB 481 SYSHRLCHITSIPATGNTTGLVPFVSWTHRSADLNNTIYSDKITQIPAVKCDNLPPVPV 540

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DB 541 VKGPGHTGGDLLQNRSTGSGVTLFLARYGLALEKAGKRYRLRYATDADIVLVNDAQI 600

QY 601 QMPKTMNPGEDLTSKTPKVAADITTLNLTADSSSLAKHNLGDPNSTLSGIVYVDRIEPI 660
DB 601 QMPKTMNPGEDLTSKTPKVAADITTLNLTADSSSLAKHNLGDPNSTLSGIVYVDRIEPI 660

QY 661 PVDETYEAE 667
DB 661 PVDETYEAE 667

RESULT 6
US-10-032-717-12
; Sequence 12, Application US/10032717
; Patent No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims

; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
; FILE REFERENCE: Pesticidal Activity Against Coleopterans
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032,717
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis (mutated)
US-10-032-717-12

Query Match 55.3%; Score 3499; DB 12; Length 673;
Best Local Similarity 99.4%; Pred. No. 3.9e-238;
Matches 669; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
1 MSPNNQNEYIIDATPSTSVSNDNRYPFANEPTNALQNDYKDYKMSAGNASEYFGSP 60
Db 1 MSPNNQNEYIIDATPSTSVSNDNRYPFANEPTNALQNDYKDYKMSAGNASEYFGSP 60
QY 61 EVLVSGQDAKAAIDIVGKLLSGLGVPFVGPVIVSLYLTQIDILWPSEKSKQWEIFMEQVE 120
Db 61 EVLVSGQDAKAAIDIVGKLLSGLGVPFVGPVIVSLYLTQIDILWPSEKSKQWEIFMEQVE 120
QY 121 ELINOKIAEYARNKALSELEGNGNYQLYLTALREWEENP-----NGSRALRDVNRFEIL 176
Db 121 ELINOKIAEYARNKALSELEGNGNYQLYLTALREWEENPNSRGRALRDVNRFEIL 180
QY 177 DLSFTQMPSPRVNPEVPLTVYMAANLHLLLLKDAISIFGEWGWSTTTINNYDROM 236
Db 181 DLSFTQMPSPRVNPEVPLTVYMAANLHLLLLKDAISIFGEWGWSTTTINNYDROM 240
QY 237 KLTAEYSDHCVKVYETGLAKLGTSAKQWVDYNOFRREMTLAVLDVVVALPNNYDTRTPM 296
Db 241 KLTAEYSDHCVKVYETGLAKLGTSAKQWVDYNOFRREMTLAVLDVVVALPNNYDTRTPM 300
QY 297 ETKAQLTRVYTDPLGAVNVSSIGSWYDKAPSGVIESVIRPHVFDYITGLTVYTQSR 356
Db 301 ETKAQLTRVYTDPLGAVNVSSIGSWYDKAPSGVIESVIRPHVFDYITGLTVYTQSR 360
QY 357 SISRARIHWAGHQISYHRVSRGSLNQMYGTNQLHSTSTFTFTNYDIYKTLSDKAVL 416
Db 361 SISRARIHWAGHQISYHRVSRGSLNQMYGTNQLHSTSTFTFTNYDIYKTLSDKAVL 420
QY 417 LDIVYPGYTIFFGMPVEPFVFNQNLNTRKTLKYNPVSKDIIASTRDSLELPPETSQ 476
Db 421 LDIVYPGYTIFFGMPVEPFVFNQNLNTRKTLKYNPVSKDIIASTRDSLELPPETSQ 480
QY 477 PNYESYSHRLCHITSIPTATGNTTGLVPVSWTHRSADLNTIYSDKITQIPAVKCDNLP 536
Db 481 PNYESYSHRLCHITSIPTATGNTTGLVPVSWTHRSADLNTIYSDKITQIPAVKCDNLP 540
QY 537 FVPVKGPGHTGGDLLOYNRSTGSGVTLFLARYGLALEKAGKYRRLRYATDADIVLHV 596
Db 541 FVPVKGPGHTGGDLLOYNRSTGSGVTLFLARYGLALEKAGKYRRLRYATDADIVLHV 600
QY 597 DAOIQMPKTNWPGEDLTSKTFKVADAITTLNLTATDSSSLAKHNLGDPNLSGIVYVDR 656
Db 601 DAOIQMPKTNWPGEDLTSKTFKVADAITTLNLTATDSSSLAKHNLGDPNLSGIVYVDR 660
QY 657 IEFIPVDETYEAE 669
Db 661 IEFIPVDETYEAE 673

RESULT 7

US-10-032-717-22
; Sequence 22, Application US/10032717
; Patent No. US20020151709A1
; GENERAL INFORMATION:

; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
; FILE REFERENCE: Pesticidal Activity Against Coleopterans
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032,717
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis (mutated)
US-10-032-717-22

Query Match 55.3%; Score 3499; DB 12; Length 673;
Best Local Similarity 99.4%; Pred. No. 3.9e-238;
Matches 669; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
1 MSPNNQNEYIIDATPSTSVSNDNRYPFANEPTNALQNDYKDYKMSAGNASEYFGSP 60
Db 1 MSPNNQNEYIIDATPSTSVSNDNRYPFANEPTNALQNDYKDYKMSAGNASEYFGSP 60
QY 61 EVLVSGQDAKAAIDIVGKLLSGLGVPFVGPVIVSLYLTQIDILWPSEKSKQWEIFMEQVE 120
Db 61 EVLVSGQDAKAAIDIVGKLLSGLGVPFVGPVIVSLYLTQIDILWPSEKSKQWEIFMEQVE 120
QY 121 ELINOKIAEYARNKALSELEGNGNYQLYLTALREWEENP-----NGSRALRDVNRFEIL 176
Db 121 ELINOKIAEYARNKALSELEGNGNYQLYLTALREWEENPNSRGRALRDVNRFEIL 180
QY 177 DLSFTQMPSPRVNPEVPLTVYMAANLHLLLLKDAISIFGEWGWSTTTINNYDROM 236
Db 181 DLSFTQMPSPRVNPEVPLTVYMAANLHLLLLKDAISIFGEWGWSTTTINNYDROM 240
QY 237 KLTAEYSDHCVKVYETGLAKLGTSAKQWVDYNOFRREMTLAVLDVVVALPNNYDTRTPM 296
Db 241 KLTAEYSDHCVKVYETGLAKLGTSAKQWVDYNOFRREMTLAVLDVVVALPNNYDTRTPM 300
QY 297 ETKAQLTRVYTDPLGAVNVSSIGSWYDKAPSGVIESVIRPHVFDYITGLTVYTQSR 356
Db 301 ETKAQLTRVYTDPLGAVNVSSIGSWYDKAPSGVIESVIRPHVFDYITGLTVYTQSR 360
QY 357 SISRARIHWAGHQISYHRVSRGSLNQMYGTNQLHSTSTFTFTNYDIYKTLSDKAVL 416
Db 361 SISRARIHWAGHQISYHRVSRGSLNQMYGTNQLHSTSTFTFTNYDIYKTLSDKAVL 420
QY 417 LDIVYPGYTIFFGMPVEPFVFNQNLNTRKTLKYNPVSKDIIASTRDSLELPPETSQ 476
Db 421 LDIVYPGYTIFFGMPVEPFVFNQNLNTRKTLKYNPVSKDIIASTRDSLELPPETSQ 480
QY 477 PNYESYSHRLCHITSIPTATGNTTGLVPVSWTHRSADLNTIYSDKITQIPAVKCDNLP 536
Db 481 PNYESYSHRLCHITSIPTATGNTTGLVPVSWTHRSADLNTIYSDKITQIPAVKCDNLP 540
QY 537 FVPVKGPGHTGGDLLOYNRSTGSGVTLFLARYGLALEKAGKYRRLRYATDADIVLHV 596
Db 541 FVPVKGPGHTGGDLLOYNRSTGSGVTLFLARYGLALEKAGKYRRLRYATDADIVLHV 600
QY 597 DAOIQMPKTNWPGEDLTSKTFKVADAITTLNLTATDSSSLAKHNLGDPNLSGIVYVDR 656
Db 601 DAOIQMPKTNWPGEDLTSKTFKVADAITTLNLTATDSSSLAKHNLGDPNLSGIVYVDR 660
QY 657 IEFIPVDETYEAE 669
Db 661 IEFIPVDETYEAE 673

RESULT 8
US-10-032-717-40
; Sequence 40, Application US/10032717
; Patent No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032,717
; PRIOR FILING DATE: 2001-10-23
; PRIOR FILING DATE: 60/242,838
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis (mutated)
US-10-032-717-40
Query Match 55.3%; Score 3499; DB 12; Length 673;
Best Local Similarity 99.4%; Pred. No. 3.9e-238;
Matches 669; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
QY 1 MSPNNQNEYIIDATPSTSVNSDNRYPFANEPTNALQNDYKDYKMSAGNASEYPCSP 60
DB 1 MSPNNQNEYIIDATPSTSVNSDNRYPFANEPTNALQNDYKDYKMSAGNASEYPCSP 60
QY 61 EVLVSGDAAKAIDIVKLLSGLGVFPVGVPIVSLYTLQIDILWPSEKQSEWEIFMEQVE 120
DB 61 EVLVSGDAAKAIDIVKLLSGLGVFPVGVPIVSLYTLQIDILWPSEKQSEWEIFMEQVE 120
QY 121 ELINOKIAEYARNKALSELGLGNNYQLYLTALKEEENP-----NGSRALRDVNRFEIL 176
DB 121 ELINOKIAEYARNKALSELGLGNNYQLYLTALKEEENPFLRMSNGSRALRDVNRFEIL 180
QY 177 DSLFTQMPSPRVNTFVPEPLTVYMAANLHLLKXDAISIFGEWGWSTTTINNYDROM 236
DB 181 DSLFTQMPSPRVNTFVPEPLTVYMAANLHLLKXDAISIFGEWGWSTTTINNYDROM 240
QY 237 KLTAEYSDHCWKVYETGLAKLKGTSAKQWVDYNOFRREMTLAVLDVVALPNDYDTRTPM 296
DB 241 KLTAEYSDHCWKVYETGLAKLKGTSAKQWVDYNOFRREMTLAVLDVVALPNDYDTRTPM 300
QY 297 ETKAQLTREYVTDPLGAVNVSSIGSWYDKAPSGVIESVIRPHVFDYITGLTVYTQSR 356
DB 301 ETKAQLTREYVTDPLGAVNVSSIGSWYDKAPSGVIESVIRPHVFDYITGLTVYTQSR 360
QY 357 SSSARYIRHWAGHQISYHRVSRGSLNQMYGTNQNLHSTSTFDFTNYDIYKTLSDKDAVL 416
DB 361 SSSARYIRHWAGHQISYHRVSRGSLNQMYGTNQNLHSTSTFDFTNYDIYKTLSDKDAVL 420
QY 417 LDIVYGYTYIFFGMPVEVFMVNLNTRKTLKYNPVSKDIIASTRDSSELELPETSQ 476
DB 421 LDIVYGYTYIFFGMPVEVFMVNLNTRKTLKYNPVSKDIIASTRDSSELELPETSQ 480
QY 477 PNTESYSHRLCHITSIPATGNTTGLVPVSWTHRSADLNTIYSDKTIQIPAVKCDNLP 536
DB 481 PNTESYSHRLCHITSIPATGNTTGLVPVSWTHRSADLNTIYSDKTIQIPAVKCDNLP 540
QY 537 FVPVWGPCHTGDLQYNRSTSGVTLFLARYGLALEKAGKVRVLRATDADIVLHVN 596
DB 541 FVPVWGPCHTGDLQYNRSTSGVTLFLARYGLALEKAGKVRVLRATDADIVLHVN 600
QY 597 DAQIQMPKTMNPGEDLTSKTFKVADAITTLNLATDSSLALKHNLGDPNSTLSGIVVYDR 656
|||||

DB 601 DAQIQMPKTMNPGEDLTSKTFKVADAITTLNLATDSSLALKHNLGDPNSTLSGIVVYDR 660
QY 657 IEFIPVDETYEAE 669
|||||
DB 661 IEFIPVDETYEAE 673
RESULT 9
US-10-032-717-24
; Sequence 24, Application US/10032717
; Patent No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032,717
; PRIOR FILING DATE: 2001-10-23
; PRIOR FILING DATE: 60/242,838
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 670
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis (mutated)
US-10-032-717-24

Query Match 55.0%; Score 3485.5; DB 12; Length 670;
Best Local Similarity 99.6%; Pred. No. 3.5e-237;
Matches 667; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 1 MSPNNQNEYIIDATPSTSVNSDNRYPFANEPTNALQNDYKDYKMSAGNASEYPCSP 60
DB 1 MSPNNQNEYIIDATPSTSVNSDNRYPFANEPTNALQNDYKDYKMSAGNASEYPCSP 60
QY 61 EVLVSGDAAKAIDIVKLLSGLGVFPVGVPIVSLYTLQIDILWPSEKQSEWEIFMEQVE 120
DB 61 EVLVSGDAAKAIDIVKLLSGLGVFPVGVPIVSLYTLQIDILWPSEKQSEWEIFMEQVE 120
QY 121 ELINOKIAEYARNKALSELGLGNNYQLYLTALKEEENP-----NGSRALRDVNRFEILDSL 179
DB 121 ELINOKIAEYARNKALSELGLGNNYQLYLTALKEEENPPLKMSRALRDVNRFEILDSL 180
QY 180 FTQYMPSPRVNTFVPEPLTVYMAANLHLLKXDAISIFGEWGWSTTTINNYDROMKLT 239
DB 181 FTQYMPSPRVNTFVPEPLTVYMAANLHLLKXDAISIFGEWGWSTTTINNYDROMKLT 240
QY 240 AEYSDHCWKVYETGLAKLKGTSAKQWVDYNOFRREMTLAVLDVVALFPNDYDTRTPMETK 299
DB 241 AEYSDHCWKVYETGLAKLKGTSAKQWVDYNOFRREMTLAVLDVVALFPNDYDTRTPMETK 300
QY 300 AQLTREYVTDPLGAVNVSSIGSWYDKAPSGVIESVIRPHVFDYITGLTVYTQSRSSIS 359
DB 301 AQLTREYVTDPLGAVNVSSIGSWYDKAPSGVIESVIRPHVFDYITGLTVYTQSRSSIS 360
QY 360 SARYIRHWAGHQISYHRVSRGSLNQMYGTNQNLHSTSTFDFTNYDIYKTLSDKDAVLDDI 419
DB 361 SARYIRHWAGHQISYHRVSRGSLNQMYGTNQNLHSTSTFDFTNYDIYKTLSDKDAVLDDI 420
QY 420 VYPGYTYIFFGMPVEVFMVNLNTRKTLKYNPVSKDIIASTRDSSELELPETSQPNY 479
DB 421 VYPGYTYIFFGMPVEVFMVNLNTRKTLKYNPVSKDIIASTRDSSELELPETSQPNY 480
QY 480 ESYSHRLCHITSIPATGNTTGLVPVSWTHRSADLNTIYSDKTIQIPAVKCDNLPFPVP 539
DB 481 ESYSHRLCHITSIPATGNTTGLVPVSWTHRSADLNTIYSDKTIQIPAVKCDNLPFPVP 540
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Qy 540 VVKGPGHTGGDLLOYNRSTGSGVTLFLARYGLALEKAGKYRRLRYATDADIVLHVNDQAQ 599
Db 541 VVKGPGHTGGDLLOYNRSTGSGVTLFLARYGLALEKAGKYRRLRYATDADIVLHVNDQAQ 600
Qy 600 IOMPKTNWPGEDLTSKTFKVADAITTLNLTATDSSSLAKHNLGDEPNSTLSGIVVVDRIEF 659
Db 601 IOMPKTNWPGEDLTSKTFKVADAITTLNLTATDSSSLAKHNLGDEPNSTLSGIVVVDRIEF 660
Qy 660 IPVDITYEAE 669
Db 661 IPVDITYEAE 670

RESULT 10
US-10-032-717-44
; Sequence 44, Application US/10032717
; Patent No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032,717
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 670
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis (mutated)
US-10-032-717-44

Query Match 55.0%; Score 3485.5; DB 12; Length 670;
Best Local Similarity 99.6%; Pred. No. 3.5e-237;
Matches 667; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 1 MSPNNQNEYIIDATPSTSVSNDNRYPFANEPTNALQMDYKYLKMSAGNASYPGSP 60
Db 1 MSPNNQNEYIIDATPSTSVSNDNRYPFANEPTNALQMDYKYLKMSAGNASYPGSP 60
Qy 61 EVLVSGQDAKAAIDIVGKLLSGLGVFPVGPVIVSLYTLQIDILWPSGKSWEIFMEQVE 120
Db 61 EVLVSGQDAKAAIDIVGKLLSGLGVFPVGPVIVSLYTLQIDILWPSGKSWEIFMEQVE 120
Qy 121 ELINQKIAEYARNKALSLEGLGNNYQLYLTALEWEENP-NGSRALDRVRNRPILDSL 179
Db 121 ELINQKIAEYARNKALSLEGLGNNYQLYLTALEWEENP-NGSRALDRVRNRPILDSL 180
Qy 180 FTQYMPFRVTFNFEVFLTVYAMAANLHLLKLDASIFGEEGWSVTTNNYDQMKLT 239
Db 181 FTQYMPFRVTFNFEVFLTVYAMAANLHLLKLDASIFGEEGWSVTTNNYDQMKLT 240
Qy 240 AEYSDHCVKVYETGLAKGTSKQWVDYNQPREMTLAVLDVVALFPNYDTRTPMETK 299
Db 241 AEYSDHCVKVYETGLAKGTSKQWVDYNQPREMTLAVLDVVALFPNYDTRTPMETK 300
Qy 300 AOLTRVYTDPLGAVNVSSIGSWYDKAPSGVIESVIRPPHVDYITGLTYTQSRIS 359
Db 301 AOLTRVYTDPLGAVNVSSIGSWYDKAPSGVIESVIRPPHVDYITGLTYTQSRIS 360
Qy 360 SARYIRHWAGHOISYHRVSRGSLQOMYGTNQNHLSTSTFDTNNDIYKLSKDAVLDDI 419
Db 361 SARYIRHWAGHOISYHRVSRGSLQOMYGTNQNHLSTSTFDTNNDIYKLSKDAVLDDI 420
Qy 420 VYPGYTYIFFGMEVEFFMVNQLNTRKTLKYNPVSKDIIASTRDSLELPPETSDQPNY 479
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Db 421 VYPGYTYIFFGMEVEFFMVNQLNTRKTLKYNPVSKDIIASTRDSLELPPETSDQPNY 480
Qy 480 ESYSHRLCHITSIPATGNTTGLVPVFSWTHRSADLNTTIYSDKITQIPAVKCMWNLFPVP 539
Db 481 ESYSHRLCHITSIPATGNTTGLVPVFSWTHRSADLNTTIYSDKITQIPAVKCMWNLFPVP 540
Qy 540 VVKGPGHTGGDLLOYNRSTGSGVTLFLARYGLALEKAGKYRRLRYATDADIVLHVNDQAQ 599
Db 541 VVKGPGHTGGDLLOYNRSTGSGVTLFLARYGLALEKAGKYRRLRYATDADIVLHVNDQAQ 600
Qy 600 IOMPKTNWPGEDLTSKTFKVADAITTLNLTATDSSSLAKHNLGDEPNSTLSGIVVVDRIEF 659
Db 601 IOMPKTNWPGEDLTSKTFKVADAITTLNLTATDSSSLAKHNLGDEPNSTLSGIVVVDRIEF 660
Qy 660 IPVDITYEAE 669
Db 661 IPVDITYEAE 670

RESULT 11
US-10-032-717-20
; Sequence 20, Application US/10032717
; Patent No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032,717
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 616
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis (truncated)
US-10-032-717-20

Query Match 51.0%; Score 3229; DB 12; Length 616;
Best Local Similarity 100.0%; Pred. No. 3.3e-219;
Matches 616; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 48 MSAGNASYPGSPVLYSGQDAKAAIDIVGKLLSGLGVFPVGPVIVSLYTLQIDILWPSG 107
Db 1 MSAGNASYPGSPVLYSGQDAKAAIDIVGKLLSGLGVFPVGPVIVSLYTLQIDILWPSG 60
Qy 108 EKSQWEIFMEQVEELINQKIAEYARNKALSLEGLGNNYQLYLTALEWEENPNSRALR 167
Db 61 EKSQWEIFMEQVEELINQKIAEYARNKALSLEGLGNNYQLYLTALEWEENPNSRALR 120
Qy 168 DVNRNRPILDSLFTQYMPFRVTFNFEVFLTVYAMAANLHLLKLDASIFGEEGWSVTT 227
Db 121 DVNRNRPILDSLFTQYMPFRVTFNFEVFLTVYAMAANLHLLKLDASIFGEEGWSVTT 180
Qy 228 INNNYDQMKLTASYSDHCVKVYETGLAKGTSKQWVDYNQPREMTLAVLDVVALFP 287
Db 181 INNNYDQMKLTASYSDHCVKVYETGLAKGTSKQWVDYNQPREMTLAVLDVVALFP 240
Qy 288 NYDTRTPMETKAOQLTRVYTDPLGAVNVSSIGSWYDKAPSGVIESVIRPPHVDYIT 347
Db 241 NYDTRTPMETKAOQLTRVYTDPLGAVNVSSIGSWYDKAPSGVIESVIRPPHVDYIT 300
Qy 348 GLTYTQSRISYSSARYIRHWAGHOISYHRVSRGSLQOMYGTNQNHLSTSTFDTNNDIY 407
Db 301 GLTYTQSRISYSSARYIRHWAGHOISYHRVSRGSLQOMYGTNQNHLSTSTFDTNNDIY 360
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QY	287	PNYDTRTPMETKAQLTREYVTDPLGAVNVSSIGSWYDKAPSGFVIESSVIRPPHVPDYI	346
Db	241	PNYDTRTPMETKAQLTREYVTDPLGAVNVSSIGSWYDKAPSGFVIESSVIRPPHVPDYI	300
QY	347	TGLTVYTQSRSSISSARYIRHWAGHQISYHRVSRGSNLQOMYGTNQNHLHSTSTFDFTNYDI	406
Db	301	TGLTVYTQSRSSISSARYIRHWAGHQISYHRVSRGSNLQOMYGTNQNHLHSTSTFDFTNYDI	360
QY	407	YKTLSDKDAVLDDIVYPGYTIFFGMPVEPFMVNQLNTRKTLKYNPVSXDIIASTRDSE	466
Db	361	YKTLSDKDAVLDDIVYPGYTIFFGMPVEPFMVNQLNTRKTLKYNPVSXDIIASTRDSE	420
QY	467	LELPPESTDQPNYESYSHRLCHITSIPATGNTTGLVPVFSWTHRSADLNNTIYSDKITQI	526
Db	421	LELPPESTDQPNYESYSHRLCHITSIPATGNTTGLVPVFSWTHRSADLNNTIYSDKITQI	480
QY	527	PAVKCNDNLPFPVVKPGHGTGGDLLQYNRSTGSGVTLFLARYGLALEKAGKYRRLRYA	586
Db	481	PAVKCNDNLPFPVVKPGHGTGGDLLQYNRSTGSGVTLFLARYGLALEKAGKYRRLRYA	540
QY	587	TDADIVLHVNDAOIQMPKTNPGEDLTSTKFKVADAITTLNLATDSSIALKHNLGEDPNS	646
Db	541	TDADIVLHVNDAOIQMPKTNPGEDLTSTKFKVADAITTLNLATDSSIALKHNLGEDPNS	600
QY	647	TLSGIVYVDRIEIPVD	663
Db	601	TLSGIVYVDRIEIPVD	617

Search completed: January 7, 2003, 05:26:10
Job time : 45 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 7, 2003, 00:49:27 ; Search time 89 seconds
(without alignments)
12477.265 Million cell updates/sec

Title: US-10-032-717-1
Perfect score: 3621
Sequence: 1 atgagtcacaaataatcaaaa.....tgattgacagtagagtaa 3621

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/1/ina/5A COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTRUS COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2565.2	70.8	3507	1	US-08-315-468-3
2	1812.2	50.0	3471	1	US-07-876-280-29
3	1812.2	50.0	3471	1	US-07-812-180A-1
4	1812.2	50.0	3471	1	US-08-315-468-1
5	1812.2	50.0	3471	4	US-07-941-650A-1
6	1180	32.6	3797	1	US-07-915-203-1
7	1180	32.6	3797	1	US-08-272-887-1
8	1180	32.6	3797	1	US-08-789-449-1
9	883.4	24.4	4344	2	US-08-532-547-4
10	883.4	24.4	4344	2	US-08-379-656B-4
11	883.4	24.4	4344	3	US-08-455-838-4
12	883.4	24.4	4344	3	US-09-019-809-4
13	883.4	24.4	4344	4	US-09-471-177-4
14	882.8	24.4	3471	4	US-09-002-285-73
15	848.6	23.4	3759	1	US-08-542-921-1
16	848.6	23.4	3759	2	US-08-880-685-1
17	848.6	23.4	3759	2	US-08-880-684-1
18	822.2	22.7	3453	4	US-09-002-285-75
19	734.2	20.3	3411	4	US-09-002-285-77
20	733.6	20.3	3414	1	US-07-973-320-3
21	731.4	20.2	3414	1	US-07-973-320-1
22	678	18.7	3934	1	US-08-100-709-3
23	678	18.7	3934	1	US-08-176-865-3
24	678	18.7	3934	1	US-08-474-038-3
25	678	18.7	3934	2	US-08-779-046-3
26	678	18.7	3934	2	US-08-881-340-3
27	673.6	18.6	4074	1	US-08-377-690-1

28	659.2	18.2	3684	1	US-08-448-170-7
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35	615.4	17.0	3567	3	US-09-314-093-58
36	615.4	17.0	3567	3	US-09-250-848-5
37	615.4	17.0	3567	4	US-09-251-885-5
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39	615.4	17.0	3567	4	US-09-337-635-58
40	615.4	17.0	3567	4	US-09-337-280-5
41	615.4	17.0	3567	4	US-09-337-280-58
42	613.8	17.0	3567	1	US-08-602-737-1
43	613.8	17.0	3567	2	US-08-980-071-1
44	613.8	17.0	3567	2	US-08-980-071-9
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ALIGNMENTS

RESULT 1
US-08-315-468-3
; Sequence 3, Application US/08315468
; Patent No. 5554534
; GENERAL INFORMATION:
; APPLICANT: Michaels, Tracy Ellis
; APPLICANT: Foncecerra, Luis
; APPLICANT: Narva, Kenneth E.
; TITLE OF INVENTION: Process for Controlling Scarab Pests
; TITLE OF INVENTION: with Bacillus thuringiensis Isolates
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/315,468
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/014,941
; FILING DATE: 01 FEB 1993
; APPLICATION NUMBER: 07/828,430
; FILING DATE: 30-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/808,316
; FILING DATE: 16-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MAY3.C2
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3507 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO

Db	3046	CGAAACGCTATACCAAATGGAGATTACCGAAATGAATTAAGTAATTGGAATCAACATCT	3105
Qy	3121	GGCGTAGAAGTACAAACAATCAATCATACATCTGCTCTTGATTCACAACTGGGATGAG	3180
Db	3106	GGTGTGAATGTACACAACAATCAATCATACATCTGCTCTTGATTCAAAATCTGGAATGAA	3165
Qy	3181	CAAGTTTCGCAACAGTTTACAGTTCCAACCGAATCAAGAATATGTGTTACAGAGTTACTGCG	3240
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Db	3346	AATACAAACGGATATAACAAATAGTGTGTACATGATCAACCGGCTATATCA	3399

US-07-876-280-29

Sequence 29, Application US/07876280
Patent No. 5262158
GENERAL INFORMATION:
APPLICANT: Payne, Jewel M.
APPLICANT: Cannon, Raymond J.C.
APPLICANT: Bagley, Angela L.
TITLE OF INVENTION: No. 5262158el Bacillus thuringiensis
TITLE OF INVENTION: Controlling Acarides
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/876,280
FILING DATE: 19920430
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M/S 104
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 3471 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bacillus thuringiensis
STRAIN: kumamotoensis
INDIVIDUAL ISOLATE: FS50C
IMMEDIATE SOURCE:
CLONE: E. coli NM522(pMYC21320) NRRL B-18769

Db 3191 ATTCTGTCATCAACGCAACCGAATGTAAATAATGTACCGGATGATTTGCTGCCAGATGTA 3250
Qy 2521 TCTCTCTGTTAACTCGGATGTTAGTATCAATCGATGCGCGCAACAAAGATGATGTAATGAC 2580
Db 3251 TCTCTCTGTTAACTCGGATGTTAGTATCAATCGATGCGCGCAACAAAGATGATGTAATGAC 3310
Qy 2581 CGTTAGAAAGTAGAAAACCGTTCTGCTGTAAGCGCGATGATTTCTTATCTTCTTATGATACA 2640
Db 3311 CGTTAGAAAGTAGAAAACCGTTCTGCTGTAAGCGCGATGATTTCTTATCTTCTTATGATACA 3370
Qy 2641 GGTGAAATCGATTACAAATGCAAAATGCGAATATGTTGTTGATTTAAAGATTACGACCA 2700
Db 3371 GGTGAAATCGATTACAAATGCGAATATGTTGTTGATTTAAAGATTACGACCA 3430
Qy 2701 GAGGATATGCAACACTCGGAAACCTAGAAATTTGGTCCGAGAGGCGCTTTATCAGAGAC 2760
Db 3431 GAGGATATGCAACACTCGGAAACCTAGAAATTTGGTCCGAGAGGCGCTTTATCAGAGAC 3490
Qy 2761 GCNTTGAAGCGTTCCGAAAGAGAGAAACAAACAGTGAAGATTTCAATGACAAAGAGAGCT 2820
Db 3491 GCNTTGAAGCGTTCCGAAAGAGAGAAACAAACAGTGAAGATTTCAATGACAAAGAGAGCT 3550
Qy 2821 GAAGAAACAGATAGAGAGATATGTCATCGAACAAGCGGTAGATCGTTTATATGCGAT 2880
Db 3551 GAAGAAACAGATAGAGAGATATGTCATCGAACAAGCGGTAGATCGTTTATATGCGAT 3610
Qy 2881 TATCAGGATCAGCAACTGATCTGATGATGAGATTTACAGATCTTACTCGCGCCCAAGAT 2940
Db 3611 TATCAGGATCAGCAACTGATCTGATGATGAGATTTACAGATCTTACTCGCGCCCAAGAT 3670
Qy 2941 CTGATCAGTCCATCTCTTACGATATATACGAAATGTTCCGAAATATCCGAGGATGAAC 3000
Db 3671 CTGATCAGTCCATCTCTTACGATATATACGAAATGTTCCGAAATATCCGAGGATGAAC 3730
Qy 3001 TATACGAGTTTACAGATTTACAGATCGATCGATCGAACAAGCGGTGAGTTGATGATCAG 3060
Db 3731 TATACGAGTTTACAGATTTACAGATCGATCGATCGAACAAGCGGTGAGTTGATGATCAG 3790
Qy 3061 CGAAATGCCATACCAATGGTGAATTTTGAATGGTGAATGGAATGCAAGCGCT 3120
Db 3791 CGAAATGCCATACCAATGGTGAATTTTGAATGGTGAATGGAATGCAAGCGCT 3850
Qy 3121 GCGGTAGAGTACAAATCAATCATCATCTGCTCTGTTGATTCGAAATGCGGATGAG 3180
Db 3851 GCGGTAGAGTACAAATCAATCATCATCTGCTCTGTTGATTCGAAATGCGGATGAG 3910
Qy 3181 CAAGTTTCGCAACAGTTTACAGTTCAACCGAATCAAGATATGTTGATGATGATGATGATG 3240
Db 3911 CAAGTTTCGCAACAGTTTACAGTTCAACCGAATCAAGATATGTTGATGATGATGATGATG 3970
Qy 3241 AGAAAGAGAGGAGTGAAGAAATGATATGTAAGTATCGTGAATGGAATCAACAGAA 3300
Db 3971 AGAAAGAGAGGAGTGAAGAAATGATATGTAAGTATCGTGAATGGAATCAACAGAA 4030
Qy 3301 ACGTTACTTTTGTAGTGAAGGATTAAGTATCAAAATGGAATGTAATACGCAAGTGC 3360
Db 4031 ACGTTACTTTTGTAGTGAAGGATTAAGTATCAAAATGGAATGTAATACGCAAGTGC 4090
Qy 3361 AATACAAATGATATACAAATATGATATGATATGATATGATATGATATGATATGATATGAT 3420
Db 4091 AATACAAATGATATACAAATATGATATGATATGATATGATATGATATGATATGATATGAT 4150
Qy 3421 TATACGCAATATATATGATATGATATGATATGATATGATATGATATGATATGATATGAT 3480
Db 4151 TATACGCAATATATATGATATGATATGATATGATATGATATGATATGATATGATATGAT 4210
Qy 3481 AGTGTGATCAATGATCAAAACCGGCTATATCAAAACAGTGAATCAATCCCGTATACA 3540
Db 4211 AGTGTGATCAATGATCAAAACCGGCTATATCAAAACAGTGAATCAATCCCGTATACA 4270
Qy 3541 GATCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3600

Db 4271 GATCAAAATGTGATGTAGATGAGTGAAGAGGATGATCTTATATAGAAAGTGTAGAA 4330
Qy 3601 TTGATTTAGACGCTAGAGTAA 3621
Db 4331 TTGATTTAGACGCTAGAGTAA 4351

RESULT 3
US-10-032-717-3
; Sequence 3, Application US/10032717
; Patent No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032,717
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3633
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3633)
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Cry12Ib-2
US-10-032-717-3

Query Match 87.0%; Score 3151.8; DB 12; Length 3633;
Best Local Similarity 92.1%; Pred. No. 0;
Matches 3353; Conservative 0; Mismatches 262; Indels 24; Gaps 2;

Qy 1 ATGAGTCCAAATATCAAAATGAATATGAATATATAGATGCGACACCTTCTTACTCTGTA 60
Db 1 ATGAGTCCAAATATCAAAATGAATATGAATATATAGATGCGACACCTTCTTACTCTGTA 60
Qy 61 TCCATGATCTTACAGATACCTTTTGGGATGAGCGCAACAAATGCGCTACCAATATG 120
Db 61 TCCATGATCTTACAGATACCTTTTGGGATGAGCGCAACAAATGCGCTACCAATATG 120
Qy 121 GATTATAAAGATTATTTAAATAATGCTGCGGAAATGCTAGTGAATACCTTGGTTCACT 180
Db 121 GATTATAAAGATTATTTAAATAATGCTGCGGAAATGCTAGTGAATACCTTGGTTCACT 180
Qy 181 GAAGTACTTGTAGCGGACAAAGATGCAAGTAAAGCCCAATGATAGTAGGTAATAATTA 240
Db 181 GAAGTACTTGTAGCGGACAAAGATGCAAGTAAAGCCCAATGATAGTAGGTAATAATTA 240
Qy 241 CTATCAGGTTTAGGGTCCCATTTTGGGCGGATAGTGAATCTTTTATCTCAACTTATT 300
Db 241 CTATCAGGTTTAGGGTCCCATTTTGGGCGGATAGTGAATCTTTTATCTCAACTTATT 300
Qy 301 GATATTTCTGGGCTTCCAGGGAAGAAAGATCAATGCGGAAATTTTATGGAACAGATGAA 360
Db 301 GATATTTCTGGGCTTCCAGGGAAGAAAGATCAATGCGGGAATTTTATGGAACAGATGAA 360
Qy 361 GAAGTCAATTAATCAAAATATAGCAAGATATGCAAGGAATTAAGCGCTTTTCGGAATTGAA 420
Db 361 GAAGTCAATTAATCAAAATATAGCAAGATATGCAAGGAATTAAGCGCTTTTCGGAATTGAA 420
Qy 421 GGATTAAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 480

QY	2623	TCTATTTCCTATTGATACAGGTGAAATCGATTCAATGAAATGCAAGAAATATCGGTTTGG	2688
DB	2635	TCTATTTCCTATTGATACAGGTGAAATCGATTCAATGAAATGCAAGAAATATCGGTTTGG	2694
QY	2683	TTTAAAGATTACGGACCCAGAGGGATATGCAACTCTCGGAAACCTTAGAATTTGGTCGAGAG	2742
DB	2695	TTTAAAGATTACGGACCCAGAGGGATATGCAACTCTCGGAAACCTTAGAATTTGGTCGAGAG	2754
QY	2743	GGACCTTTATCAGGAGACGCATTAGAACGCTTCCAAAGAGAAGAACCAACAGTGGAAAGATT	2802
DB	2755	GGACCTTTATCAGGAGACGCATTAGAACGCTTCCAAAGAGAAGAACCAACAGTGGAAAGATT	2814
QY	2803	CAAAATGACAAGAGACGTCGAGGAACAGATAGAGAGGTATATGCGATCGAAAACAGCGGTA	2862
DB	2815	CAAAATGACAAGAGACGTCGAGGAACAGATAGAGAGGTATATGCGATCGAAAACAGCGGTA	2874
QY	2863	GATCGTTTATATGCCGATTATCAGGATCAGCAACTGAAATCCTGATGTAGAGATTACAGAT	2922
DB	2875	GATCGTTTATATGCCGATTATCAGGATCAGCAACTGAAATCCTGATGTAGAGATTACAGAT	2934
QY	2923	CTTACTGCGGCCCAAGATCTGATPACAGTCCATTCTTACGTATATACGAAATGTTTCCCA	2982
DB	2935	CTTACTGCGGCCCAAGATCTGATPACAGTCCATTCTTACGTATATACGAAATGTTTCCCA	2994
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DB	2995	GAATATCACAGGGAGTAACATATATACGAAAGTTTACAGATTATACAGATCGATCCCAACAGCG	3054
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DB	3055	TGGAGTTTGTATGATCAGCGAAATGCCATACCAATGCGTCAATTTTCGAAATGCGTTAAAGT	3114
QY	3103	AAITGGAAITGCAACGCGCTGGCGTAGAAGTACACAAATCAATCATCATCTGCTCTTG	3162
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QY	3163	ATTTCAAAATCGGGATCAGCAAGTTTTCGCAACAGTTTACAGTTCCAACCGATCAAGATAT	3222
DB	3175	ATTTCAAAATCGGGATCAGCAAGTTTTCGCAACAGTTTACAGTTCCAACCGATCAAGATAT	3234
QY	3223	GTGTTACGAGTTACTCGCGAAGAAAGGGGTAGGAAATGGAATGTAAAGTATCCGTGAT	3282
DB	3235	GTGTTACGAGTTACTCGCGAAGAAAGGGGTAGGAAATGGAATGTAAAGTATCCGTGAT	3294
QY	3283	GGTGGAAATCAACAGAAACGCTTACTTTTAGTGCAGCGATTATGATCAAAATGGAATG	3342
DB	3295	GGTGGAAATCAACAGAAACGCTTACTTTTAGTGCAGCGATTATGATCAAAATGGAATG	3354
QY	3343	TATTAATACGCAAGTGTCCAAATACAAATGATATAACACAAATAATCGGTATATAACAA	3402
DB	3355	TATTAATACGCAAGTGTCCAAATACAAATGATATAACACAAATAATCGGTATATAACAA	3414
QY	3403	GCATCGAGTACAAACGGATATAACGCCAAATAATATGTATAATACGCAAGCATCGAATACA	3462
DB	3415	GCATCGAGTACAAACGGATATAACGCCAAATAATATGTATAATACGCAAGCATCGAATACA	3474
QY	3463	AACGGATATAACAAATAGTGTGTACATATGATCAAAACGGCTATATATCAAAAAACAGTG	3522
DB	3475	AACGGATATAACAAATAGTGTGTATCAATATGATCAAAACGGCTATATATCAAAAAACAGTG	3534
QY	3523	ACATTATCCCGGTATACAGATCAAAATGTGGAATGAGATGAGTGCAGACAGAGGTACATTTC	3582
DB	3535	ACATTATCCCGGTATACAGATCAAAATGTGGAATGAGATGAGTGCAGACAGAGGTACATTTC	3594
QY	3583	TATATAGAAAGTGTAGAAATGATTGTAGACGTAGAGTAA	3621
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RESULT 4

RESULT 4
US-10-032-717-28
; Sequence 28, Application US/10032717
; Patent No. US20020151709A1

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 7, 2003, 00:42:52 ; Search time 3176 Seconds
(without alignments)

18464.691 Million cell updates/sec

Title: US-10-032-717-1

Perfect score: 3621

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: em_esthum.*
3: em_estin.*
4: em_estnu.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
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9: gb_est1.*
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11: gb_htc.*
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13: gb_est4.*
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15: em_estfun.*
16: em_estom.*
17: gb_gss.*
18: em_gss_hum.*
19: em_gss_inv.*
20: em_gss_pln.*
21: em_gss_vrt.*
22: em_gss_fun.*
23: em_gss_mam.*
24: em_gss_mus.*
25: em_gss_other.*
26: em_gss_pro.*
27: em_gss_rod.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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c 4	53.6	1.5	531	13	BJ438828
5	53.6	1.5	617	13	BJ410977
6	53.6	1.5	619	13	BJ389714

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10	53	1.5	759	17	CNS060XV
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12	52.8	1.5	1101	17	CNS00001
c 13	52.6	1.5	773	17	BM651171
14	52.6	1.5	1300	13	BM468018
c 15	52.4	1.4	415	13	BJ355703
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18	52	1.4	883	17	AZ535659
19	51.6	1.4	938	17	AZ528417
20	51.2	1.4	619	14	BQ451864
21	51.2	1.4	886	17	CNS075DF
22	51.2	1.4	1007	17	CNS06X9S
23	50.8	1.4	1001	17	CNS01400
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32	49.8	1.4	1101	17	CNS0182P
33	49.6	1.4	691	10	AW622044
34	49.4	1.4	740	17	CNS02VRZ
35	49.4	1.4	783	17	CNS00A1S
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c 37	49.4	1.4	1101	17	CNS017Y0
c 38	49.2	1.4	583	12	BG852416
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ALIGNMENTS

RESULT 1

CNS0039G/c

LOCUS

DEFINITION

Accession

Version

Keywords

Source

Organism

Reference

Authors

Title

Journal

Comment

CNS0039G 1101 bp DNA linear GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
AL063921
AL063921.1 GI:4941778
GSS.
Drosophila melanogaster.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammose in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial


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/strain="AX4"
/db_xref="taxon:44689"
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/clone_lib="Dictyostelium discoideum cDNA library, VF"
/sex="mat A"
/dev_stage="Growth phase"
161 a 70 c 56 g 236 t 8 others
BASE COUNT
ORIGIN

Query Match 1.5%; Score 53.6; DB 13; Length 531;
Best Local Similarity 49.3%; Pred.No. 0.015;
Matches 134; Conservative 0; Mismatches 138; Indels 0; Gaps 0;

QY 3226 TTACGAGTTACTCGAGAAAGAGGGGTAGGAAATCGATATGTAAGTATCCGTGATGGT 3285
DB 462 TTGCCATCATCCGATGATGAAATTTTGATGATGATGATGATGATGATGATGATGAT 403
QY 3286 GGAATCAAAACAGAAACGCTTACTTTTGTGCGAAGCATTTATGATACAAATGGAATGTAT 3345
DB 402 GATGATGAAAATAATAGCAGTCAAGTGGTGAAATATGATATTAATCTACCAATATNAAT 343
QY 3346 AATACGCAAGTGTCCATACAAATGATATTAACACAATATGCGTATATATACACAGCA 3405
DB 342 AATAATAATATGTCATACGAATAATGATACCAATATAATATAACATAGTAATACT 283
QY 3406 TCGAGTACAAACGGATATACGCAATAATATGTATTAATACGCAAGCATCGAATACAAAC 3465
DB 282 ACACTACTAATAATATAATAACATGATAGTAATAATTTCAAACTCTANTATAATAAT 223
QY 3466 GGATATAACCAAAATAGTGTGTCACATGATCA 3497
DB 222 AATAATAATAATAATAATAATAATAATAATAATGA 191

RESULT 5
BJ410977
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BJ410977 617 bp mRNA linear EST 10-MAR-2002
BJ410977 Dictyostelium discoideum cDNA library, VF Dictyostelium
discoideum CDNA clone ddv2f16 3', mRNA sequence.
BJ410977
BJ410977.1 GI:19323672
EST.
Dictyostelium discoideum.
Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bases 1 to 617)
Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
Full length cDNA of Dictyostelium discoideum at the vegetative
stage
Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
1. .617
/organism="Dictyostelium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
/clone="ddv2f16"
/clone_lib="Dictyostelium discoideum cDNA library, VF"
/sex="mat A"
/dev_stage="Growth phase"
278 a 37 c 99 g 202 t 1 others
BASE COUNT
ORIGIN

Query Match 1.5%; Score 53.6; DB 13; Length 617;
Best Local Similarity 53.1%; Pred.No. 0.016;
Matches 138; Conservative 0; Mismatches 119; Indels 3; Gaps 1;

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QY 3258 AATGGATATGTAAGTATCCGTGATGGGAAATCAACAGAAAGCGTTACTTTTAGTGC 3317
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 89 AATATTAAATGAAGTATTGAATTAATGAATGAATGAATGAATGAATGAATGAATGA 148
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3318 AAGCGATTATGATCAAAATGAATGTATAATACCGCAAGTGCCAAATGATGATATAA 3377
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 149 AA---ATGAAGATTAAATATAATATAATATAATATAATATAATATAATATAATGA 205
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3378 CACAAATAATCGTATATACACAGCATCGAGTACAAACGATATACGCAATATAT 3437
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 206 TAATGATAATGATAATGATAATATAATATAATATAATGATGATGATAATATAATAT 265
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3438 GTATAATACGCAAGCATCGAATACAAACGATATAACCAATAGTGATGATCAATGATCA 3497
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 266 AATAATGGAATATAACATATAATATAATATAATATAATATAATATAATATAATGA 325
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3498 AACCGGTATATCAAAAAA 3517
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 326 AATAATGGAATGGAAGAA 345
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 6
BJ389714 619 bp mRNA linear EST 08-MAR-2002
LOCUS
DEFINITION
    BJ389714 Dictyostelium discoideum cDNA library, SF Dictyostelium
    discoideum cDNA clone dds19f23 5', mRNA sequence.
ACCESSION
    BJ389714
VERSION
    BJ389714.1 GI:19300800
SOURCE
    Dictyostelium discoideum.
ORGANISM
    Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE
    1 (bases 1 to 619)
AUTHORS
    Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
TITLE
    Full length cDNA of Dictyostelium discoideum at the slug stage
JOURNAL
    Unpublished (2002)
COMMENT
    Contact: Tadasu Shin-i
    Center For Genetic Resource Information
    National Institute of Genetics
    1111 Yata, Mishima, Shizuoka 411-8540, Japan
    Tel: 81-559-81-6856
    Fax: 81-559-81-6855
    Email: tshini@genes.nig.ac.jp.
    Location/Qualifiers
FEATURES
    source
        1..619
        /organism="Dictyostelium discoideum"
        /strain="AX4"
        /db_xref="taxon:44689"
        /clone="dds19f23"
        /clone_lib="Dictyostelium discoideum cDNA library, SF"
        /sex="mat A"
        /dev_stage="slug stage"
BASE COUNT 278 a 38 c 99 g 203 t 1 others
ORIGIN
    Query Match 1.5%; Score 53.6; DB 13; Length 619;
    Best Local Similarity 53.1%; Pred. No. 0.016;
    Matches 138; Conservative 0; Mismatches 119; Indels 3; Gaps 1;

QY 3258 AATGGATATGTAAGTATCCGTGATGGGAAATCAACAGAAAGCGTTACTTTTAGTGC 3317
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 89 AATATTAAATGAAGTATTGAATTAATGAATGAATGAATGAATGAATGAATGAATGA 148
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3318 AAGCGATTATGATCAAAATGAATGTATAATACCGCAAGTGCCAAATGATGATATAA 3377
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 149 AA---ATGAAGATTAAATATAATATAATATAATATAATATAATATAATATAATGA 205
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QY 3378 CACAAATAATCGTATATACACAGCATCGAGTACAAACGATATACGCAATATAT 3437
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 206 TAATGATAATGATAATGATAATATAATATAATATAATGATGATGATAATATAATAT 265
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3438 GTATAATACGCAAGCATCGAATACAAACGATATAACCAATAGTGATGATCAATGATCA 3497
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Db 266 AATAATGGAATATAACCAATATAATATAATATAATATAATATAATATAATGA 325
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QY 3498 AACCGGTATATCAAAAAA 3517
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 326 AATAATGGAATGGAAGAA 345
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 7
BJ389815 638 bp mRNA linear EST 08-MAR-2002
LOCUS
DEFINITION
    BJ389815 Dictyostelium discoideum cDNA library, SF Dictyostelium
    discoideum cDNA clone dds20m04 5', mRNA sequence.
ACCESSION
    BJ389815
VERSION
    BJ389815.1 GI:19300901
KEYWORDS
    EST.
SOURCE
    Dictyostelium discoideum.
ORGANISM
    Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE
    1 (bases 1 to 638)
AUTHORS
    Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
TITLE
    Full length cDNA of Dictyostelium discoideum at the slug stage
JOURNAL
    Unpublished (2002)
COMMENT
    Contact: Tadasu Shin-i
    Center For Genetic Resource Information
    National Institute of Genetics
    1111 Yata, Mishima, Shizuoka 411-8540, Japan
    Tel: 81-559-81-6856
    Fax: 81-559-81-6855
    Email: tshini@genes.nig.ac.jp.
    Location/Qualifiers
FEATURES
    source
        1..638
        /organism="Dictyostelium discoideum"
        /strain="AX4"
        /db_xref="taxon:44689"
        /clone="dds20m04"
        /clone_lib="Dictyostelium discoideum cDNA library, SF"
        /sex="mat A"
        /dev_stage="slug stage"
BASE COUNT 289 a 38 c 110 g 201 t
ORIGIN
    Query Match 1.5%; Score 53.6; DB 13; Length 638;
    Best Local Similarity 53.1%; Pred. No. 0.017;
    Matches 138; Conservative 0; Mismatches 119; Indels 3; Gaps 1;

QY 3258 AATGGATATGTAAGTATCCGTGATGGGAAATCAACAGAAAGCGTTACTTTTAGTGC 3317
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 73 AATATTAAATGAAGTATTGAATTAATGAATGAATGAATGAATGAATGAATGAATGA 132
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3318 AAGCGATTATGATCAAAATGATGATATACCGCAAGTGCCAAATGATGATATAA 3377
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 133 AA---ATGAAGATTAAATATAATATAATATAATATAATATAATATAATGAAGTGA 189
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3378 CACAAATAATCGTATATACACAGCATCGAGTACAAACGATATACGCAATATAT 3437
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 190 TAATGATAATGATAATGATAATATAATATAATATAATGATGATGATGATGATATAT 249
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3438 GTATAATACGCAAGCATCGAATACAAACGATATAACCAATAGTGATGATCAATGATCA 3497
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 250 AATAATGGAATATAACCAATATAATATAATATAATATAATATAATATAATGA 309
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3498 AACCGGTATATCAAAAAA 3517
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 310 AATAATGGAATGGAAGAA 329
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RESULT 8
CNS0106X 1101 bp DNA linear GSS 26-JUL-1999
LOCUS
DEFINITION
    Drosophila melanogaster genome survey sequence T7 end of BAC
    BACN03K20 of DrosBAC library from Drosophila melanogaster (fruit
    fly), genomic survey sequence.

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DEFINITION EST569551 PyBS Plasmodium yoelii yoelii CDNA clone PYCOB51 5' end.
mRNA sequence.

ACCESSION BM167028
VERSION BM167028.1 GI:17300260
KEYWORDS EST.
SOURCE Plasmodium yoelii yoelii.
ORGANISM Plasmodium yoelii yoelii
REFERENCE Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 412)
AUTHORS Carlton, J.M., Daly, T.M., Long, C.A., Bergman, L.W., Vaidya, A.B.,
Fraser, C.M. and Carucci, D.J.
TITLE Plasmodium yoelii EST project at TIGR
JOURNAL Unpublished (2001)
COMMENT Contact: Jane Carlton
Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-530-9319
Fax: 301-838-0208
Email: carlton@tigr.org
For clone info, please contact the Malaria Research and Reference
Reagent Resource Center, ATCC
http://www.malaria.mr4.org/mr4pages/index.html
Seq primer: ADF.

FEATURES
source Location/Qualifiers
1. 412
/organism="Plasmodium yoelii yoelii"
/strain="17XL"
/db_xref="taxon:73239"
/clone="PYCOB51"
/clone_lib="PyBS"
/dev_stage="Asexual blood stages"
/lab_host="E. coli XL-1 Blue"
/notes="Vector: PAD-GAL4; At 20-25% parasitemia, blood was
collected from BALB/cByJ mice infected with Pyl7XL
parasites, and leukocytes removed by passage over
microcrystalline cellulose columns. Total RNA was
isolated using the guanidinium isothiocyanate method, and
mRNA isolated using oligo(dT)-cellulose chromatography.
First strand cDNA synthesis was completed using a 50-base
primer and reverse transcriptase in the presence of
5-methyl dCTP. After second strand synthesis, uneven
termini were treated with Pfu DNA polymerase and EcoRI
adaptors ligated to the blunt ends. The sample was cleaved
with XhoI and separated on a Sephacryl S-500 column.
Size-fractionated cDNA was precipitated and ligated to
HybriZAP arms directionally using EcoRI-XhoI cleaved arms
After packaging, the phagemid vector (PAD-GAL4) was
excised from the HybriZAP vector and plasmid DNA
isolated."

BASE COUNT 226 a 20 c 62 g 104 t
ORIGIN

Query Match 1.5%; Score 53; DB 13; Length 412;
Best Local Similarity 49.5%; Pred. No. 0.02;
Matches 137; Conservative 0; Mismatches 140; Indels 0; Gaps 0

QY 3241 AGAAAGAGCGGTAGGAATATGGAATATGTAAGTATCCGTGATGTTGGAAATCAACAGAA 3300
DB 81 AGCATAAATGGGGAATGTATTGAAATCTGAATGATTCAGAAAATAATAATGGTAATAAA 140
QY 3301 ACGCTTACTTTTAGTGCAGCGATTTATGATACAAATGGAATGTGTAATAATCGCAAGTGTC 3360
DB 141 AATGGTAATAGTAATGATAATAATAATGGTAATAATAATGTTAATAATGATGATAATAAT 200
QY 3361 AATCAAAATGGATATAACAAATAATCGGTATTAATACACAAGCATCGAGTCAACACGA 3420
DB 201 AATGATAATAAAATGGTAATAATAATGATGATAATAAAATGGTAATAATAATGATGAT 260
QY 3421 TATACGCCAAATAATATGTTATAATACGCAAGCATCGAATACAAACGGGATATAACAAAT 3480
DB 261 AATAATAATGATGATAGAAAACAGCAAAAAAATAAAAAATGAAAAATTTGAATAATAAT 320

[illegible]


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Oy 3378 CACAAATAATCGGTATTAATACACAGCATCGAGTACAAACGGATATACGCAAAATATAT 3437
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
632 AAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAA 573
Oy 3438 GTATTAATACGCAAGCATCGAATACAAACGGATATACACAAATAGTGTGTAATGATCA 3497
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
572 AAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAA 513
Oy 3498 AACCGCTTATTCACAAACAGTGCACATTCATCCGTATACAGATCAATCGGATGGA 3557
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
512 AAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAA 453
Oy 3558 GATGAGTCAGACAGAGGTACATCTTATATAGAAAGTGTAGAAATGA 3604
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
452 AAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAA 406

RESULT 14
BM468018 1300 bp mRNA linear EST 05-FEB-2002
LOCUS AGENCOURT 6437618 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5532913
DEFINITION 5', mRNA sequence.
ACCESSION BM468018
VERSION BM468018.1 GI:18517060
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1300)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM1216 row: p column: 02
High quality sequence stop: 434.

FEATURES             source
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            /clone_lib="NIH MGC 71"
            /tissue_type="leiomyosarcoma"
            /lab_host="DH10B (phage-resistant)"
            /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
            Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
            Average insert size 2.1 kb."
BASE COUNT          586 a 102 g 112 t 388 others
ORIGIN
    1..1300
        Query Match      1.5%; Score 52.6; DB 13; Length 1300;
        Best Local Similarity 25.9%; Pred. No. 0.039;
        Matches 196; Conservative 0; Mismatches 560; Indels 0; Gaps 0;

Oy 2792 AGTGGAGATTCAAATGACAAGACGCTGAAGAAACAGATAGAGGTATATGCGCATCA 2851
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
507 ANNNNNNANNNNANNNNANNNNANNNNANNNNANNNNANNNNANNNNANNNNANNA 566
Oy 2852 AACAAACGGTAGATCGTTTATATGCGGATATACAGGATCAGCAACTGAATCCTGATG 2911
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
567 AAANNANANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 626
Oy 2912 AGATTACAGATCTTACTGCGGCGCAAGATCTGTATACAGTCCATCTCCTAGTATATAACG 2971
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
627 AAANNANNNNNNANNNNNNANNNNANNNNANNNNANNNNANNNNANNNNANNNNANNA 686

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Oy 2972 AAATGTTCCCAAGAAATACCGGGATGAACCTATATACGAAGTTTACAGAAATTAACAGATCGAC 3031
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
687 NNAAAAAAAAANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 746
Oy 3032 TCCAAACAGCGGTGGAGTTTGTATGATCAGCGAAATGCGCATACCAAATGGTGTATTTTCGAA 3091
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
747 NNNNANNNANNNANNNANNNANNNANNNANNNANNNANNNANNNANNNNNNNNNNN 806
Oy 3092 ATGGGTAAAGTAAATGGGAATCAACGCTGCGGTAGAGTACAAACATCAATCATCATCAT 3151
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
807 AAAANNNANNNANNNANNNANNNANNNANNNANNNANNNANNNANNNANNNANNA 866
Oy 3152 CTGCTCTTGATTTCCAAATCGGATGAGCAAGTTTCGCAACAGTTTACAGTTTCAACCGA 3211
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
867 AANANNNANNNANNNANNNANNNANNNANNNANNNANNNANNNANNNANNNANNA 926
Oy 3212 ATCAAAGATATGTTACGAGTTACTGCGAGAAAGAGGGGTAGGAAATGGATATGTA 3271
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
927 AANANNNANNNANNNANNNANNNANNNANNNANNNANNNANNNANNNANNNANNA 986
Oy 3272 GTATCCGTGATGGTGGAAATCAACACAGAAACGCTTACTTTTAGTGCAGCGGATTTATGATA 3331
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
987 AANANNNANNNANNNANNNANNNANNNANNNANNNANNNANNNANNNANNNANNA 1046
Oy 3332 CAAATGGAATGTATAATACGCAAGTGTCCAATACAAATGGATATAACACAAATATATGCGT 3391
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1047 AANANNNANNNANNNANNNANNNANNNANNNANNNANNNANNNANNNANNNANNA 1106
Oy 3392 ATAATACACAGCATCGAGTACAAACGGATATACGCAAAATATATGTATATATACGCAAG 3451
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1107 AAAAAAAAAAAAAAAAAANNNANNNANNNANNNANNNANNNANNNANNNANNNANNA 1166
Oy 3452 CATCGAATACAAACGGATATACCAATAGTGTGTAATGATCAATGATCAATCAATATATCA 3511
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1167 ANAANNNANNNANNNANNNANNNANNNANNNANNNANNNANNNANNNANNNANNA 1226
Oy 3512 CAAAAACAGTGACATTCATCCGCTATACAGATCAAA 3547
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1227 NAAAAAAAAANNNANNNANNNANNNANNNANNNANNNANNNANNNANNA 1262

RESULT 15
BM355703/c 415 bp mRNA linear EST 07-MAR-2002
LOCUS BM355703 Dictyostelium discoideum cDNA library, AF Dictyostelium
DEFINITION discoideum cDNA clone dda57022 3', mRNA sequence.
ACCESSION BM355703
VERSION BM355703.1 GI:19255297
KEYWORDS EST.
SOURCE Dictyostelium discoideum.
ORGANISM Dictyostelium discoideum.
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE 1 (bases 1 to 415)
AUTHORS Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
TITLE Full length cDNA of Dictyostelium discoideum at the aggregation
stage
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@gene.nig.ac.jp.
location/Qualifiers
    1..415
        /organism="Dictyostelium discoideum"
        /strain="AX4"
        /db_xref="taxon:44689"
        /clone="dda57022"
        /clone_lib="Dictyostelium discoideum cDNA library, AF"
        /sex="mat A"

FEATURES             source
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            /strain="AX4"
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            /clone_lib="Dictyostelium discoideum cDNA library, AF"
            /sex="mat A"

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QY 121 ELINOKIAEYARNKALSELEGLNNGYQLYLTALBEEWENPNNGSALRDVRRNREILDSLF 180
DB 121 ELINOKIAEYARNKALSELEGLNNGYQLYLTALBEEWENPNNGSALRDVRRNREILDSLF 180
QY 181 TOTMPSFRVTNFEVPELTVYVYMAANLHLLLDKASIFGEEWGHSTTTINNYIDROMKLT 240
DB 181 TOTMPSFRVTNFEVPELTVYVYMAANLHLLLDKASIFGEEWGHSTTTINNYIDROMKLT 240
QY 241 EYSDHCWKVETGLAKLGTSAKQWVDYNOFRREMTLAVLDVVALFNYDTRTYPMETKA 300
DB 241 EYSDHCWKVETGLAKLGTSAKQWVDYNOFRREMTLAVLDVVALFNYDTRTYPMETKA 300
QY 301 QLTREYVTDPLGAVNVSSIGSWDKAPSGFVIESVIRPPHVDIYITGLVYITQSRSS 360
DB 301 QLTREYVTDPLGAVNVSSIGSWDKAPSGFVIESVIRPPHVDIYITGLVYITQSRSS 360
QY 361 ARVIRHWAGHOISYHRVRSRNSLOOMGTQNLHSTSTFTFTNYDIYKTLSDKAVLLDIV 420
DB 361 DRYMRYWAGHOISYKHIGTSTSTFTQMTGTQNLQSTSNFDTFTNYDIYKTLSDKAVLLDIV 420
QY 421 YPGVYTIFFCMPEVEFPMVQNLNTRKTLKYNPVSKDIIASTRDSLELEPPETSDQNYE 480
DB 421 YPGVYTIFFCMPEVEFPMVQNLNTRKTLKYNPVSKDIIASTRDSLELEPPETSDQNYE 480
QY 481 SYSHRLCHITSPATGNTTGLVPVFSWTHRSADLNNTIYSDKITQIPAVKCDNLPFPV 540
DB 481 SYSHRLCHITSPATGNTTGLVPVFSWTHRSADLNNTIYSDKITQIPAVKCDNLPFPV 540
QY 541 VKPGHGTGDLQVNRSTGVTGLFARYGLALEKAKYRVLAYADIVLHV-----N 596
DB 541 VKPGHGTGDLQVNRSTGVTGLFARYGLALEKAKYRVLAYADIVLHV-----N 596
QY 597 DAOIOMPKT-MNPGC-DLTSKTFKVAADITLNLATDSSLKALHNLGDNSTLSGIVVY 654
DB 597 DAOIOMPKT-MNPGC-DLTSKTFKVAADITLNLATDSSLKALHNLGDNSTLSGIVVY 654
QY 655 DRIEFTPVDETYEAEQDLAKAVNALFTNTKDGRLPGVTDYEVNQANLVECLSDLL 714
DB 655 DRIEFTPVDETYEAEQDLAKAVNALFTNTKDGRLPGVTDYEVNQANLVECLSDLL 714
QY 715 PNEKRLLFDAVRAKRLSEARNLQDDPQFQINGENGWASTAGTGLEIYEGDALFKGRYLRL 774
DB 715 PNEKRLLFDAVRAKRLSEARNLQDDPQFQINGENGWASTAGTGLEIYEGDALFKGRYLRL 774
QY 775 PGAREIDTETPTLYOKVEGVLPKPYTRVRLGRFVSSQGLREFTIRHOTNRIVKQVND 834
DB 775 PGAREIDTETPTLYOKVEGVLPKPYTRVRLGRFVSSQGLREFTIRHOTNRIVKQVND 834
QY 835 DLLPDPVSPVNSDGSINRCSEQKYNSRLEVENRSGEAHEFSIPIDTGEIDYNNENAGI 894
DB 835 DLLPDPVSPVNSDGSINRCSEQKYNSRLEVENRSGEAHEFSIPIDTGEIDYNNENAGI 894
QY 895 FKITDPEGYATLGNLEVEGPLSGDALERLOREQQWKIOMTRREEDRBYWASQAV 954
DB 895 FKITDPEGYATLGNLEVEGPLSGDALERLOREQQWKIOMTRREEDRBYWASQAV 954
QY 955 DRLYADYQDQALNPVBEITDLTAAQDLIQSIPIYVYNMFPEIPGMNTYKTFELTDLRQQA 1014
DB 955 DRLYADYQDQALNPVBEITDLTAAQDLIQSIPIYVYNMFPEIPGMNTYKTFELTDLRQQA 1014
QY 1015 WSLYDQRNAIPNGDFRNLGNWNAATPGVQOQINHTSVLVPINWDEQVSOQFTVPQNR 1074
DB 1015 WSLYDQRNAIPNGDFRNLGNWNAATPGVQOQINHTSVLVPINWDEQVSOQFTVPQNR 1074
QY 1075 VLRVTKARKEGVGYSIRDCGQOTELTFPSASDYDTNGMNTQVSNNGYNTNNAINTQ 1134
DB 1075 VLRVTKARKEGVGYSIRDCGQOTELTFPSASDYDTNGMNTQVSNNGYNTNNAINTQ 1134
QY 1135 ASSTNGYNANMNTQASNTNGYNTNSVNDQTCYITKVTFTFYPTQMTIEMSETGTF 1194
DB 1135 ASSTNGYNANMNTQASNTNGYNTNSVNDQTCYITKVTFTFYPTQMTIEMSETGTF 1194
QY 1157 EYSDYCVKWKYKIGLKLKGTTSKWLNTYHQFREMTLLVLDLVALFPNYDTHMYPIETTA 299
DB 1157 EYSDYCVKWKYKIGLKLKGTTSKWLNTYHQFREMTLLVLDLVALFPNYDTHMYPIETTA 299

RESULT 2
C8AA_BACUK
ID C8AA_BACUK STANDARD; PRT; 1157 AA.
AC Q45704;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pesticidal crystal protein cry8Aa (insecticidal delta-endotoxin
DE CryIIIA(a) (Crystalline entomocidal protoxin) (131 kDa crystal
DE protein).
GN CRY8AA OR CRYVIIIA(A).
OS Bacillus thuringiensis (subsp. kumamotoensis). Bacillus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=132267;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL B-18746 / PS50C;
RA Payne J.M., Sick A.J., Ponceirada L.;
RT "Novel coleopteran-active Bacillus thuringiensis isolate and a novel
RT gene encoding a coleopteran-active toxin.";
RL Patent number EP0498537, 12-AUG-1992.
CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF COLEOPTERA.
CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPORELIATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
CC N-TERMINUS.
CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U04364; AAA21117.1; -
DR HSSP; P07130; 1DLIC.
DR InterPro; IPR001178; Endotoxin.
DR Pfam; PF00555; endotoxin; 1.
KW Toxin; Sporulation.
SQ SEQUENCE 1157 AA; 131009 MW; 687B5C49DE93683B CRC64;

Query Match 62.4%; Score 3950.5; DB 1; Length 1157;
Best Local Similarity 65.5%; Pred No. 9.1e-213;
Matches 804; Conservative 120; Mismatches 211; Indels 93; Gaps 19;

QY 1 MSPNNQVEYIIDATPSTSVNSDNNRYPANPTNALQNDYKYLKMSAGNASYPGSP 60
DB 1 MSPNNQVEYIIDATPSTSVNSDNNRYPANPTNALQNDYKYLKMSAGNASYPGSP 60
QY 61 EYLVSGQDAKAADIVGKLGLGYPVGVPTVSLYTQILDILWPSGEKSQWEIFMBOVE 120
DB 61 EYLVSGQDAKAADIVGKLGLGYPVGVPTVSLYTQILDILWPSGEKSQWEIFMBOVE 120
QY 61 ETPIIS-SSTIQTGIGVIRILGALGVFFASQIASFYSFVIGLWPSKSDVIMGEIMERVE 119
DB 61 ETPIIS-SSTIQTGIGVIRILGALGVFFASQIASFYSFVIGLWPSKSDVIMGEIMERVE 119
QY 121 ELINOKIAEYARNKALSELEGLNNGYQLYLTALBEEWENPNNGSALRDVRRNREILDSLF 180
DB 121 ELINOKIAEYARNKALSELEGLNNGYQLYLTALBEEWENPNNGSALRDVRRNREILDSLF 180
QY 120 ELVDQKIEKYVKDKALAEKGLGNALDVYQOSLEDWLENNDARTSVVSNQFIADLNP 179
DB 120 ELVDQKIEKYVKDKALAEKGLGNALDVYQOSLEDWLENNDARTSVVSNQFIADLNP 179
QY 181 TOTMPSFRVTNFEVPELTVYVYMAANLHLLLDKASIFGEEWGHSTTTINNYIDROMKLT 240
DB 181 TOTMPSFRVTNFEVPELTVYVYMAANLHLLLDKASIFGEEWGHSTTTINNYIDROMKLT 240
QY 180 VSSIPSFAVSGHEVLLAVYAQAANLHLLLRDASIFGEEWGFPGCEISFRFNRQQLTA 239
DB 180 VSSIPSFAVSGHEVLLAVYAQAANLHLLLRDASIFGEEWGFPGCEISFRFNRQQLTA 239
QY 241 EYSDHCWKVETGLAKLGTSAKQWVDYNOFRREMTLAVLDVVALFPNYDTRTYPMETKA 300
DB 241 EYSDHCWKVETGLAKLGTSAKQWVDYNOFRREMTLAVLDVVALFPNYDTRTYPMETKA 300
QY 240 EYSDYCVKWKYKIGLKLKGTTSKWLNTYHQFREMTLLVLDLVALFPNYDTHMYPIETTA 299
DB 240 EYSDYCVKWKYKIGLKLKGTTSKWLNTYHQFREMTLLVLDLVALFPNYDTHMYPIETTA 299
```

[illegible]

RESULT 3

RESUMI 3	C8CA BACTP	STANDARD;	PRT; 1160 AA.
ID	AC Q45706;		
DT	30-MAY-2000	(Rel. 39, Created)	
DT	30-MAY-2000	(Rel. 39, Last sequence update)	
DT	30-MAY-2000	(Rel. 39, Last annotation update)	

Pesticidal crystal protein cry8Ca (Insecticidal delta-endotoxin protein) (Crystalline entomocidal protoxin) (130 kDa crystal protein).

GN CRY8CA OR CRYVIII(CA) OR CRYIII.

OS Bacillus thuringiensis (subsp. japonensis).

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI_TaxID=128936;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Buibui;

RX MEDLINE=94259659; PubMed=7764305;

RA Sato R., Takeuchi K., Ogiwara K., Minami M., Kaji Y., Suzuki N.,

RA Hori H., Asano S., Ohba M., Iwahana H.;

RT "Cloning, heterologous expression, and localization of a novel crystal protein gene from Bacillus thuringiensis serovar japonensis strain buibui toxic to scarabaeid insects.";

RT Curr. Microbiol. 28:15-19(1994).

RL [2]

RN SEQUENCE OF 1-14 AND 56-64, AND CHARACTERIZATION.

RX MEDLINE=94259659; PubMed=8200856;

RA Hori H., Suzuki N., Ogiwara K., Himejima M., Indrasith L.S.,

RA Minami M., Asano S., Sato R., Ohba M., Iwahana H.;

RT "Characterization of larvicidal toxin protein from Bacillus thuringiensis serovar japonensis strain Buibui specific for scarabaeid beetles.";

RT J. Appl. Bacteriol. 76:307-313(1994).

RL J. FUNCTION: PROMOTES COLLOIDSMORTIC LYSIS BY BINDING TO THE MIDGUT EPITHELIAL CELLS OF INSECTS. ACTIVE ON VARIOUS SCARABAEID BEETLES SUCH AS ANOMALA CUPREA, A. RUFOCUPEA AND POPILLIA JAPONICA.

CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART OF THE SPORE COAT.

CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-TERMINUS.

CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.

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CC EMBL; U04366; AAA21119.1; --

DR HSP; P07130; IDLC.

DR InterPro: IPR001178; Endotoxin.

DR Pfam; PF00555; endotoxin; 1.

KW Toxin; Sporulation.

SQ SEQUENCE 1160 AA; 130425 MW; C16C3D912EEB8751 CRC64;

Query Match 48.4%; Score 3066; DB 1; Length 1160;

Best Local Similarity 50.3%; Pred. No. 2.1e-163;

Matches 63; Conservative 180; Mismatches 298; Indels 146; Gaps 23;

Qy 1 MSPNQNEYIIDA TPSTVSNDSNRYPFANEPTNALQNNDYDKYKMGAGNASEYEGSP 60

Db 1 MSPNQNEYIIDA LPTSVDNSIRYPLANDQNTLNQNNYDKYKMGAGNASEYEGSP 60

Qy 61 EVLVSGQDAKAAIDIVKLLGLGVFPVFGIVTSLYLTQLIDILWPSGEKSWEIFMQVE 120

Db 61 GTFTISAQDAVGTGIDIVSTTIISGLIGIPVLGEVFSILGSLIGLLWPSNNENWQIFMNRVE 120

Qy 121 ELINOKIATYARNKALSELGSLGNVQLYLTAAEEENPNGSRALDVRNRFEILDLSLF 180

Db 121 ELIDDKILDSVRSRAIADLANSTRVVEYQNALEDWRKNPSTSAALVXERPGNAEAIL 180

Qy 181 TQYMPSPRVNTFVFPFTLYVMAANLHLLLKDAISFGEEWGSTTTTNNYVDRQMKLTA 240

Db 181 RTNMGSPQTYETPLPTTAQAASLHLVWRDVQIVGKEWGPQNDIDILFYKEQVSYTA 240

Qy 241 EYSDHCVKWYETGLAKLGKTSAKQWVDYNOFRREMTLAVLDVVALFPNYDTRTPYMETKA 300

Db 241 RYSDHCQVWYNAGLNKLGRTGAKQWVDYNNRFRRENNVMVLDLVALFPNYDIARYPLETNA 300
Qy 301 QLTREVYTDPLGAV---NVSSIGSWYD---KAPSGVIESVIRPPHVPDYITGLTYVT 353
Db 301 ELTREIFTPDVGSVVTGSSYSLISWYDMIPALPSFSTLE-NLLRKPDPFFLLQOEIRMT 359
Qy 354 QSRISARIYIRHWAGHOISYHRSVRSGLNQMTGNTONLHS-----TSTFDTNVDIY 407
Db 360 SFRQNGTIEYNYNGQRLT-----LSYIGSSFNKYSGLVLAGAEDIIPVQNDIY 410
Qy 408 KTLKSDAVLLDIVPG-YTYIFFGMPVEVFPWVWLNQNLNTRTKYNPNVSKDIIASTRDS 466
Db 411 RVV-----WTYIGRTNLLGVNPVTFYF---SNNTKTYS-KPKQFAGGKITDSDG 458
Qy 467 LELPETSQPNYESYSHRLCHITS--IPATGNTT-GLVPVFSWTHRSADLNNTIYSDKI 523
Db 459 BELTYE-----NYOSYSHRVYIISFEIKSTGGTVLGVPIPGWTHSSASRNNIYATKI 513
Qy 524 TQIPAVKC-----WDNLFPV---PVRKPGHGTGDLLOYNRSTGSGVGLFLARYGL 571
Db 514 SQIPINKASRTSGGAVNMFQSLYNGPVMKLSG-SGSOVINLRVATDAKGA----- 564
Qy 572 ALEKAGKVRVLRVATDADIVLHN-----DAQIOMPKWNPCEDLTSKTFKVAD 621
Db 565 ---SQRIRIRIRYASDRAGKFTISSRSPENPATYSIAIYNTMTNASTYTFAYAE 620
Qy 622 AITTLNLTADSS---LALKHNLGEDPNSTLSGTVVVDRIEFTPVDTYEAODLEAAK 676
Db 621 S-GPINIGISGSRFTDISITKEAG-----ANLYIDRIEFTPVNTLFEABEDLVAK 672
Qy 677 KAVNALFTNTDGLRPGVTDYEVNQANLVCLSDLYPNEKRLFLDVAERAKRLSEARN 736
Db 673 KAVNGLFTNEKDALQTSYTDYQVNOAANLIECLSDLYPNEKRLMDAVKEAKRLVQARN 732
Qy 737 LQDPDFQEIENGNGWTASTGIEVEGALPKGRVLRPLPGAREIDTETPTYLKQVEEG 796
Db 733 LQDGTGNRINGNGWTGSTGIEVEGDLFKDRSLRLTSAREIDTETPTYLQOQIDES 792
Qy 797 VLKPYTVRLRPGVSSOGLIEFTIRHCTNRIVKNVPDPLLDPVSPVNSDGSINRCSBK 856
Db 793 LLKPYTRYKLKGFIGSSODLEIKLIRHRANQIVKNVPDNLPLDPVSPVNSDGVKCSQQ 852
Qy 857 YVNSRLEVENR-----SGEAHEFSIPDTGTIDYENAGIIVGPKITDPGEYATLGNLE 910
Db 853 YVDANLALENNGENGNMSSDASHFSDITGTIDLNENTGIWIVFKIPTTNGNATLGNLE 912
Qy 911 LVEGGLSGDALERLQREEQWQKQMTRRRETDRLRYMASKQAVDRLYADYDQQLNPDV 970
Db 913 FVEEGPLSGETLEWAQQEQOQWQDKARAKRAASEKTYTAAKQAIQDLRFADYDQQLNSGV 972
Qy 971 EITDLTAADLIQSIPIVYVYVNFPEIPGMNTYKFTELDRLOQAWSLYDORNAIPNGDPR 1030
Db 973 EMSDLLAQNVLQSIPIVYNALPEIPGMNTYKFTELDRLOQAWSLYDORNAIPNGDPR 1032
Qy 1031 NGLSNWNPATPGVEVQOQINHISVLVIPPNDQVSOQFTVPQNRQYVLRVATKRGVNGYV 1090
Db 1033 NGLSNWNPATSVNQVQQLSDTSVLVIPPNNQSVSOQFTVPQNRQYVLRVATKRGVNGYV 1092
Qy 1091 SIRGGNQTETLTSASDYDTNGMYNTQVNTNGYNTNAYNTQASSTNGYNNMYNTQ 1150
Db 1093 IIRDCANQTETLTNICDDDT-GVLST----- 1118
Qy 1151 ASNTNGYNTNAYNTQVNTQVNTQVNTQVNTQVNTQVNTQVNTQVNTQVNTQVNTQ 1206
Db 1119 -----DOTSYIINKVEFTSTEQVWIDNSETGEVFNIESVELVLEEE 1160

RESULT 4

C9CA_BACTO

ID C9CA_BACTO STANDARD; PRT; 1157 AA.

AC Q45733;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE CRYIXC(a) (Crystalline entomocidal protoxin) (130 kDa crystal
DE protein).
GN CRY9CA OR CRYIXC(A).
OS Bacillus thuringiensis (subsp. tolworthi).
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1442;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=BTS02618A;
RX MEDLINE=96141404; PubMed=8572715;
RA Lambert B., Buysse L., Decock C., Jansens S., Piens C., Saey B.,
RA Seurinckx J., Van Audenhove K., Van Rie J., Van Vliet A., Peferoen M.,
RT "A Bacillus thuringiensis insecticidal crystal protein with a high
RT activity against members of the family Noctuidae.";
RL Appl. Environ. Microbiol. 62:80-86(1996).
CC -!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF LEPIDOPTERA LARVAE. HAS A FAIRLY BROAD
CC SPECTRUM OF ACTIVITY AGAINST MEMBERS OF THE FAMILIES PYRALIDAE,
CC PLUTELLIDAE, SPHINGIDAE, AND NOCTUIDAE. IT IS THE FIRST
CC INSECTICIDAL CRYSTAL PROTEIN WITH ACTIVITY AGAINST CUTWORMS. NO
CC ACTIVITY IS OBSERVED AGAINST SOME BEETLES, SUCH AS COLORADO POTATO
CC BEETLE.
CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART OF
CC THE SPORE COAT.
CC -!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-
CC TERMINUS.
CC -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC
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CC
CC EMBL; Z37527; CAA85764.1; --
DR HSP70; P07130; IDLC.
DR InterPro; IPR001178; Endotoxin.
DR Pfam; PF00555; endotoxin; 1.
KW Toxin; Sporulation.
SQ SEQUENCE 1157 AA; 129775 MW; C3643918F7DFB8A CRC64;

Query Match 41.0%; Score 2595.5; DB 1; Length 1157;
Best Local Similarity 44.1%; Pred. No. 3.8e-137;
Matches 554; Conservative 197; Mismatches 348; Indels 157; Gaps 22;
Qy 1 MSPNNQNEYIIDATPSTSVSNDNRYPPANEPTNALQNNMDYKDLKMSAGNASBPGSP 60
Db 1 MRRNNQNEYIIDAPHGCGPSDDDDRVYPLASDPNALQNNMDYKDLQNTDEYDTSINP 60
Qy 61 EVLVSGQDAKAAADIVGKLLSGLVGPFVGVIVSLYXQLIDILWPSGKSEWEIPEQVE 120
Db 61 SLSISGRDAVQTALTVVGRILGALGVFPFSQIVSFYQFLNTLWPNVDTAIWEAFQVE 120
Qy 121 ELINQKTAEBARNKALSELGLGNNYQIYLTAEWEENPNSPALRDVNRPIILSLP 180
Db 121 ELVNQQITTEFARNQALRQGLGDSFNVYQSRQLNWLAADRNTNLNSVVRQAQFTALDLDF 180
Qy 181 TOVNPFSRVNTFVPPLTVYMAANLHLLLLKQASIFGEEGWSSTTNNYNYDRQMKLTA 240
Db 181 VNAIPLFVNGQQVPLSVTAQAVNLHLLLLKQASLFGEGGFTQGEISTYIDQLEUTA 240
Qy 241 EYSDHCVKVYETGLAKGTSAKOWVDYNNRFRRENNVMVLDLVALFPNYDIARYPLETNA 300
Db 241 KYTNVCEWTYNTGLDRLGRTNTESLRYHQFRRENTLVLDVLDVVALFPYDVLRYPTGSP 300
Qy 301 QLTREVYTDPL---GAVNVSSISGW-----YDKAPSGVIESVIRPPHVPDYITGLTYVT 353
Db 301 QLTREVYTDPLFVFNPPANVGLCRWGTNPYN---TFSELENAFIRPPHLPFLRLSLTI-S 356

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QY 354 QSRISARYIRHWAGHOISYHRVSRGSLNQOMYG-----TNQNLHSTSTDFNTYD 405
DB 357 SNRPVSNFMDYSGHTLRSYLANDSAVQSDSLTITATINPGVDGTRISTAVD 416
QY 406 IYKTLSDAVLLDVIYPGYTYIFFGMEPEVEPFMVNQNLNTRKTLKYNPVSKDIIASTRDS 465
DB 417 FRSALIG-----IYGVNRASFPVGLFNGT--TSPANGGCRDLY-----DT 455
QY 466 ELELPPTSOPNYESYSHRLCHITSIPATCN-----TTGLVPVFSWTHRSADLNNTIY 519
DB 456 NDELPPDEST-----GSSHRLSHVTFPSFQTNQAGSIANAGSVTYVWTRDRVDLNNIT 511
QY 520 SDKITQIPAVKCMNDLPVVPVKGHGTDGLLOVNRSTGSGVTLFLARYGLALEKAGKY 579
DB 512 PNRITQIPLVKASAPVSGTIVLKGFGTGGILR--RTINGTFTL---RVTVNSPLTQOY 567
QY 580 RVLRYATADIVLH-----VNDAGIQMPKTMNPFGEIDTSK-----TP 617
DB 568 RLRVFASTGNFIRVLRGVSGVIGDVLRLGSTMNRQGLTYESFPTRETTTGPFPNPTF 627
QY 618 KVADAITLNLATSSALKNLGDEPNSTLSGIVYVDRIEPIFVDETYEAEODLEAKK 677
DB 628 TQAEIILTVAEGVST-----GGEYIIDRIEIVPNPAREAEEDLEAKK 672
QY 678 AVNALFTNTKDLRPGVTVDYEVNOANLVECLSDLYNEKRLLFDAVREAKRLSEARNL 737
DB 673 AVASLFTRTDGLQVNTDYQDQANLVCLSDBOYGHDKMLLEAVRAAKRLSRNRL 732
QY 738 LQDPDPQOING--ENGWTPASTGIEVIGDALFKGRYLPLGAREIDTETPTIYLYQKVE 795
DB 733 LQDPDFNTINTEENGWKAASGVITSEGGPFKGRALQASAR-----ENYPTIYQKVA 788
QY 796 GVLKDYTRYLRGFGVSSQGLIEFTIRQTNRIKVNVDLDPVSPVNSDGS-----INRC 852
DB 789 SVLKPYTRYLRDGFVKSSQDLIEDLIHFKHVLKXNVPDNL---VSDTYSQSGCSGINRC 845
QY 853 SEQKYVNSRLVEN-----BSGEAHSFIPIDTGEIDYENENAGIWWGFKITDPEGYATL 906
DB 846 DEQHQVNDQDAEHHPMDCCBAQAQTHEFSYINTGDINASVDQGLIWWVLKVRTDGYATL 905
QY 907 GNLEVERGPLSGDALERLQREBOQWKIQMTRRREEDRRYRMAKQAVDRLYADYQDOOL 966
DB 906 GNLEIVEVGPLSGSELEQRDNKNAELGKRAEIDRVYLAQAQAINHLFVDYQDOOL 965
QY 967 NPDVEITDLTAAQDLIOSIPYVNEFPEIPGMNNTKTELTDRLQQAWSLYDQRNAIPN 1026
DB 966 NPEIGLAEINEASNLVESISGVSDTLQIPGINYEIVTELSDRLQQAASLYTSRNAVQN 1025
QY 1027 GDFPGLSNWATPGVEVQOINHTSVIYIPNWDEOVSOQFTVPQNRVYLVRTARKEGVG 1086
DB 1026 GDFNSGLDSWNTWDASVQDDGNMFLVLSHWDQAQVSOQLRVNPKYVLRVLTARKVGGG 1085
QY 1087 NGYVIRGCGNOTETLTFSADYDNTGMYNTQVNTGNTGNTNAYNTQASSTNGYNANNM 1146
DB 1086 DGYVIRGAGHQQEILTNAQDYVNGY-----1114
QY 1147 YNTQASNTGNTNAYNDQGTIYTKTYTPIPTQPMIEMSETGTFYIESVELI 1202
DB 1115 -----VNDNS-----YITEEVVFPYETKHMVVESESGSFYIDSIEFI 1153

RESULT 5
C9DA BACTP STANDARD; PRT; 1169 AA.
AC O06014;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE Pesticidal crystal protein cry9Da (insecticidal delta-endotoxin
DE CryIXD(a)) (Crystalline entomocidal protoxin) (132 kDa crystal
DE protein).
GN CRY9DA OR CRYIXD(A).
```

```
OS Bacillus thuringiensis (subsp. japonensis).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
RN [1]_TaxID=128936;
RP SEQUENCE FROM N.A.
RC STRAIN=N141;
RA Asano S.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPIHELIAL CELLS OF INSECTS.
CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPOREULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
CC -!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
CC N-TERMINUS.
CC -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; D85560; BAAL19948.1; -.
CC HSPSP; P07130; 1DLCL.
CC InterPro; IPR001178; Endotoxin.
CC Pfam; PF00555; endotoxin; 1.
CC Toxin; Sporulation.
CC SQ SEQUENCE 1169 AA; 132228 MW; 659AB25729DE5E9 CRC64;
Query Match 40.4%; Score 2558.5; DB 1; Length 1169;
Best Local Similarity 43.8%; Pred. No. 4 4e-135;
Matches 555; Conservative 188; Mismatches 356; Indels 169; Gaps 25;
QY 1 MSPNNQNEYIIDIATPSTSVSNDNRYPFANEPTNALQNMDYKDYLMQASAGNASEYEGSP 60
DB 1 MNRNNQNEYVIDAPHGCPADVVVKYPLTDDPNAGLQNNYKEYLQYGDYTDPLNP 60
QY 61 EVLVSGDAAKAAIDIVGKLLSGLGVFPVPIVSLYTLQIDILWPSCGKQWELFMQVE 120
DB 61 NLSVSGKDVIVQVGINIVGRLLSFFGFPFSSQWTVTYLLNSLWLPDDENSVDAMERVE 120
QY 121 ELINOKTAERYARKNSELSEGLGNVQLYLTAALEENENPNSGRALDRVNRPIILSLF 180
DB 121 ELIDQKISEAVKGRALDDLTGLQVNYLYVEALDEWLNRPNGAKSL--VSORFNILSLF 179
QY 181 TQVMPST---RVTNFVPEPLTVYMAAANLHLLKLDASIFGEEWGWSTTTNNYIDROM 236
DB 180 TQFMPFSGSGGSONYATILLPVYQAANLHLLKLDADIVGARWGLNQIQIDQFHSRQQ 239
QY 237 KLTAEYSDHCVKYETGLAKLGTSAKOWDYNOFRREMTLAVLDVVALPNYDTRYPM 296
DB 240 SLTQTYTHNCVTAANDGLAELRGTTAESWFKYQYRREMTLTAMDVALFPYNYLRQYD 299
QY 297 ETKAQLTREVYT---DPLGAVNVSSIGSWYDKAP-----SFGVISSVIRPPHVPDYI 346
DB 300 GTNPQLTREVYTDPIAFDPLEQPTQICRSWYINPAFRNHLNFSVLENSLRPPHLLERL 359
QY 347 TGLVTVYQSRISISSARYIRHWAGHOISYHRVSRGSLNQOMY-----GTNQLHSTSTF 399
DB 360 SNLQILVNYQTNGSA-----WRGSRVRYHYLHSSIIQEKSYGLLSDPVGANINQ----- 409
QY 400 DFTNYDIYKTLSDAVLLDVIYPGYT-----YIFGMEPEVEFFWVNO 441
DB 410 ---NNDIYQIISQVSNFASPVGSSYSVMDTNFYLSSGQVSGISGYTQGIIPAV---CLQQ 463
QY 442 LNNTRKTLKYNPVSKDIIASTRDSLELELPPTSOPNYESYSHRLCHITSI----- 492
DB 464 RNSTDDELPSLNP-EGDII-----RNYSHRLSHITQYRFOATQSGS 502
QY 493 PATGNTTGLVPVFSWTHRSADLNNTIYSDKITQIPAVKCMNDLPVVPVKGFGHTGGDLL 552
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Db 503 PST--VSANLPTCVTHRDVLDNTITANQITOLPLVKAHELSSCATVVKGGFTGSDVI 560
QY 553 QYNSTSGVGLFLARVGLALEKAGKRVRYRATADIVLHVND-----QIOMPMTMN 607
Db 561 R-RTNTGCGFAIRVSVGPLTQ---RYRIRPRYASTIDFDFVTRGGTTINNFRFTTMN 616
QY 608 PGEDLTSTKPKVADAITLNLATDSSIALKHNLEDNPNSTLSGIVYVDRIEFIPVDIYE 667
Db 617 RQGSRYESTVETFTPTNFNTQSDIIRTSIOGLSGN---GEVILDRIBIIPNPAE 672
QY 668 ABQDLEAAKXAVNA-LFTNTKXGRLPGVTDYEVNAQANLVECLSDDLYPNEKRLFLDAVR 726
Db 673 AEDLEAAKAAARQNLFTRTRDGLQVNVTDYQVDAANLVSCLSDQYGHDKMLLEAVR 732
QY 727 EAKLSARNLLQDPDFQEQING--ENGWASTGIEVTEGDALFKGRYLRLPGAREIDTET 784
Db 733 AAKLSERNLLQDPDFNTINSTENGWASKANGVTISEGGFFFKGRALQLASAR-----EN 788
QY 785 YPTLYQKVEEGLKPYTRYRLRGVSSQGLEIFTIRHOTNRIVKXNPVDDLLPDVSPVN 844
Db 789 YPTIYQKVASLKPTRYRLRDLGVKSSQDLEIDLHYHKVHLVKVNPDLN---VSDTY 845
QY 845 SDGS---INRCSEQKYNRSLEVEN-----RSGEAHEFSIPIDTGBIDYNNAGIWWG 894
Db 846 SDGSCGMRCEEQMNAQLETEHHHPMDCCAAQTHEFSSYINTGDLNASVDQGIWV 905
QY 895 FKTDPSGYATLGNLVEGPLSGDALERLQREBQKWIQMTRRREBTDTRYWASKOAV 954
Db 906 LKVRTDGYATLGNLVEGPLSGESLERQDRONAKWNAELGRKRAEIDRVYLAQAI 965
QY 955 DRLYADYQDQQLNPDEITDLTAQDLTQSIPTVYVYNNMFPPIGWNKYTKFTELDRLOA 1014
Db 966 NHLFVDYQDQQLNPDEITDLTAQDLTQSIPTVYVYNNMFPPIGWNKYTKFTELDRLOA 1025
QY 1015 WSLYDQRNAIPNGDFRNGLSNNAATPGVEVQOINHTSVLVIPIPNDEQVSOQFTVPQRY 1074
Db 1026 SYLYTSRNAVQNGDFNSGLDSMNNTTASVQDGNMFLVLSHWDASVQSLRVNPNCKY 1085
QY 1075 VLRVTARKEGVNGVYIRDCGNQTEILTFASDYDINGMYNTQVNTNGYNTNNAVNTQ 1134
Db 1086 VLRVTARKVGGDGYVIRDGAHQETLTFNACDYVNGTY----- 1126
QY 1135 ASSTNGYNANNMYNTQASNTNGYNTNSVYNDQTVITKTVTFTFVPTQMWLEMSSTGTF 1194
Db 1127 -----VNDNS-----YIEEVVYFETKHMWVEVSESGSF 1157
QY 1195 YIESVELI 1202
Db 1158 YIDSIEPI 1165

RESULT 6
C9EA_BACTA STANDARD; PRT; 1150 AA.
ID C9EA_BACTA
AC Q9ZNL9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pesticidal crystal protein cry9Ea (insecticidal delta-endotoxin
DE CryIXE(a)) (Crystalline entomocidal protoxin) (130 kDa crystal
DE protein).
GN CRY9EA OR CRYIXE(A).
OS Bacillus thuringiensis (subsp. aizawai).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1433;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SSK-10;
RA Midon N., Oyama K.;
RT "Bacillus thuringiensis cry gene for insecticidal crystal protein."
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT

```

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CC EPIITHELIAL CELLS OF INSECTS.
CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
CC -!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
CC N-TERMINUS.
CC -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC -----
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CC -----
DR EMBL; AB011496; BAA34908.1; -.
DR HSSP; P07130; 1DLC.
DR InterPro; IPR001178; Endotoxin.
DR Pfam; PF00555; endotoxin; 1.
KW Toxin; Sporulation.
SQ SEQUENCE 1150 AA; 129895 MW; 7D6AB93D6EDC97EB CRC64;

Query Match 38.7%; Score 2449; DB 1; Length 1150;
Best Local Similarity 43.4%; Pred. No. 5.6e-129;
Matches 541; Conservative 198; Mismatches 362; Indels 146; Gaps 30;

QY 1 MSPNNQNEVEIIDATSTSVSNDNRPYFANEPNALQNNQNDYKDKLMSAGNASIEYRGS- 59
Db 1 MNRNNPNEVEIIDAPYCGCPDSDVRYPLASDPNAAFQNNMYKEYLQYDG---DYTGSL 57
QY 60 --PEVLVSGQDAKAIDIVKLLSGLPVPGVIVSLVLTQILDLWPSGEKQWEIEME 117
Db 58 INPNLSINPRDVLQTGINIVGRILGFLGVFAGQLVTFYTFLLNQLMPTNDNAVWEAFMA 117
QY 118 QVELINQIKAEYARNKALSELGLGNVLYLTALTEENENPENGSRALDRVNRPIILD 177
Db 118 QIEELIDOKISAQVNRNALDDLTGLHDHYEYLALEWLERENGARA-NLVQRFENLH 176
QY 178 SLFTQWMPSPRV---TNFVPPPLTVYMAANLHLLLDKASIFGSEWGSTTTINNYD 233
Db 177 TAFVTRMPSPSGTGFQSDAVALTVYQAANLHLLLDKAEIVGARWGLQGOINLYFN 236
QY 234 ROMKLAIEYSDHCXKVEYGLAKLKTSAQWVDYVQPREMTLAVLDVVALPENVYTRT 293
Db 237 AQQERTYIYNHCVETYNRGLEDVGRGNTESWLNHRFREMTLMAAMDVALPFFVNVQ 296
QY 294 YPMETKAQLTRREYVTDPL---GAVNVSSIGSWYDKA-PGFGVIESSVIRPPHVPDYITGL 349
Db 297 YPNGANPOLTRREYVTDPIVYVPPANOGICRRWGNPNYTFSELENAFIRPHLPERLRL 356
QY 350 TV-----YTSRSISSARYIRHWAGHOISYHRVSRGSLNQOMYGTNQNLHSTDFDFTNYD 405
Db 357 TISRNYTAPTINS---FLDYWSGHTLQSOHANNPTTYETSYG-QITSNTRLENTN-- 409
QY 406 IYKLSKDAVLVDIVPGYIYF---FGPEVEFF---MVNQLNTRKLYKNVPSKDI 459
Db 410 -----GARIDSRRARNFGNLYGVSSLNIFPTGVMSSEITNAANTCRODLTTE-- 460
QY 460 ASTRDSELEPPPTSDQPNYESYSHRLCHITSIPATGNTT-----GLVPVPSWTHRS 511
Db 461 -----ELPLENN-----FNLLSHVFL--RPNTTQGGFLATLGFVPVYVWTRD 503
QY 512 ADLNTIYDKITQIPAVKCDNLFPVVPVKGPGHTGGDGLQVNRSTSGVGTFLARYGL 571
Db 504 VDFNTITADRIQTLPKWKASEIGGGTIVVKGPGTGGDILR-RTDGAAGVTI---RANV 559
QY 572 ALEKAGKYRVLRYATDAIV--LHVND--AQIQMPTNPGEDLTSTKPKVADAITTLN 627
Db 560 NAFLTQOYRIKRYASTYFVWNLFFVNSAAGTFLPSTMAQNSGLSTYESFNTLEVTIIR 619
QY 628 LATDSSLAKHNLGDPNPNSTLSG-IYVDRIEPIVDETVESQDLEAKKAYNALPNT 686

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Db 620 F-SQSDTTLRLNI-----FPSISGQEVYVDKLEIVIPINPTREABEDLEDAKAVASLEFRT 674
Qy 687 KQGLRPGVTDYEVNQANLVCLSDLLYPNEKRLLEFLDAVRAKRLSEARNLLQDPDQEI 746
Db 675 RDGLQVNTDYQVDDQANLVCLSDQEGHDKMLLEAVRAKRLSRNLLQDPDQNEI 734
Qy 747 NG--ENQWTASTGIEVIEGDALFKGRVLRLEPGAREIDTETPTLYQKVEGVLPKPTRY 804
Db 735 NSTEENCKWASNGVTISEGGPFPAKRALQALASAR---ENYPTIYQKVDASTLKPTRY 790
Qy 805 RLKGFVSSQGLEIFTRHQTNRIRVKNVDPDLLPDPVSPVNSDGS---INRCSEOKYNSR 861
Db 791 KLKDFVQSSQDLEIDLHKKHVLVKNVNDL---VSDTYSGSCSGINRCSEHQVDVQ 847
Qy 862 LEVEN-----RSGEAHEFSPIDTGRIDYNNENAGIWDGFKITDPEGVATIGNLELVEG 915
Db 848 LDAEDHPKDCCEAAQTTFEFSYIHTGDLNASVDQGIWVLQVTRTDTGATVIGNLELVEG 907
Qy 916 PLGSDALERLQREBQWKIQMTRREBETDRRYMASKQAVDRLYADYQDQQLNPQVEITDL 975
Db 908 PLGSESLEREQDNKAWNEEVGRKRAETDRIYQDAKQAINHLFVDYQDQQLSPVGMADI 967
Qy 976 TAAQDLIQSPYVNEPPEIPGANYKFTPTLDRLOQAWSLYDQRNAIPNGDFRNGLSN 1035
Db 968 IDAQNLTASISDVYSDAVLQIPGINEMYETLSNRLQOASLYTSRNVVQNGDFNSGLDS 1027
Qy 1036 WNATPGVEVOQINHTSVLIPNWDQVSOQFTVQPNORVLRVLTARKEGVNGVYSIRDG 1095
Db 1028 WNATTDVAVQDGNHFLVLSHWDQVSOQFRVQPNCKYVLRVTAKRKVGNGDGVITQDG 1087
Qy 1096 GNQETILTFGSADYDTGMVNTQVSNNGYNTNAYNTQASSTNGYNANNMYNTQASNTN 1155
Db 1088 AHRETLTFNACDYDVNGTH-----1107
Qy 1156 GYNTNSVNDQGTGHTKVTPIPTDQWIMSETEGTFYIESVELI 1202
Db 1108 -VNDNS-----YITKELVFPKTEHMMVEVSETEGTFYIDSIEFI 1146

RESULT 7
CIXA_BACTM STANDARD; PRT; 1215 AA.
ID CIXA_BACTM AC Q45715;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pesticidal crystal protein cry1Ka (insecticidal delta-endotoxin
DE Cry1K(a)) (Crystalline entomocidal protoxin) (137 kDa crystal protein).
GN CRY1KA OR CRY1K(A) OR CRY1K.
OS Bacillus thuringiensis (subsp. morrisoni).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1441,
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=F190;
RX MEDLINE=96102856; PubMed=8586263;
RA Koo B. T., Park S. -H., Choi S. -K., Shin B. S., Kim J. I., Yu J. H.;
RT Cloning of a novel crystal protein gene cry1K from Bacillus
RT thuringiensis subsp. morrisoni."
RL FEMS Microbiol. Lett. 134:159-164(1995).
CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPIGUTAL CELLS OF INSECTS. SELECTIVELY TOXIC TO ARTOGEDIA RAPAE
CC AND NOT ACTIVE ON PLUTELLA XYLOSTELLA.
CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPOREULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
CC N-TERMINUS.
CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC -----
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CC -----
DR EMBL; U28801; AAB00376.1; -
DR HSSP; P02965; 1CIY.
DR InterPro; IPR001178; Endotoxin.
DR Pfam; PF00555; endotoxin; 1.
DR Toxin; Sporulation.
SQ SEQUENCE 1215 AA; 137378 MW; 7CA7A33311893D9B CRC64;

Query Match 38.1%; Score 2415.5; DB 1; Length 1215;
Best Local Similarity 42.9%; Pred. No. 4.5e-127;
Matches 538; Conservative 201; Mismatches 421; Indels 95; Gaps 28;

Qy 1 MSPNQNEYEIIIDATSTSVNSDNRYPFANEPTNALQNMDDYKDYLMKMSAGNASEYEGSP 60
Db 1 MNSNRKNEIINAIISPVSNSHAQVMDLSPDAR-----IEDSLCAEAGNNID----P 49
Qy 61 EVLVSGQDAAKAIDIVGKLLGLGVPPFVGVPIVSLYLTQLIDILWPSCKEKOWEIFMEOVE 120
Db 50 FVSAAS---TVQTSISAGRIAGLVGVPPFAGQLASFYSFLVGLWPSG-RDPWEILFMEHVE 105
Qy 121 ELI-NQKIAEYARKALSELEGNNYQLYLTALAEWEENPNNGSRALRDVNRPEILDLSL 179
Db 106 QIVRQQIITDSVSDTAARLEGLGRGYSYQQALETWLDNRNDARSRIIRERVIALELD 165
Qy 180 FTQMPFSRVTVNEVEPLTVYMAANLHLLLLKDAISFGEEWGSTTTINNYDRQMKLT 239
Db 166 ITTAIPLFSIRNEVEPLLMYQAANLHLLLRDASLFGSEWGMSSADVNAQYQEQIRYT 225
Qy 240 AYSYDHCWKVYETGLAKTGTSAKQVVDYQNPQREMTLAVLDVVVLPFNPYDTRYPMETK 299
Db 226 EYSNHCVMQNTGLNRKRGTTAETWVRYNQPRDLFLGVLVDLVALPSPDTRYPITPT 285
Qy 300 AQLTREYVTDPLGAVNVSSISGWDYKAPSGVIESVIREPPHVDYITGLTVYTSRSIS 359
Db 286 AQLTREYVTDPLGVV-AGPNNSMFRNGASFSAIENAIIRQPHLYDPLTNLTITR-RSQV 343
Qy 360 SARYIRHWAGHQSIRHVRSGSNLQMGYNQNLHSTSTDFNTYDIYKTLSDKDALDI 419
Db 344 GTTIMNLWAGHRTFNRIOGGSSEMYGAIITNPVSVSDIPFVNRDRVYRTVSLAGGSL 403
Qy 420 VYFGYTVIFPGMEVEFEFMYNQLNTRKT-LKYNPVSKDIIASTRDSLELPPTSDPN 478
Db 404 -----SGIRYGLTRVDPMIFRNHPDIVTGLFVHPHAGIATQVKDSDELPPPTTQPN 458
Qy 479 YESYSHRLCHITSIPATGNTTGLVPVFSWTHRSADLNTIYSDKITQIPAVKCDNLPFV 538
Db 459 YRAFSLLSHISMGPTTQD---VPPVYVSWTHQSADRNTINSRITQIPLVKAHTLQSGT 515
Qy 539 PVKPGHGTGDDLQVNRSTGSGVTLEFLARYGLALEKAGKYRVLRYATDADIVLHND 598
Db 516 TVKVGPGFTGGDILR-RTSG--GPEAFSNVNLDFNLQRYRARIYASTNLRIYVTV 571
Qy 599 -----QIQMPKTNPGEDLTSKTKVADAITTLNLA-----TDSSLAKHNLGSDPNSTL 648
Db 572 GERIPAGQFQKTDWAGAPLTFQSFVA-----TINTAFTFPERSSSL-----TIGADTFSS- 622
Qy 649 SGIVYVDRIFPIVDETYEAEQLEAAKAVNALFTNTKD-GLRPGVTDYEVNQANLVE 707
Db 623 GNEVYVDRFELIQVATFAESDLERAKAVNALFTSTNPRGLKTDVTDYHIDQVSNLVE 682
Qy 708 CLSDLYPNRKLLFDVAEREAKRLSEARNLLQDPDQNEI-----ENGWTASTGIEVIEGDA 765
Db 683 CLSDEFCLDKKRELLEEVKAKRLSDERNLQDPTFTSISQOTDRGWIGSTGISIQGDD 742
Qy 766 LFKGRVLRLEPGAREIDTETPTLYQKVEGVLPKPTRYELRGVSGSQGLEIFTRHQT 825
Db 743 IFKENYVRLPFT--VD-ECYPTLYQKIDESQLKSYTRYQLRGYIEDSQDLIELIYRNA 799
Qy 826 NRIVKNVDDLLP----DVSPVNSDGSINRCSEOKYNSRLEVENRSGE-----AHEFSI 876
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Db 800 KHTLSVPGTESPWPSSGVPSGRCBPNRCAPRIEMWNPDLDCSCRYGKCVHSHHFSL 859
Qy 877 PIDTGEIDYENAGIWGFKITDPEGVATLGNLELVEBGLSGDALERLOREQWQIOM 936
Db 860 DIDVCGTDLNEDLGGWIFIKITQDGHAKGNLFIEBKPLGKALSKVKAERKWDKY 919
Qy 937 TRREEDRRYMASQAVDRLYADYQDQOLNPDVEITDLTAAQDLIQSIPIVYNEMPEI 996
Db 920 EKLOLETKRVYTEAKESVDALFVDSQYDKLOANTNIGIIHGADQVHRIEPIYSELPI 979
Qy 997 PGMYTPTTELTLRLOQAWSLYDORNAIPNGDFRNGLSNNWATPGVEVQOQNHNTSVLIP 1056
Db 980 PSINAAIPEELEHGFHFRAYSILYDARNVTKNGDFNGLSCMNKGVHDVQONHRSVLVS 1039
Qy 1057 NWDSVQSQFTVQPNQRYLVARTARKEGNGVGVYSIRGGNQGTETLTPSASDYDTNGYN 1116
Db 1040 EWEAEVSQKVRVCPDRGYILRVATYKGYEGGCVTIHEFEDNTDLKFP--RNFVEEYVP 1097
Qy 1117 TVQSNNGYNTNAYNTQASSTNGYNA-----NNMNTQAS-----NTN 1155
Db 1098 NNTVTCNDYTNQSAEGSTDACNSYRGYEDGYENRYEPNPSAPVNYTPTVEEGMYTDTQ 1157
Qy 1156 GYN---TNSVNDOT---GYITKTFTPIPTDQWIMSEMSTEGTFYIESVELIV 1203
Db 1158 GYNHCVSDRGYRNHTPLPAGVYVLELVEFPETEQWIEGTETGTFIVGSVELLL 1212

RESULT 8
C7AB_BACUA STANDARD; PRT; 1138 AA.
ID C7AB_BACUA
AC Q45707;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pesticidal crystal protein cry7AB (insecticidal delta-endotoxin
DE CryIIA(b)) (Crystalline entomocidal protoxin) (130 kDa crystal
DE protein)
DE CRY7AB OR CRYVIIA(B).
OS Bacillus thuringiensis (subsp. dakota).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=132268;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD511;
RA Payne J.M., Fu J.M.;
RT "coleopteran-active Bacillus thuringiensis isolates and genes encoding
RT coleopteran-active toxins.";
RL Patent number US5286486, 15-FEB-1994.
CC -!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPIITHELIAL CELLS OF COLEOPTERA.
CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPORELIATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART OF
CC THE SPORE COAT.
CC -!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-
CC TERMINUS.
CC -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC -----
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CC -----
CC EMBL; U04367; AAA21120.1; -.
CC HSSP; P07130; 1DLC.
DR InterPro; IPR001178; Endotoxin.
DR Pfam; PF00555; endotoxin; 1.
KW Toxin; Sporulation.
SQ SEQUENCE 1138 AA; 129778 MW; 01DF702C074CE88 CRC64;
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Query Match 37.9%; Score 2397; DB 1; Length 1138;
Best Local Similarity 42.4%; Pred. No. 4.4e-126;
Matches 524; Conservative 208; Mismatches 367; Indels 138; Gaps 30;

Qy 1 MSPNNQNEYEIIIDATSTSVNSDNRYPPFANETNALQNDYKDYLRKMSAGNASEYPGSP 60
Db 1 MNLNLNGGYE-----DSNRTLNLSNYPTOKALSPSLKNNYQDFLSITERE-----QP 49
Qy 61 EVLVSGDAAKAALDIVKGLSLGVFPVGVPIVSLYLTQLDILWPSGEKSWELFMEOVE 120
Db 50 EALASGNTAINTVSVVGATLSALGVPGASFITNFKITGLLWPH-NKNINDEFMTEVE 108
Qy 121 ELINOKIARYARNKALSEGLGNNYQLYLTALEEENPNGRALRDVNRREILSLF 180
Db 109 TLEQKIEQVARNKALAEGLGNNLTIIYQALDMLNPPDPATITRVIDRFRILDALP 168
Qy 181 TQMPSPRVNFEVPLTVYAMAANLHLLKQASIFGEEWGWSTTTNNYIDROMKLT 240
Db 169 ESMPSFVAGYBIPLTVYAQAANLHLLRDSTLYGDKWGTQNNIEENYANRQKHIS 228
Qy 241 EYSDHCVKVETGLAKLKGTSAKOWVDYNOFRREMTLAVLDVVALPNYDTRTYPMETKA 300
Db 229 EYSHCVKWTNGLSLRNGSTYEQWYNINFRREMILWLDIAAFPIYDFRMYMETST 288
Qy 301 QLTREVYTDPLGAVNVSSIGSWYDKAPSGFVIESSVIRPPHVEDYITGLTVYTQSRSS 360
Db 289 QLTREVYTDPI-SLSISN-----PDIGPSFSQMENTAPRTHLVLDYLDLYIYSKYKAFS 343
Qy 361 ARY---IRHWAGHQISYHRVSRGNSLQQ---MYGTNQLHSTSTFDFTNYDIYKTLSDAV 415
Db 344 HEIQPDLFTWCVHKVSPKK-SEQSNLYTTGIYKTSYISSGAYSPAGNDIYRTLAAPSV 402
Qy 416 LLDIVVPGYTIFFGMPVEVEFFVWNLNTRKTLKYNPVSKDIIASTRDSLELELPETSD 475
Db 403 ---VVIP-YIQ-NYGEQVEFYGVKGHVHVRGNKYD-----LYTSDIDQLPDP--G 447
Qy 476 QPNYESYSHRLCHITSI-----PATGNTTGLVPVFSWTHRSADLNNTTYSKTIQIPAVKC 531
Db 448 EPIHEKYTHLCHATAISKSTPDYDNAT--IPIFSWTHRSAEYNNRYPNKKIPAVKM 505
Qy 532 WDLNLPFVVPVKGPGHGGDLLQVNRSTGVSVGTFLARYGLALEKAGKYRVLRYATDADI 591
Db 506 YKLDLSTVVKVPGFTGGDLVK-RGSNGYIGDI-KATVNSPLSQ--KYRVRYRYATSVSG 561
Qy 592 VLHV--NDAQIOMPK-----TWNPGEGLTSTKPKVADAITLNLATDS---SLALKEN 639
Db 562 LFNVFIND-BIALQKQFQSTVETIGEGLUTYGSFGYIEYSTTIQPPNEHPKITLHNLH 620
Qy 640 LGEDPNSTLSGIVVVDRIEPIPVDETYEARQDLAEAAKAVNALFTNTKGLRPGVTDYEV 699
Db 621 SNNSP-----FVDSIEPIPVVNYDEKEKELEKAKAVNTLFTGRNALQKYVTDYKV 673
Qy 700 NQANLVECLSDLLYNEKPLLFDAVREAKRLSEARNLLQDDPDPQIRING--ENGWTA 757
Db 674 DVQSILVDCISGDLVYNEKRELQNLVKARLSYRNLLDPTFDSINSSENGWYGSNG 733
Qy 758 IEVLGDALFKGYRLPGARETDTETPYLYKYVEEGLVKPYTRYLRGFGVSSGOGL 817
Db 734 IVNGGDFVFGNGLYLFSGYN--DTQ-YPTLYQKIDESKLEYSRYKLGKGFTESSQDLE 790
Qy 818 IFTRHQTNRIKVNPPDLLPDVSPVNSDGSINRCSEQKYVNSRLEVENRSGE----- 870
Db 791 AVYIRYDAKHRTLDVSDNLLPDILPENTCGEPNRCAAQQLD-----ENFSSCSNMQDG 845
Qy 871 ----AHEFSPIDTGEIDYENAGIWGFKITDPEGVATLGNLELVEBGLSGDALERLQ 926
Db 846 ILSDSHSFSNLNIDTGSINHNENLGIWLFKISTLEGYAKFENLEVEDGDPVIGEARLVK 905
Qy 927 REEQWQKIOWTRREEDRRYMASQAVDRLYADYQDQOLNPDVEITDLTAAQDLIQSI 986
Db 906 RQETKWRNKLAQMTTQAIYTRAKQALDNLFANAQDHLKIDVTFABIAARQVQSIR 965
Qy 987 YVYNEMFPEIPGMNYTKFTELTDLRQAWSLYDQRNAIPNGDFRNGLSNNWATPGVEVQO 1046
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Db 966 EVTMSLVVPGVHPIFTSLGRVORAFQDYDVRNVRNGRFLNGSLDWIVTSNVQOE 1025
Qy 1047 INHTSVLVIPWDEQVSOQTPQPNQRYLVRTARKEGVGVSVIRDDGNGQOTETLPSA 1106
Db 1026 ENGNNVLVNNWDAQVRNVKLGQDRGVLRVTVARKIGIGEGYITITDEEGHDTQURFTA 1085
Qy 1107 SDYDTNGMYNTQVNTNGYNTNAYNTQASSTNGYNANNMYNTQASNTNGYNTNSVNDQ 1166
Db 1086 CE-----EIDASNAF-----I 1096
Qy 1167 TGVITKTVFIPPTDQWMIEMSTEGTFYIESVELIV 1203
Db 1097 SGYITKELEFPPTDQWMIEMSTEGTFYIESVELIV 1133

RESULT 9
C1BB_BACTU
ID C1BB_BACTU STANDARD; PRT; 1229 AA.
AC Q45739;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE Pesticidal crystal protein cryIIb (insecticidal delta-endotoxin
DE CryIIb(b)) (crystalline entomocidal protoxin) (140 kDa crystal protein).
GN CRYIIB OR CRYIIB(B) OR CRYETS.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxId=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EG5847 / NRRL B-21110;
RA Donovan W.P., Tan Y., Jany C.S., Gonzalez J.M. Jr.;
RT "Bacillus thuringiensis cryet4 and cryet5 toxin genes and proteins
RT toxic to lepidopteran insects.";
RL Patent number US5322687, 21-JUN-1994.
CC -!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF MANY LEPIDOPTERAN LARVAE.
CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPORE FORMATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
CC -!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
CC N-TERMINUS.
CC -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
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Db 106 QLIRQOVTVNTNTAIAARLEGLGRGYSYQQALETWLDNRNDARSRIILERVVALELDI 165
Qy 181 TQYMSFRVTNEVPLTYVYAAANLHLLLLKQASTFGEWGHSTYITNNYDROKMLTA 240
Db 166 TTAIPLFIRNEVPLVMVYAANLHLLLDASLFGSEWGNASSDVNQYQOEIRYTE 225
Qy 241 EYSDHCVKWYETGLAKLKGTSAKQVVDVNOFRREMTLAVLDVVVALPPNYDTRYPMETKA 300
Db 226 EYSNHCQWNTYGLNLRGTNAESWLRVYNQFRDLTLGVLDLVALPSPDYTRYPINTSA 285
Qy 301 QLTREYVTDPLGAVNVSS---IGSWY-DKAPSGFVIESVIRPPHVFYITGLTVVYQSR 356
Db 286 QLTREIYTDPIGRTNAPSFGASTNWFNNAPSFAEAAIFRPHLLDPPEQLTIYSASS 345
Qy 357 SISSARYIRHWAGHOISYHRVSRGSLNQMYGTNQNLHSTSTFDETNYYDIYKTLSDAVL 416
Db 346 RWSSTOHMYVWGHRLNFRPTIGTTLNTSTQGLTNTSINPVLQFTSRDYRTESNAG-- 403
Qy 417 LDIVYPGYTIYFP-----GMPEVEPFVWNLN-NRKTLLKYNPVSXDIITASTRDSLELP 470
Db 404 -----TNILFTYPVNGVPAWFNPINQNIYERGATTYQPYQGVGIQLPDSLETLP 455
Qy 471 PETSQPNYESYSHRLCHITSIPATGNTTGLVPVPSWTHRSADLNNTIYSDKITQIPAVK 530
Db 456 PETTERPNYESYSHRLSHIGLI--IGNTL-RAPVYSWTHRSADRTWTIGPNRITQIPLVK 512
Qy 531 CWDNLPFPVVPVKGPGHGTGDLLOYRSTSGVTLFLARYGLALEKAKGRVRLRYA--TD 588
Db 513 ALNLHSGVTWVGPGFTGGDIIL-RTNTGTGDI---RLNINVPLSQRYRIRYASTTD 568
Qy 589 ADIVLHVNDQIQM---PKTMNPGEDLTSTFKVADAITTLATDSSSLAKHNLGEDPN 645
Db 569 LQFFTRINGTTVNIQNFSTRMGRGNLEYSRPTAGFSTPFPLNAQS---TFTLAQSF 625
Qy 646 STLGSIVYVDRIEFIPVDETYEAEQDLAAKAVNALFTNTKD-GLRPGVTYDEVNQAAN 704
Db 626 SNOE--VYIDRVFVPAEVTPEAYEDLERAQKAVNALFTSTNPRRLKTDVTDVHIQVSN 683
Qy 705 LYECISDDLYPNEKRLLPDAVREKLSARNLLODPDFQEING----- 748
Db 684 MVACISDEFCLDEKRELFEKVAKRLSDERNLLODPNFTFISGQSFASIDQSQSNFPSI 743
Qy 749 ----ENGWTAAGIEVIEDGALFKGRYLRLPGAREIDTETPTLYLQKYVEGVKPYTRY 804
Db 744 NELSEHGWSGANVTIOEGNDVFKENYVTLPGT---FNECYPNLYQKIGESLKYTRY 800
Qy 805 RLRGFVSSQGLEIFTRHOTNRIKVNVP--DLLLP--DVSPVNSDGSINRCSQKYVNS 860
Db 801 QLRGVIEDSQDLEILYIRYNAXHETLDVPGTDSLWPLSVESPIGRGCEPNRCAPHEWNP 860
Qy 861 RLEVENRSGE-----AHEFSIPDITGEIDYNNAGIWWGFKITDPEGYATLGNLELVEEG 915
Db 861 DLDSCSRDGERCAHSHHFETLDVGTDLHENLGVVWVFKIKTOEGYARLGNLEFIEEK 920
Qy 916 PLSGDALERLQREOQKOWTMRREETDRRYMAKQAVDRLYADYQDOQLNPDVETDL 975
Db 921 PLIGELSRVKAABKKRDKREKLQETKRVTEAKEADALFVDSQYDQLQADTNIGMI 980
Qy 976 TAAQDLIQSIPYVYNNMFPEIFGMNYTKETELTDRLQQAWSLYDQRNAIPNGDFRNLGN 1035
Db 981 HAADKLVRHIREAYLSLSELPVIFGVNAEIPFEELEGHITITAMSLYDAENVKNGDFNGLIC 1040
Qy 1036 WNAATGVEVQOQNNHRSVLVIPNWDQVQSQQFTVQPNQRVLRVARTARKEGVGVSVIRDG 1095
Db 1041 WNVKGHVDVQOQSHRSDDLVIPEWEAEVSQAVRCPGRGVIILRVYAKYEGEGCVTIHEI 1100
Qy 1096 GNOTETLTSADYDINGMYNTQVNTNGYNTNNAVNTQASSTNGYNANNMYNTQASNTN 1155
Db 1101 ENNTDELKE--KNCSEEVYPTDGTGTCNDYTAHQG-----TAACNSRNAGYEDAYEDTTA 1154
Qy 1156 GYNTNSVYNDQF-----GYITKTVTPIPTDQWMIEMSETE 1191
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Db 1155 SVNYKPYEBETDVRDNCHEYDRGVNYPVPAGVYVTKLEYFFETDTVWISIGETE 1214
QY 1192 GTFVIESVELIV 1203
Db 1215 GKFIIVDSVELLL 1226

RESULT 10
C7AB_BACUK
ID_C7AB_BACUK STANDARD; PRT; 1138 AA.
AC Q45708;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pesticidal crystal protein cry7ab (Insecticidal delta-endotoxin
DE CryVIIA(b)) (Crystalline entomocidal protoxin) (130 kDa crystal
DE protein).
GN CRY7AB OR CRYVIIA(B).
OS Bacillus thuringiensis (subsp. kumamotoensis).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=132267;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD867;
RA Payne J.M., Fu J.M.;
RT "Coleopteran-active Bacillus thuringiensis isolates and genes encoding
RT coleopteran-active toxins";
RL Patent number US5286486, 15-FEB-1994.
CC -!- FUNCTION: PROMOTES COLEOPTEROTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF COLEOPTERA.
CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
CC -!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
CC N-TERMINUS.
CC -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC
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CC
CC EMBL; U04368; AAA21121.1; -;
DR HSP; P07130; IDLC.
DR InterPro; IPR001178; Endotoxin.
DR Pfam; PF00555; endotoxin; 1.
KW Toxin; Sporulation.
SQ SEQUENCE 1138 AA; 129658 MW; E12DC80C0A56D1DA CRC64;

Query Match 37.78; Score 2388; DB 1; Length 1138;
Best Local Similarity 42.3; Pred. No. 1.4e-125;
Matches 521; Conservative 208; Mismatches 374; Indels 130; Gaps 28;

QY 1 MSPNNQNEYIIDAPTSPVSDNSRNPFPANEPTNALQNMDDYKDYKMSAGNASEYGPSP 60
Db 1 MNLNLCGYE-----DSNRTLNLSNLYPTQKALSPSLKNNYQDFLSITER-----QP 49
QY 61 EVLVSGQDAKAAIDIVKGLSGLGVPFVGPVIVSLYTLQIDILMPGSKSQWEIFMEQVE 120
Db 50 EALASGNTAINTVSVTGATLSALGVPASFTITFYLKITGLLWPH-DKNIWDEFMTVE 108
QY 121 ELINQKTAENARKALSELEGNNYQLYLTALBEEWENPMSRALDRVRNFILSLF 180
Db 109 TLIEQKIEQVARNKALAELEGNNLTYYQQALEDWLNPPDPATITRVIDRFRILDALF 168
QY 181 TOYNMPSFRVTNFEVPELTVYAMANLHLLKLDASIFCEEWGWSITTNINYYDRQMKLTA 240
Db 169 ESYMPSFRVAGYEPLLTIVYQAQANLHLLLRDSTLYGDKWEFTQNNIENYNNRQKHIS 228
QY 241 EYSDHCVKWVETGLAKLKGTSKQWVDYVQFRRWTLAVLDWVALFPNYPNDRTPYMETKA 300

Db 229 EYSHNCVKWYNSGLSRLNGSTYEQWYNFRREMILWLDIAAVFPYIDPRMYSMETST 288
QY 301 QLTREVYTDPLGAVNVSSIGSWTDKAPSGVIESSVIRPPHVDYITGLTVYTSRIS 360
Db 289 QLTREVYTDPI-SLSISNPGI-----GPSFSQMENTAIRTPHLVDYLDLYTSKYKAPS 343
QY 361 ARY---IRHWAGHQISVHRVSRGSLNQ--MYGTNQNLHSTSTFDFTNYDIYKTLSDAV 415
Db 344 HEIQPDLFYMSAKVSP-KOSEQSNLYTTGIYKTSYSSGAYSGFNGNDIYRLAAPS 402
QY 416 LLDIVPGYTYPIFGMPPEVEFFMVNQLNTRKTLKXNPVSKDIIASRDSSELELPPTSD 475
Db 403 ---VYIP-YTQ-NVGVEQVEFYGVKGVHVRGDKYD-----LTYSDIDQLPPD--G 447
QY 476 QPNYESVSHRLCHITST-----PATGNTTGLVPVPSWTHRSADLNNIYSDKIQIIPAVK 531
Db 448 EPIHEKYTHRLCHATAISKSTPDYDNAT--IPFSWTHRSABEYNNRYPNKKITKIPAKM 505
QY 532 WDLNLPFVVPVKGPGHTGGDLQVNRSTGVTFLFARYGLALEKAGKYRVLRYATD--A 589
Db 506 YKLGDTSTVVGPGPTGGDLVK-RGNGYIGDI-KATVNSPLSQ--NYRVRYATVNSG 561
QY 590 DIVLVNDAQIOMPK-----TNPGBEDLTKTPKADAITTLNLTATDSSLALKHNLGED 643
Db 562 QFNVYINDKITLQKQFQNTVETIGEGKDLTYGSFYIEYSTTIQPPDKPKITLHLS 621
QY 644 PNSTLSGIVVVDRIETPIVDUETTEAEQDLAAKAVNALNTKDGRLPGVTVYEVNQAA 703
Db 622 NNSSF-----YVDSIEFIPVDVNYDEKEKAKAVNTLFTEGRNALQKDVTDYKVDQS 677
QY 704 NLVECLSDLLYPNEKLLFDVAERAKLSERNLQDPDFQIEG--ENGWTAATGTEVI 761
Db 678 ILVDCISGDLYPNEKELQNLVYAKLSYRNLLLDPTFDSINSSENGWYSGNLVIG 737
QY 762 EGDALFKGRYLRLPGAREIDTETPTLYYQKVEEGLKPYTRYRLRGFGVSSQGLEIFTI 821
Db 738 NGDFVFGNYLIPSGTN--DTQ-YPTLYQKIDESKLKEYTRYKLGFISSQDLEAYVI 794
QY 822 RHQTNRVKVPDDLLPDVSPVNSDGSINRCSEKQYVNSRLEVENRSGE-----870
Db 795 RYDAKHRTLDVSDNLLPDILPENTCGENRCAAAQVLD-----ENPSECSMMDGILSD 849
QY 871 AHFSPIDPIDGEIDYNNAGIWWGFKITDPGEVATLGNLELVEEGLSGDALERLQREEQ 930
Db 850 SHSFSNLIDIGSINHNENGLIWLFLISTLEGAKFNGLEVIDGPPVIGELAKRVKQET 909
QY 931 QWKIQMTRREEDRRYMASQAVDRLYADYQDQQLNPDPVEITDLTAAQDLIQSIPVYN 990
Db 910 KWRNKLAQLTTQTAIYTRAKQALDNLFANAQDHLKIDVTFAEIAAARKIVQSIREAYM 969
QY 991 EMPPEIPGMNYYTKETELDRLOQAWSLYDORNALPNGDFRGLSNWNATPGVEVQOINHT 1050
Db 970 SWLSVVGPNVHPIFTELSERVQBAFQLYDVNRVNRGRFLNGLSDMTVTSDVKVQENGN 1029
QY 1051 SVLVIPNWDQVSOQFTVQPNORYLVRVTARKEGVNGVYISRDGNGQTETLTFASDYD 1110
Db 1030 NVLVNNDWAQVLQNVKLYODRGYILVTRAKIGIGEGYITIDEEGHTVQLRPTACEV- 1088
QY 1111 TNGMYNTQVSTNGYNTNNAYNTOASSTNGYNANNMYNTOASNTNGYNTNSVYNDQTGYI 1170
Db 1089 -----IDASNAF-----ISGYI 1100
QY 1171 TKVTFTFIPYTDQWMIEMSETEGTFYIESVELIV 1203
Db 1101 TKSELEFPDTEKWHIEIGETEGIFLVIESIELFL 1133

RESULT 11
C1BD_BACTZ
ID_C1BD_BACTZ STANDARD; PRT; 1231 AA.
AC O92A25;
DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Peptidicidal crystal protein cryIbD (Insecticidal delta-endotoxin
 DE CryIb(d)) (CryIb(d) entomocidal protoxin) (140 kDa crystal protein).
 GN CRYIbD OR CRYIbD OR CRYIa OR CRYIe.
 OS Bacillus thuringiensis (subsp. wuhanensis).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=52024;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HD-525;
 RX MEDLINE=20153386; PubMed=10688690;
 RA Kuo W.-S., Lin J.-H., Tzeng C.-C., Kao S.-S., Chak K.-F.;
 RT "Cloning of two new cry genes from Bacillus thuringiensis subsp.
 RT wuhanensis strain";
 RL Curr. Microbiol. 40:227-232(2000).
 CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
 CC EPITHELIAL CELLS OF LEPIDOPTERAN LARVAE. TOXIC TO PLUTELLA
 CC XYLOSTELLA.
 CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPOREULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
 CC OF THE SPORE COAT.
 CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
 CC N-TERMINUS.
 CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
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 CC -----
 CC ENBL; U70726; RAD10292.1; --
 DR HSPSP; P02965; IC1Y.
 DR InterPro; IPR001178; Endotoxin.
 DR Pfam; PF00555; endotoxin; 1.
 KW Toxin; Sporulation.
 SQ SEQUENCE 1231 AA; 139654 MW; 129A0371CDBBE52 CRC64;

 Query Match 37.3%; Score 2359.5; DB 1; Length 1231;
 Best Local Similarity 41.1%; Pred. No. 6.1e-124;
 Matches 525; Conservative 197; Mismatches 433; Indels 121; Gaps 26;

 QY 1 MSPNNQNEYIIDATPSTSVNSDNRYPANEPHALQMDYKDKLMSAGNASEYFQSP 60
 DB 1 MTSNRKNEINEINALSIPAVNSHSAQMDLSLAR-----IEDSLCIAEGN-----NI 47

 QY 61 EVLVSGQDAKAAIDIVGKLLSGLVFPVGPVLSLYTQIDILWPSGKSOWEIFMEQVE 120
 DB 48 NPLVSA-STVQTGINIAGRIIGLVGPVAGQASLYSFLVGLMFSG-RDPWEIFLEHVE 105

 QY 121 ELINQKIAEYARNKALSELGLGNQYLYLTALBEEWENPNNGSRALDRVNRFEILDSLF 180
 DB 106 QLIRQVTEVNTAIALREGLGRGYSYQQALETWLDNRNDARSIIERYVALELDI 165

 QY 181 TOYMPSFVTVNPEVFLTVYMAANLHLLLKDAISFGEWGNSTTTNNYYDRQMKLTA 240
 DB 166 TTAIPFLFRIRNEEVLPLVYAQAANLHLLLRDASLFGSEWGNASSDVNQYEQIRYTE 225

 QY 241 EYSDHCWKVYETGLAKLGTSAKQWVDYVNOFRREMTLAVLDVVALFPVNYDTTYPMETKA 300
 DB 226 EYSHCVQWYNTGLNLRGTNAESMLRNQFRDUTLGLVDLVALFPSTYDTRTYPNTSA 285

 QY 301 QLREVTYDPLGAVNVSS----IGSWY-DKAPSGFVIESVIRPPHFVDFITGLTVYTSQR 356
 DB 286 QLREIYTDPIGRTNAPSGFSTWNNNAPSFAIEAAIFPPHLLDFPEQLTIYSASS 345

 QY 357 SISSARYIRHWAGHIOISYHRVSRGNLQOMYGTGNLHSTSTFDTNVDIYKTLSDAVL 416
 DB 346 RWSSTOHNWYVGHRLNFRPIGTTLNTSTOGLTNTNTSINPVTLOQTSRSDVYRTESNAG-- 403

QY 417 LDIVPGYTYIFF-----GMPEVEFPFVNVQLN-NTRKTLKYNPVSKDIIASTSDSELELP 470
 DB 404 -----TNILEFTFVNGVPWFARFNFIPQNIYERGATTYSQPYQGVQLDFSETLP 455

 QY 471 PETSDOPNYESYSHRLCHITSIPATGNTTGLVPVFSWTHRSADLNNTIYSDKLTQIPAVK 530
 DB 456 PETERPNIYESYSHRLSHIGLI--IGNTL-RAPVYSWTHRSADRTWTIGNRRITQIPAVK 512

 QY 531 CWDNLFPV---PVVKGFGHTGGDLLOYNRSTGVSGLTFLARYGLALEKAG-KYRVRLRYA 586
 DB 513 G-----REFLNGSVISGPGFTGGDVLRNRNGNIQNRGYEVPIQFTSTSTRYRVRVYA 568

 QY 587 TDADIVLHVN--DAQI---OMPTKMPGDELTSTKTKFVADAITLNLATDSSALKXNLG 641
 DB 569 SVTSELNVNLGNSSIFPTLPATAASLDNLQSDGFGYVEINNAFTSATSNIVGAR----- 624

 QY 642 EDNSTLSGLVYVDRIEFIPVDETYEAOLEAKKAVNALFTNTKD-GLRPGVTDYEVN 700
 DB 625 ---NFSANAEEVIIDRFEPITVATFEAYDLERAQKAVNALFTSTNPRRLKTDVTDTHID 681

 QY 701 QAANLVECLSDDLLYPNEKRLLFDAVREAKELSEARNLLQDPDFQEING----- 748
 DB 682 QVSNWVACLSDDECLDEKRELFEKVKYAKGLSDERNLLQDPNFTFISGQLSFASIDGQSN 741

 QY 749 -----ENGWASTAGIEVIEGDALFKGYRLRPGAREIDTETYPYLYKQVEEGVLPK 800
 DB 742 FTSINELSERGWGSENVITQEGNDVFNKYVTLPGT---FNECYPNLYKIGESLKA 798

 QY 801 YTRYLRGFGVSSQGLEIFIRHQTNRIKVNVP--DLLP--DVSPVNSDGSINRCSEQK 856
 DB 799 YTRYQLRGYIEDSQDLEIYLRINAKHETLDVPGTDSLWPLSVKSPIGRCGPNRCAPHF 858

 QY 857 YVNSRLREVENRSGE-----AHEFSIPIDTGEIDYENENAGIWWGFKITDPGAYATLGNLEL 911
 DB 859 EWNPDLDSCSDGRCERCAHSHHFTDIDVCTDLHENLGVVWVFKIKTQSGYARLGNLEF 918

 QY 912 VEEGLSGDALERLQREEQWKIQMTRRRRETDERRRYNASKQAVDRLYADYQDQOLNPDVE 971
 DB 919 IEKPLIGEALSRVKRAEKKRDKREKLQLETKRVVYTEAKETVDALFVDSHYNRLQADTN 978

 QY 972 ITDLTAAODLIQSIPIYVYNEMFPEIPGMNYTKETELTDRLQQAWSLYDQRNAIPNGDPN 1031
 DB 979 IGMTHAADRLVHRHIEAYLPELPPIGINAVIPEELNRISTAFSLDARNVIKNGDPNN 1038

 QY 1032 GLSNWNAIPGVEVQIQIHNTSVLIPNWDQVSOFTVQPNQRYVLRVTARKEGVNGYVS 1091
 DB 1039 GLSCWNVKGHVVDVQSHRSDLVIPWEAEVSQAVRCPGEGYILRVYAYKEGEGCVT 1098

 QY 1092 IRDGNQOTELTFESADYDTNGMYNTQVSNYNTNGYNTNNAYNTOASSTNGYNNANMYTQA 1151
 DB 1099 IHEIENNTDELKF--KNCEEEVYPTDTGTCNDYTAHQG---TAACSRNAGYEDAYEV 1152

 QY 1152 SNTNGYNTSVYNDQT-----GYITKTVPFIPYTQMWIEM 1187
 DB 1153 DTTASVNYKPYEBETVTVDRDNHCEYDRGVNYPVPAGYVTKLEYFPETDVTWIEI 1212

 QY 1188 SETEGTFVIESVELIV 1203
 DB 1213 GETEGKFIVDSVELLL 1228

 RESULT 12
 CLIBE_BACTU
 ID CLIBE_BACTU STANDARD; PRT; 1227 AA.
 AC O85805;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Peptidicidal crystal protein cryIbE (Insecticidal delta-endotoxin
 DE CryIb(e)) (CryIb(e) entomocidal protoxin) (139 kDa crystal protein).
 GN CRYIbE OR CRYIbE OR 158C2B.
 OS Bacillus thuringiensis.
 OG Plasmid pMYC2383.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1428;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL B-18972 / PS158C2;
 RA Payne J.M., Cummings D.A., Cannon R.J.C., Narva K.E., Stelman S.;
 RT "Bacillus thuringiensis genes encoding lepidopteran-active toxins."
 RL Patent number US5723758, 03-MAR-1998.
 CC -!- FUNCTION: PROMOTES COLLOIDAL LYSIS BY BINDING TO THE MIDGUT
 CC EPIHELIAL CELLS OF MANY LEPIDOPTERAN LARVAE.
 CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPORE FORMATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
 CC OF THE SPORE COAT.
 CC -!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
 CC N-TERMINUS.
 CC -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
 CC
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; AF077326; AAC32850.1; -
 DR HSSP; P07130; 1DLC.
 DR InterPro; IPR001178; Endotoxin.
 DR Pfam; PF00555; endotoxin; 1.
 DR Toxin; Sporulation; Plasmid.
 KW SEQUENCE 1227 AA; 139084 MW; CBA847BEA0B34CD3 CRC64;
 SQ
 Query Match 37.2%; Score 2356.5; DB 1; Length 1227;
 Best Local Similarity 41.5%; Pred. No. 8.9e-124;
 Matches 526; Conservative 200; Mismatches 433; Indels 109; Gaps 23;
 QY 1 MSPNNQNEYIIDATPTSTSYSDNSRYPFANEPTNALQNDYKDYKXMSAGNASEYGPSP 60
 DB 1 MTSNRKNEEIIINALSIPAVNSHAQ-----MNLSTDAIEDSLCIAEGNNID---P 49
 QY 61 EVLVSGDAAKAIDIVGKLLSGVFPVGPVIVSLYQLDILWPSGEKQWEIFMEQVE 120
 DB 50 FVSAS---TVQTGINAGRIGLVGLVFPAGQIASFYSFLGELWPRG-RDPWEIFLHVE 105
 QY 121 ELNQKIAEYARNKALSELGLGNVYQLYLTALFEWENPNNGSRALRDVNRPIILDSLF 180
 DB 106 QLRQQTENTRTALRLOGLNSFRAYQOSLEDWLENRDDARTSRVLYTQYIALSLDP 165
 QY 181 TQYMPGFRVTNFEVFLTVYAMAANHLHLKDKASIFGEWGWSTTTNNYNDQMKLTA 240
 DB 166 LNAMPLFAIRNQEVPLLMVYAAQANLHLLLRDASLFGSEFGLTSQEIQRYERQVEKTR 225
 QY 241 EYSDHCKVETETGLAKGTSKQWVDYQVQPRREMTLAVLDVVALFNYDTRTPMETKA 300
 DB 226 EYSDYCARWNTGLNLRGTNAESWLRYNQPRDLTGVLVDLVALFPSYDTRVPMNTSA 285
 QY 301 QLTREYVTDPLGANVSS---IGSWY-DKAPSGFVIESSVLRPPHVDYIYGLTVYQSR 356
 DB 286 QLTREYVTDPIGRNAPSGFSTWFWNNAPSAIAEAVRPHLLDPFQLIFSVLS 345
 QY 357 SISRARIYRWAGHQISYHRVSRGNSLQOMYGTQNLHSTSTPFTNYDIYKTLSDAVL 416
 DB 346 RWSNTQYMYWVGHRLS-SRTIRGLSTSTHGTNTSINPVTQLQTSRDVYRTESFAGIN 404
 QY 417 LDIVYPGYTIYFGMPVEVFWVQNLNTRTKLYKNPVSKDIIASTRDSLELPEPESDQ 476
 DB 405 ILLTTP-----VNGVPWARENWRNPLNSRGLSLTYTYGYTGVGQLFDSSELPETTER 459
 QY 477 PNYESYSHRLCHITSIPATGNTTGLVPVFSWTHRSADLNNTIYSDKTOIPAVKCDNLP 536
 DB 460 PNYESYSHRLNRLI---SGNTL-RAPVYSWTHRSADKNTISSDSITQIPLVKSFLNS 516
 QY 537 FVPVVKGFHGTGGDLLQYNRSTGSGVGLFLARYGLALEKAGKYRVRLYATDADIVLHV- 595

DB 517 GTSVVSQPGFTGGDIIRTN-VANGSVLSMGLNFNNTSLQ---RYRVRVRYAASQTVMLRVT 572
 QY 596 ----NDAQIQMPKTNPGEDLTSKTEKVDADAITLNL--ATDSSLALKNLGEDPNSTLS 649
 DB 573 VGGSTTFDQGFSTMTSANGSLTSQSFRPAEPFVGISASGQTAGISISNAGRQ----- 626
 QY 650 GIVYVDRIEFPVDETYEAEQDLAAKAVNALFTNTKD-GLRPGVTDYEVNQAANLVEVC 708
 DB 627 -TFHFKIEFIPITAFEAEDLERAQAVNALFTNTNPRRLKATGTYDHIDEVSNLVAC 685
 QY 709 LSDDLIPNEKRLFLDAVREAKRLSEARNLLQDDPPOEIN-----G 748
 DB 686 LSDFECLDEKRELLKVKYAKRLSDERNLLQDDPNFTSINKQDPFISTNEQSNFTSIHEQS 745
 QY 749 ENGWTASTGIEVLEGDALPKGYRLRLPGAREIDTETPTLYOKVEGVLKPYTRVRLRG 808
 DB 746 EHWGENSENTIQEGNDVFKENVILPGT---FNECYPIYLYOKIGAEALKATRVQLSG 802
 QY 809 FVGSSQGLEIFITIRHQTRIVKRVDPD---LLPDVSPVNSDGSINRCSEQKTVNSRLEV 864
 DB 803 YIEDSQDLIELYLRVNAKHETLDVPGTESVWPLSVESPIGRCGEPNRCAPHFENPDLC 862
 QY 865 ENRSGE-----AHEPSIPIDTGBIDYNAGIWWGPKITDPEGYATLGNLELVEBGLSG 919
 DB 863 SCRDEGKCAHSHHFLSDIDVGCIDLHENLGVWVVPKIKTQEGHARLGNLEFTEEPKLLG 922
 QY 920 DALERLQREBQWIKIQTWTRREBETDRRYMASKQAVRLVADYQDQQLNPDVEITDILTAQ 979
 DB 923 EALSVRKRAEKWRDKREKLQLETKRVTYEAKEAVDALFVDSQYDRLQADNTNIGMHAAD 982
 QY 980 DLTSQSPYVYNEMFPIPGMNYTKFTELDRLOQAAVSLYDQARNALPNDGPRNGLSNWAT 1039
 DB 983 KLVHRIEAVLSLSVPGVNAEIFELEGRIITALSLYDARNVKNKGFNGLACWNVK 1042
 QY 1040 PGVEVQOINHTSVLIPNDWDEQVSQFTVPQNRQYVLRVYRTARKEGVNGVYSIRDGNQT 1099
 DB 1043 GHVDVQSHRSVLVTPWEAEVSAQVRVCPGRGYTLRVYAYKEGYGEGCVTTHIEINNT 1102
 QY 1100 ETLTFESADYDTNGMYNTQVSTNGYNTNAYNTQASSTNGYNNANNMYNTQASNTNGYNT 1159
 DB 1103 DELKP--KNCBEEVYPTDTGTCDNYTAHQG-----TAACNSRNAGYEDAYEVDTTASVNY 1156
 QY 1160 NSVYNQDT-----GYIKTVTFPIYTDQMIEMSETEGTFY 1195
 DB 1157 KPYEETTYDVRDNHCEYDRGVVYVPPVAGYMTKELFFETDKVWIEIGETGEKFI 1216
 QY 1196 IESVELIV 1203
 DB 1217 VDSVELLL 1224
 RESULT 13
 C7AA_BACTU STANDARD; PRT; 1138 AA.
 ID C7AA_BACTU AC Q03749;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Pesticidal crystal protein cry7Aa (insecticidal delta-endotoxin
 DE CryVIIA(a)) (Crystalline entomocidal protoxin) (129 kDa crystal
 DE protein).
 GN CRY7AA OR CRYVIIA(A) OR CRYIIIC.
 OS Bacillus thuringiensis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1428;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92384571; PubMed=1514800;
 RA Lambert B., Hofte H., Annys K., Jansens S., Soetaert P., Peferoen M.;
 RT "Novel Bacillus thuringiensis insecticidal crystal protein with a
 RT silent activity against coleopteran larvae."
 RL Appl. Environ. Microbiol. 58:2536-2542 (1992).

CC -!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
 CC EPITHELIAL CELLS OF COLPOPTERA. THIS PROTEIN IS NOT TOXIC IN ITS
 CC NATURAL FORM. IT IS HIGHLY TOXIC TO COLORADO POTATO BEETLE LARVAE
 CC AFTER AN IN VITRO SOLUBILIZATION AND TRYPSIN ACTIVATION STEP.
 CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPOREULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART OF
 CC THE SPORE COAT.
 CC -!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-
 CC TERMINUS.
 CC -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
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 CC -----
 CC EMBL; M64478; AAA22351.1; -
 CC EMBL; A07236; CAA00646.1; -
 CC HSP; P07130; IDLC.
 CC InterPro; IPR001178; Endotoxin.
 CC Pfam; PF00555; endotoxin; 1.
 CC Toxin; Sporulation.
 CC KW
 CC SEQUENCE 1138 AA; 129391 MW; 69D8676D4F6A1FAC CRC64;
 CC -----
 CC Query Match 37.1%; Score 2348; DB 1; Length 1138;
 CC Best Local Similarity 41.7%; Pred. No. 2.4e-123;
 CC Matches 512; Conservative 211; Mismatches 385; Indels 120; Gaps 27;
 CC -----
 CC QY 1 MSPNNQNEYIIDATPSTSVNSNRPANPEPTNALQNDYDYKLVKMSAGNASEYGPSP 60
 CC Db 1 MNLNLDGYE-----DSNRTLANSINPTQKALSPSLKNNYQDFLSITERE-----QP 49
 CC QY 61 EVLVSGDAAKAIDIVKLLSGLGVFPVPIVSLYLTQLIDILWPSEKQWEIEMFQVE 120
 CC Db 50 EALASGNTAINTVSVTGATLSALGVGASPTNPFYKLAGLLWPENCKI-WDEFMTEVE 108
 CC QY 121 ELINOKIAEVARNKALSELGLGNVQLYLTALEEWEENENGSGALRDVNRFEILDSLF 180
 CC Db 109 ALIDQKIEEYVRNKALAEGLDGLSALDKYQKALADWLGKQDDPEALISVATEFRILDSLF 168
 CC QY 181 TOTMPSFRVTNFEVPLTVTYAMAANLHLLKQASIFGEWGWSTTTNNYDROMKLT 240
 CC Db 169 EFSMPSFKVGYRIPLTLVTAQANLHALLRDLSTLYGDKWFTQNNIENYRQKRIS 228
 CC QY 241 EYSDHCVKYETGLAKUGTSAKQWVDYNQFRREMTLAVLDVVALFPNYDRTYPMETKA 300
 CC Db 229 EYSDHCTKWTNSGLSRLNGSTYEQWYNFRFRREMILMALDLVAVFPFDPHPRYSMETST 288
 CC QY 301 QLTREYVYDPLGAVNVSSIGSWYDKAPSGFVIESSVIRPHVPIYIGLTVYTSRIS 360
 CC Db 289 QLTREYVYDPLGAVNVSSIGSWYDKAPSGFVIESSVIRPHVPIYIGLTVYTSRIS 343
 CC QY 361 ARY---IRHWAGHOISVHRVSRGSLNQQ---MYGTQNMHLSTSTDFNTDYITKLSKDAV 415
 CC Db 344 HETQDPLFYSAHKVSEFK-SEQSNLYTGYIGKTSYSGVSGAYSFHNDIYRILAPSV 402
 CC QY 416 LLDIVYGYTYIFPGMEVEFFFMVNLNTRKTLKYNPVSKDIIASTRDSLELPPTSD 475
 CC Db 403 ---VYVP-YTQ-NYGVQEVFYGKGVHVRGDNKYD-----LTVDSIDQLPPD--G 447
 CC QY 476 QPNYESVSHRLCHITSI-----PATGNTGLVPFSWTHRSADLNTYSDKITOIPAVKC 531
 CC Db 448 EPIHEKYTHLCHATAIFKSTPDYDNAT--IPIFSWTHRSAYYNNRYPNKITIPAVKM 505
 CC QY 532 WDNLPFPVVPVKGPGHCTGDLLOYNRSVGCTFLARYGLALEKAGYRVLRYATD--A 589
 CC Db 506 YKLDDEPSTVVGPGFTGDLVK-RGSTYIGDI-KATVNSPLSQ--KIRVRYATVNSG 561
 CC QY 590 DIVLVNDAQIQMPK-----TMMFGDLTSKTFKVAADAITTLMATDSSIALKHLNGED 643

Db 562 QFNVYNDKILQTKFQNTVETIGEGKDLTYSGFGVIEVSTTIQFPDEHPKITLHLSL 621
 QY 644 PNSTLSGIYVVRIBRIPVDVETAEADQLEAKAKAVNALFTNTKGLRGVTDYEVNQAA 703
 Db 622 NNSSF---YVDSIEFIPVDVNVYAEKEKLEKAKAVNTLFTFEGRNALQKDVTDYKVDQS 677
 QY 704 NLVECLSDLLPYNEKRLLDVAREAKRLSEARNMLLODPOFQEING--ENGWTAFTSTGLIEVI 761
 Db 678 ILVDCISGLDYPNEKRELQNLVKYAKRLSVSRNLLDPTFDSINSSEENGWYSGNGIVIG 737
 QY 762 EGDALFKGYRLPGAREIDTETYPYLYKQVEGVLPYRYRLRGFVGVSSGGLFTI 821
 Db 738 NGDFVFGKGYLIPSGYN--DTQ-YPTLYLQKIDSEKLYRYKLGKGFIESQDLAEYI 794
 QY 822 RHQTRIVKXNPDDLDPVSPVNSDGSINRCSQKTVNSRLEVENRS-----GEAHEFS 875
 Db 795 RYDAKHTLDVSNLLPDLIPENTCGEPNRCAAQVLDENPSPSCSMQDGLSDSHSFS 854
 QY 876 IPIDTGEIDYENAGIWFQKIDTPEGYATLGNLEIVBEGFLSGDALERLQREEQWKIQ 935
 Db 855 LNIIDTGSINHNENLGIWLFKISTLEGYAKFGNLEIVEDGPIVIGEALARKVROETKWRNK 914
 QY 936 MTRREERTERYMAKQAVDLVADYQDQOLNPDVEITDLTAAQDLIOSTPYVYNEMFPE 995
 Db 915 LAQTTTQAIYTRAKOQDLNLFANQDSHLKRDVTFAETAAARKIVQSIREAMSWLSV 974
 QY 996 IPGMNTKTELTDLRQQAWSLYDQNAIPNGDFRNLGSNNWATPGVEVQIQNHSTVLVI 1055
 Db 975 VFGVNHPIFTELSGRVQAFQLDVNRVNRGFRFLNGLSDWIVTSVKVQEEGNNVLVL 1034
 QY 1056 PNWDEQVQOFTVOPNORYVLRVTRKEGVNGVYSIRDGNGNOTETLTTPSASDYDTNGMY 1115
 Db 1035 NNWDAQVLQNVKLYQDRGYLHVLTARKIGIGEGYITTBEGHTDQLRFTACE----- 1087
 QY 1116 NTOVSNYNGVYNNAYNTQASSTNGYNNANNMYTQASNTNGYNTSVNDQTVITKVT 1175
 Db 1088 --EIDASNAF-----ISGYITKELE 1105
 QY 1176 FIPVTQMMIEMSETEGTFVIESVELIV 1203
 Db 1106 FFPDTEKVIHIEGTEGIFLVESIELFL 1133
 RESULT 14
 ID CLBA BACTK STANDARD; PRT; 1228 AA.
 AC P05517; Q45731;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Pesticidal crystal protein crylBa (Insecticidal delta-endotoxin
 DE CrylB(a)) (Crystalline entomocidal protoxin) (140 kDa crystal protein).
 GN CRYIIB OR CRYIIB(A) OR CRYA4.
 OS Bacillus thuringiensis (subsp. kurstaki), and
 OS Bacillus thuringiensis (subsp. entomocidus).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=29339, 1436;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=B.t.kurstaki; STRAIN=HD-2;
 RX MEDLINE=88203216; PubMed=3362680;
 RA Brizzard B.L., Whiteley H.R.;
 RT "Nucleotide sequence of an additional crystal protein gene cloned
 RT from Bacillus thuringiensis subsp. thuringiensis.";
 RL Nucleic Acids Res. 16:2723-2723 (1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=B.t.entomocidus; STRAIN=HD-110;
 RA Soetaert P.;
 RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
 CC EPITHELIAL CELLS OF INSECTS.
 CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING

SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART OF THE SPORE COAT.
-1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-TERMINUS.
-1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
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EMBL; X06711; CAA29898.1; -;
ENBL; X95704; CAA65003.1; -;
PIR; S00873; S00873.
HSP; P07130; IDLC.
InterPro; IPR001178; Endotoxin.
Pfam; PF00555; endotoxin; 1.
Toxin; Sporulation.
VARIANT 150 150 Y -> H (IN STRAIN HD-110).
SEQUENCE 1228 AA; 139647 MW; C8E3A19FB5D98575 CRC64;
Query Match 37.0%; Score 2340; DB 1; Length 1228;
Best Local Similarity 42.1%; Pred. No. 7.5e-123;
Matches 533; Conservative 193; Mismatches 435; Indels 106; Gaps 26;
QY 1 MSPNNQNEYIIDATPSTVNDNRYPFANEPNALQNDYKYLKMSAGNASYEGSP 60
DB 1 MTSNRKNEIINA-----VSNHSAQ-----MDLLPDARIEDSLCIAEGNNID----P 44
QY 61 EVLVSGQDAKAAIDIVKLGSLGVPVGVPIVSLYLTOLIDLMPSEKESQWEIPEMVE 120
DB 45 FVSAS-----TVGTGINAGRIIGVGVPPAGQASIFSLVGLMPRG--RDWEIFLEHVE 100
QY 121 ELINQIAEYARNKALSLEGNGNYQLYLALEEWENPNPNSRALRDVRNRFELDSL 180
DB 101 QLINOQITENARTALARLGLGDSFRAYQOSLEDWLENRDDARTSVLYTQYIALELDF 160
QY 181 TQYMPFRVTNFEVFLTVYMAANLHLLKLDASIFGEEWGWSTTTNNYIDROMKLT 240
DB 161 LNANPLFAIRNOEVPFLMVYQAANLHLLRDASLFGSEFLTSQEIQRYYERQVETR 220
QY 241 EYSDHCVKWTETGLAKGTSAKOWVDYNQPERMTLAVLDVALFPVYDTRTYPMETKA 300
DB 221 DSDYCVWEYNTGLNSLGTNAASWVRNQFRDUTLGLVDLVALFPSIDRTYPTINTSA 280
QY 301 QLTREVYTDPLGA--VNVSSIGSWY-DKAPSGVIESSVIRPPHVFDITGLTVYTQSR 357
DB 281 QLTREVYTDAGTCVNWASM-NWYNNAPSFSAEAAIRSPHLLDFLEQLTIFSASSR 339
QY 358 ISSARYIRHAGHOISYHRVSRGSLQOMYGTQNLHSTSTFDFTNYDIYKLSKDAVLL 417
DB 340 WSNTRHMTYWRGHTYQSRPIGGLTSTHGATNTSINPV-TLRFASRDVYRTESVAGVLL 398
QY 418 DIVVPGTYIIFGPEVEFFWVQNLN-NRKTLYKNPVSKOIIASTRDSLELPETSQ 476
DB 399 ---WGIVLEPIHGVTFRFTNTPONISDRGTANTSYQYESPGLQKDSLELPETTER 455
QY 477 PNYESYSHRLCHITSIPATGNTTGLVPVFSWTHRSADLNNTYSKITQIPAVKWCNDLP 536
DB 456 PNYESYSHRLSHIGILQSRVN---VPVYSWTHRSADRTNTPGRIITQIPMKVASELPQ 512
QY 537 FVPVVGPGHTGGDLLQNRNRTSGVTLFLARYGLALEKAGKRVRLRYADADIVLHVN 596
DB 513 GTTVVRGFGFTGGDILR-RTNTGFGFIRVTVNGPLTQ---RYRIGFYASTVDFDFVS 568
QY 597 DA-----QIQMPKTNPCGDLTSKTFKVADAITTLNLTSSSLAKHNL-GEDPNSTLSG 650
DB 569 RGGTTVNNFRFLTNWSGDELKYGNF-VRRAPFTFTTQIQDIIRTSIQGLSGN----- 623
QY 651 IVYVDRIEFIPVDETYEAEQDLAAKAVNALFTNTKD-GLRPGVTDYEVNQANLVECL 709

DB 624 EYIDKIEIIPVTAPEAYDLEAQAVALFTNTPRELKTQDVTYHIDQVSNLVA 683
QY 710 SDDLYPNEKELLDPDAVEAKLSLSEARNLLQDPDFQEN-----GE 749
DB 684 SDFCLDEKRELLKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNFTSIHQSE 743
QY 750 NGWTAFTGIEVIEGADALFKGRLPARGIBIDTETPTLYLYQKVEEGVLKPYTYRLRGF 809
DB 744 HGWGSSENIITQSGNDVFKENYVTLPGT---FNECYTYLYQKIGESLKYATYQLRGY 800
QY 810 VGSQGLIEFTIRHQTNRIVKNVP--DDLPL--DVSPNSDGSINRCSQKYNVSRLEVE 865
DB 801 IESQDLEIYLIRYNAKHETLDVPGTESLWPLSVESPIGRCEPNRCAPHFENPDLDCS 860
QY 866 NRSCE-----AHEPSIDTGEIDYNENAGIWCFKITDPGYATLGNLELVEEGPLSGD 920
DB 861 CRDGKCAHSHHPSLDIDVGCTDLHENLGVVVFVKIKTQEGHARLGNLEFIEBKPLGE 920
QY 921 ALERLQREEQWKIOMTRREBEETDRRYMAKQAVDRLYADYQDQOLNPDVEITDLTAAQD 980
DB 921 ALSRVKAEKKWRDKREKLQLETKEVYTEAKEAVDALFVDSQYDLQADTNIGMHAADK 980
QY 981 LIQSIPIVYNEMPEIPIGMNYTKFTLTDRLQQAWSLYDQNAIPNGDFRNLGNMNA 1040
DB 981 LVHRIREAYLSLSELPVIGVNAEIPFEELEGHITAILSYDARNVVVKGDFNNGLTGWNVKG 1040
QY 1041 GVEVQQLNHTSVLYIPNWDQSVSQOFTVQPNQRYLVRTAKEGVNGYVSIROGNGTE 1100
DB 1041 HVDVQSHHRSDLVPEWEAAVSVQAVRVCPCGVILRYATYKEGYGCVCVTIHEINNTD 1100
QY 1101 TLTFASDYDNTGMYNTQVSNNTGNTNNAYNTOASTNGYNNMNTYNTQASNTNGYNTN 1160
DB 1101 ELKP--KNREEEVPTDTGTCNDYTAHOGTACDACNSNAGYDAYEVDVTTASVNYK 1158
QY 1161 SVYNDQT-----GYTKTVTFIPYTDQWMIEMSETEGTFYI 1196
DB 1159 PTVEETVTDVRRNHCEYDRGVYVPPVAGYVTKLEVPETDTVWIEIGETEGKPIV 1218
QY 1197 ESVELIV 1203
DB 1219 DSVLELL 1225
RESULT 15
CLBC_BACTM
ID CLBC_BACTM STANDARD; PRT; 1233 AA.
AC Q45774;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Pesticidal crystal protein cryIbC (Insecticidal delta-endotoxin
DE CryIb(c)) (Crystalline entomocidal protoxin) (140 kDa crystal protein).
GN CRYIbC OR CRYIbC(C) OR CRYIbC.
OS Bacillus thuringiensis (subsp. morrisoni).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1441;
RN [1]
RP SEQUENCE FROM N.A.
RA Bishop A.H., Bone E.J., Ellar D.J.;
RT "Cloning of novel Bacillus thuringiensis delta-endotoxin";
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION. PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF INSECTS.
CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
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CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
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OM protein - protein search, using sw model

Run on: January 7, 2003, 05:03:13 ; Search time 83 Seconds
(without alignments)
2993.889 Million cell updates/sec

Title: US-10-032-717-2
Perfect score: 6332
Sequence: 1 MSPNNQNEYIIDEATSTSV.....MSRETEGTFYIESVELIIVDVE 1206

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTEMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_podent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2440	38.5	1144	2 Q45745	Q45745 bacillus th
2	2342	37.0	1228	2 Q93775	Q93775 bacillus th
3	2332	36.8	1228	2 Q93775	Q93775 bacillus th
4	2184.5	34.5	1189	2 Q91877	Q91877 bacillus th
5	2075.5	32.8	1180	2 Q955V8	Q955V8 bacillus th
6	2070.5	32.7	1176	2 Q45736	Q45736 bacillus th
7	2068	32.7	1160	2 Q937F9	Q937F9 bacillus th
8	2055.5	32.5	1176	2 Q9RC30	Q9RC30 bacillus th
9	2054.5	32.4	1171	2 Q06894	Q06894 bacillus th
10	2048	32.3	1155	2 Q9F296	Q9F296 bacillus th
11	2027	32.0	1177	2 Q45735	Q45735 bacillus th
12	2024	32.0	1155	2 Q93721	Q93721 bacillus th
13	2021	31.9	1177	2 Q03743	Q03743 bacillus th
14	2020.5	31.9	1178	2 Q9R826	Q9R826 bacillus th
15	2017.5	31.9	1178	2 Q45768	Q45768 bacillus th
16	2005	31.7	1174	2 Q45749	Q45749 bacillus th

17	1961.5	31.0	1176	2 Q9S514	Q9S514 bacillus th
18	1902	30.0	1128	2 Q9FDC0	Q9FDC0 bacillus th
19	1867	29.5	1280	2 Q8VUK9	Q8VUK9 bacillus th
20	1860	29.4	1118	2 Q9AM83	Q9AM83 bacillus th
21	1823	28.8	1118	2 Q9AM82	Q9AM82 bacillus th
22	1793	28.3	1236	2 Q939T3	Q939T3 bacillus th
23	1688.5	26.7	1118	2 Q9AM81	Q9AM81 bacillus th
24	1562.5	24.7	1254	2 Q8VUL0	Q8VUL0 bacillus th
25	1523	24.1	1270	2 Q8VUL1	Q8VUL1 bacillus th
26	1514	23.9	719	2 Q93NJ5	Q93NJ5 bacillus th
27	1512	23.9	719	2 Q8S796	Q8S796 bacillus th
28	1491	23.5	719	2 Q9F0P8	Q9F0P8 bacillus th
29	1212.5	19.1	723	2 Q9S4B5	Q9S4B5 bacillus th
30	1194.5	18.9	652	2 Q9S6N9	Q9S6N9 bacillus th
31	1167	18.4	1155	2 Q9AM80	Q9AM80 bacillus th
32	1103.5	17.4	645	2 Q9S603	Q9S603 bacillus th
33	1046.5	16.5	526	2 Q93308	Q93308 bacillus th
34	1028	16.2	558	2 Q8VW63	Q8VW63 bacillus th
35	1025	16.2	638	2 Q87654	Q87654 bacillus th
36	1012.5	16.0	620	2 Q45720	Q45720 bacillus th
37	966.5	15.3	618	2 Q93306	Q93306 bacillus th
38	962	15.2	618	2 Q45737	Q45737 bacillus th
39	955.5	15.1	558	2 Q8VW61	Q8VW61 bacillus th
40	937	14.8	607	2 Q45721	Q45721 bacillus th
41	933	14.7	660	2 Q8RQU6	Q8RQU6 bacillus th
42	906.5	14.3	381	2 Q45740	Q45740 bacillus th
43	710.5	11.2	666	2 Q8VW62	Q8VW62 bacillus th
44	635	10.0	650	2 Q8VNX2	Q8VNX2 bacillus th
45	624.5	9.9	688	2 Q8VNX1	Q8VNX1 bacillus th

ALIGNMENTS

RESULT 1

Q45745 PRELIMINARY; PRT; 1144 AA.
ID Q45745
AC Q45745;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Delta-endotoxin (Fragment).
GN CRYIX GENE.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94085596; PubMed=8262221;
RA Shevelev A.B., Svarinsky M.A., Karasin A.I., Kogan Y.N.,
RA Chestukhina G.G., Stepanov V.M.;
RT "Primary structure of the cryX**the novel Delta-endotoxin-related
RL gene from Bacillus thuringiensis ssp. galleriae.";
RL FEBS Lett. 336:79-82(1993).
DR EMBL; X75019; CAA52927.1; -.
DR HSSP; P07130; 1DLG.
DR InterPro; IPR001178; Endotoxin.
DR Pfam; PF00555; endotoxin; 1.
FT NON_TER 1
SQ SEQUENCE 1144 AA; 129399 MW; 7D28594A19C4B065 CRC64;

Query Match 38.5%; Score 2440; DB 2; Length 1144;
Best Local Similarity 44.0%; Pred. No. 6.6e-132; Indels 146; Gaps 25;
Matches 534; Conservative 177; Mismatches 357;

QY 42 YKDYLMKSNAGNASEYFGSPVELVSGQDAKAAADIYVGLKLSGLGVPFVPGIVSLYTOLID 101

Db 20 YKDYLMKSGSDYIDSYINPGNVRTG---LQTGIDIVAVVVGALGGPVGGLTGLFLSLFG 76

QY 102 ILMPSEKSKQWEITFMQVEELINQKIAEYARNKALSEGLEGNYYQIYLTALSEWENPN 161

Db 77 FLWPSNDQAVWEAFIEQMEELIEQRIISDQVVRTALDGLTGIQNYNQYLLTALKEWERPN 136

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QY 162 GSRALDRVRNRFEILDSLTQYMPSF-----RVTFVFPFLTVYMAANLHLLILKDSAP 217
DB 137 GVRA-NLVQRFELHALFVSSMFSFGSGSQRFQALLVVYQAANLHLLILKDAEY 195
QY 218 GEBGWSSTTINNYYDROMKL-TAEYSDHCVKWYETGLAKGTSAKOWVDYNOFRREMT 276
DB 196 GARWGLRESOIGNLYFNELOTRDRYTNHCNVANNGLAGLRGTSABSWLKHQFRREAT 255
QY 277 LAVLDVVALPNDYTRYPMETKALQREVYTDPLGAVNUSS-----IGSWYD-KAPS 328
DB 256 LMAMDLLALPPYNNRYPIAVNPQLREVYTDPLGVSESSLPPELRCURWQETSAMT 315
QY 329 FGVIESVIRPPHVDYITGLTVTQGRSIS-SARYIRHWAGHOISYHVRSGSN--LQ 385
DB 316 FSNLENALISPHLFDYINNLMYTGFSVHLTNQLEGWGHVSSTSLASGTTVLRR 375
QY 386 MYGTNQNHLSTSTDFNTDYIYKLSK-----DAVLLDIV---YPGVYIYFPGMPE 433
DB 376 NYGSTTSI--VNYFSFNDRDYVQINTRSHTGLGFQNAFLGITRAQFYPGGT 426
QY 434 VEFPMNQLNTRKTLKYNPVSKDIIASTRDSLELPETSDQPNYSYSHRLCHITS-- 491
DB 427 ----SVTQRNALTCQYNSID-----ELPSLDNEPIRSYSYSHRLSHITSYL 470
QY 492 ----IPATGNTTGLVPVFSWTHRSADLNTIYSDKITQIPAVKCMWNLPPFVVPVKGPGH 546
DB 471 HRVLTIDGINIYSGNLTYVWTHRDVLTNTIADRITQLPLVKSFEIPAGTIVVRGPGF 530
QY 547 TGGDLQYNRSTGSGVTLFLARYGLALEKAGKYRRLRYA--TDADIIVLHVNDQI--- 601
DB 531 TGGDIL--RRTG-VGTGTRVTRTAPLQRYRIRFRFASTNLTNLTGIRVQDRQVNYFD 586
QY 602 MPKTMNPGEDLTSKTFKVADAITLNLATDSSL-----ALKHNLGEDNSTLSGVYVDRI 657
DB 587 FGTMNRGDELRYESFATREFTTDFNFRQPOELISVFANAFSAQOE-----VYFDRI 638
QY 658 EFLPVDYTAEOLEAKKAVNALFTNTKDLRPGVTDYEVNQANLVECLSDLYPNE 717
DB 639 EILPVPNAREAKEDLEAKKAVASLFTTRDGLQVNVKDYQVDAQANLVCLSDBOQYD 698
QY 718 KRLLFDVAREAKRLEARNLQDPDFOBING--ENGWASTGIEVIEGDALEFKGRYRLP 775
DB 699 KCMLEAVRAAKRSRNLQDPDFNTINSTENGWAKSANGVTISEGGPPYKGRALQLA 758
QY 776 GABEDTETPTLYLYOKVEEGLKPYTYRLRGFVSGSGLIEITIRHOTNRIVKNVDD 835
DB 759 SAR-----ENPTYIYQKVDASELKPYTRYSDGFFVKSSQDLEIDLIIHHKHVHLKQVNDPN 814
QY 836 LLPVSPVNSDGSINRCSQKYVNSRLIVEN-----RSGEAHEFSIPIDTGEIDYNNEN 888
DB 815 LVSDTYDDSCSGINRCQOQWNAQLETEHHHPMDCCAAQTHEFSYIYDGLNSSVD 874
QY 889 AGIIVGFKITDPEGYATLGNLEVEBGLSGDALERLQREBQCKIOMTRREBTRDRYM 948
DB 875 QGIWAIKVRITDGYATLGNLEVEBGLSGESLEREQDNTKSAELGRKRAETDRVYQ 934
QY 949 ASKQAVDLVADYQDQOLNPEVEITDLTAADLQSIPIYVYNEMPEPEIPGMNYKFTLT 1008
DB 935 DAKOSINHLFVYQDQOLNPEIGMADINDAQNLVASIDSVYSDAVLOIPGINYRIYELS 994
QY 1009 DRLOQANSLVDORNAIPNGDPFNGLSNNNATPGVEVQOINHTSVLVI PNWDEQVSQQFTV 1068
DB 995 NRLOQASVLTSRNAVQDGFNGGLSDSNATAGASVQDQGNTHFLVLSHWDAQVSQFV 1054
QY 1069 QPNQRYLVRVARKGVNGVYSIRDGNQOTETITFASDYDTNGMYNTQVSNNGYNTN 1128
DB 1055 QPNCKYVLRVTAEKVGGDGYVITRDGAHHTETITFNACDYDINGTYT----- 1103
QY 1129 NAYNTQASSTNGYNNMNYNTQASNTNGYNTNSVNDQGTIYTKVTPIPTDQWNIEM 1188
DB 1104 -----DNT-YLTKEVIFYSTHEMWEVN 1126
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QY 1189 ETEGTFYIESVELI 1202
DB 1127 ETEGAFHIDSIEFV 1140
RESULT 2
Q93T75 PRELIMINARY; PRT; 1228 AA.
AC Q93T75;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)
DE Delta-endotoxin Cry1Ba2.
GN CRY1BA2.
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria, Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=1436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD-9;
RA Mat Isa M.N., Abdullah M.A.F., Mahadi N.M.;
RT "Characterization of cryIB gene and its flanking regions cloned from
RL Bacillus thuringiensis subsp. entomocidus HD-9.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF363025; AAK51084.1; -.
DR InterPro; IPR001178; Endotoxin.
DR Pfam; PF00555; endotoxin; 1.
SQ SEQUENCE 1228 AA; 139621 MW; 3DA2A4DBF59C95C3 CRC64;

Query Match 37.0%; Score 2342; DB 2; Length 1228;
Best Local Similarity 42.1%; Pred. No. 3.3e-126;
Matches 533; Conservative 193; Mismatches 435; Indels 106; Gaps 26;

QY 1 MSPNNQNEYEIIIDATSTSVNSDNRYPFANEPNALQNDYKDYLRKMSAGNASEYPGSP 60
DB 1 MTSNRKNENBIINA-----VSNHSAQ-----MDLLPDARIEDSLCIAEGNNID----P 44
QY 61 EVLVSGQDAKAADIVKLLSLGLVGPVGPVYSLYLTQLDILWPSCGKQWEIFMEQVE 120
DB 45 FVSA-----TVQTGINIAGRILGVLPFAGQLASFSYFLVGLWPRG-RDQWELFISHVE 100
QY 121 ELINQKIAEYARKNALSLEGLGNVYLYLTALFEEWENPNSRALRDVNRPRILSLP 180
DB 101 QLNIQQTENARNTALARQLGDSFRAYQOSLEDWLENRDDARTSVLHTQYIALSILDP 160
QY 181 TQWPSFRVTVNFEVPLTVYMAANLHLLILKDAIPGEBGWSSTTINNYYDROMKLT 240
DB 161 LNAMPLFAIRNQEVPLIMVYAQAANLHLLILKDAISLFGSEFGLTSQEIQRYERQVTR 220
QY 241 EYSDHCVKWYETGLAKGTSAKOWVDYNOFRREMTLAVLDVVALPNDYTRYPMETKA 300
DB 221 DYSYCVIEWNTGLNSLRGTNAASWRYNQFRRLDITLGLVDLVALFSDYTRTYPINTSA 280
QY 301 QLREVTYTDPLGA--VNVSSIGSWY-DKAPSFVIESVIRPPHVFYITGLTVYTOSRS 357
DB 281 QLREVTYTDALGATGVNWSM-NWYNNNAPFSAIEAARSPHLLDFLQLTIFSSSR 339
QY 358 ISSARYIRHWAGHOISYHVRSGSNLQOMYGTNQNHLSTSTFTPTNYDYIKLSKDAVLL 417
DB 340 WSNTRHMTYWRGHTIOSRPIGGGLNSTHGATNTSNPV-TLRFASRDVYRTESYAGVLL 398
QY 418 DIVYPGTYIYFPGMPEVFPVNVQLN-NTRKTLKYNPVSKDIIASTRDSLELPETSDQ 476
DB 399 ---WGYLEPIHGVTFRVFTPNQNTSDRGTYNSOFYSPGSLQKDSLETPEPPER 455
QY 477 PNYESYSHRLCHITSIPATGNTTGLVPVFSWTHRSADLNTIYSDKITQIPAVKCMWNL 536
DB 456 PNYESYSHRLSHIGIILQSRVN---VPVYSWTHRSADRTNITGNRITQIPWVKASELP 512
QY 537 FVPVVKPGHGTGDLQYNRSTGSGVTLFLARYGLALEKAGKYRRLRYATDADIVLHVN 596
DB 513 GTTVVRGFGTGGDILA-RTNTGGFGPIRVTVNGPLTQ---RYRIGPRYASTVDFDFVS 568
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Qy 597 DA-----QIQPKTMNPGEDLTSKTFKVADAITTLNLTADSSLSLAKHNL-GEDPNSTLSG 650
Db 569 RGGTVNNFRFLTMNSGDELKYNF-VRRAPFTTPTTQIQDIIRTSIQGLSGN---G 623
Qy 651 IVTVDRLEFIPVDETYEABODLEAKKAVNALFTNKD-GLRPGVTYEVNQAAANLVECL 709
Db 624 EYIDKIEIIPVATPEAYDLERAQAVNALFTNTPRLKTDVTDYHIDQVSNLVAEL 683
Qy 710 SDDLYPNEKELLFDVAREAKLSARNLLODPDOEIN-----GE 749
Db 684 SDFCLDEKKELEKVKYAKRLSDERMLLODPNTSINKQDPFISTNEQSNFTSIHQSE 743
Qy 750 NGWTAAGIEVIGDALFKGRIYLPKGLAREIDTETPTLYQKVEEGLPYTYRRLRGF 809
Db 744 HGWGSENIITQEGNDVFNKENVYTLPGT---FNECYPTLYQKIGESLKAAYTRYQLRGY 800
Qy 810 VGSQGLIEFTIRHQTNRIVKQNP--DDLIP--DVSPNSDGSINRSCQKYVNSRLEVE 865
Db 801 IEDSQDLIEILIRYNAKHETLDVPGTESLWPLSVESPIGRGCEPNRCAPHFEMNPDLCDS 860
Qy 866 NRSGE-----AHEPSIPIDTGEIDYNENAGIWWGFKITDREGYATLGNLELVEGSLSGD 920
Db 861 CRDGEKCAHSHHPSLDDVCGCTDLHENLGVVWVFKITQEGHARLGNLEFIEBKPLUGE 920
Qy 921 ALERLQREBOQWKIOMTRREEDTDRRYMAKQAVDRLYADYQDQQLNPDPVEITDLTAQD 980
Db 921 ALSRVKAEKWRDKREKLOLETKRVVTEAKEADVALFVDSQYDLQADTWIGMHAADK 980
Qy 981 LIQSIPVYNEMPEIFPGMNTKTELTDLRQQAWSLYDQNAIPNGDFRNLGNWNAATP 1040
Db 981 LVHRIEAYLSLSELPVPGVNAEIPFEELEHIIITAILSDARNVVKNGDFNGLTCWNVKG 1040
Qy 1041 GVEVOQINHTSVLIPNWDQVSOQFTQPNQORVILRTARKEGVNGYVIRGNGOTE 1100
Db 1041 HVDVQOHSRSDLVPEWEAEVSOAVRCPGCGYILRVYATYKEGYGEGCVTIHIEENTD 1100
Qy 1101 TLFPASDYDTNGMYNTQVSTNGYNTNAYNTQASSTNGYNNMNTQASNTNGYNTN 1160
Db 1101 ELKF--KNRESEEVYPTDTGTCNDYTAHQTAGCADACNSNAGYEDAYEDVTASVNYK 1158
Qy 1161 SVYNDQF-----GYTKTFTPTPTDQMIEMSETEGTFVI 1196
Db 1159 PTYEEETVDVRRDNHCEYDRGYVNPVPAGYVTKLEYFETDVTWIEIGTEGKPIV 1218
Qy 1197 ESVELIV 1203
Db 1219 DSVLELL 1225
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RESULT 3
Q93NM5 PRELIMINARY; PRT: 1228 AA.
AC Q93NM5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Cyl1Ba.
GN Cyl1Ba.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
SEQUENCE FROM N.A.
RP Zhang J., Song F., Huang D.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AP368257; AAK63251.1; -
DR InterPro: IPR001178; Endotoxin.
DR Pfam: PF00555; endotoxin; 1.
SQ SEQUENCE 1228 AA; 139666 MW; E86D9842341P8439 CRC64;
Query Match 36.8%; Score 2332; DB 2; Length 1228;
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Best Local Similarity 42.0%; Pred. No. 1.2e-125;
Matches 532; Conservative 193; Mismatches 436; Indels 106; Gaps 26;
Qy 1 MSNNQNEVEIIDATSTSVSNDNSRYPFANEPNTALQNMWDYKDYLMKMSAGNASEYEGSP 60
Db 1 MTSNRKNNEIINA-----VSNHSAQ-----MDLUPDARIEDSLCIAEGNID-----P 44
Qy 61 EVLVSQDAAKAIDIVGKLLSGLGVFPFVGVPIVSLYTLQILIDILWPGSEKQSWEIFMEQVE 120
Db 45 FVGSAS---TVQTGINIAGRILGVLPFAGQLASFYSFLVGLWPRG-RDQWEIFLEHVE 100
Qy 121 ELNQKIAEVARKALSELEGLGNVQLYLTALBEEENPNSGSRALDVRNRREILDSLF 180
Db 101 OLINOQITENARNTALRQLGLDSFRAYQQSLEDLENRDDARTSRVLTQVIALSLDF 160
Qy 181 TOYMPFRVNFVFPFLTVYMAANLHLKLDASIFGEWGWSTTTNNYDQRMKLT 240
Db 161 LNAMPFAIRNQEVPLWVYQAANLHLRLDASIFGSEFGLTSQEIQRYEYQVERTR 220
Qy 241 EYSDHCYKMYETGLAKLKGTSKQWVDYNOFREMTLAVLDVVVALPNYDTRTYPMETKA 300
Db 221 DYSYCVVWNTGLSLRGNTAAASVRYNQFRDLTLGLVDLVALFSDYDTRTYPINTSA 280
Qy 301 QLTREVTTDPLGA--VNVSSIGSWY-DKAPSGVIESSVIRPHVFPYIITGLTYVTQSR 357
Db 281 QLTREVYTDAGATGVNMASM-NWYNNNAPFSAIAAAIRSPHLLDFLEQLTIFSSASR 339
Qy 358 ISSARIYRHAGHOISVHRVSRGSLQMYGTQNLHSTSTFTNYDVIYKTLISKDAVLL 417
Db 340 WSTRHTMYWRGTIOGRPIGGGLTSTHGATNTSINPV-TLRPASRDVTRTESYAGVLL 398
Qy 418 DIVVPGYTIFFGMEPEFEMVNLN-NTRKTLKYNPVSKDIIASTRDSLELPETSDQ 476
Db 399 ---WGIYLEPIHGVTVRFNFTPNQISDRGTANYSPQYSPGLQKDSLETPEPPER 455
Qy 477 PNTESYSHRLCHITSIPATGNTTGLVPFNSWTHRSADLNTIYSDKLTQTPAVKCNWNL 536
Db 456 PNTESYSHRLSHIGIILQSRVN--VPVSWTHRSADRTNTIGPNRITQIPMVKASELPQ 512
Qy 537 FVPVKGPGHGTGDLQYNSTGSGTFLARYGLALEKAGKYRVRRLRYATDADIVLHN 596
Db 513 GTTVVRPGFTGDIUR-RNTGSGFGPIRVTVNGPLTQ---RYRIGFRYASTVDFDFVS 568
Qy 597 DA-----QIQPKTMNPGEDLTSKTFKVADAITTLNLTADSSLSLAKHNL-GEDPNSTLSG 650
Db 569 RGGTVNNFRFLTMNSGDELKYNF-VRRAPFTTPTTQIQDIIRTSIQGLSGN---G 623
Qy 651 IVTVDRLEFIPVDETYEABODLEAKKAVNALFTNKD-GLRPGVTYEVNQAAANLVECL 709
Db 624 EYIDKIEIIPVATPEAYDLERAQAVNALFTNTPRLKTDVTDYHIDQVSNLVAEL 683
Qy 710 SDDLYPNEKELLFDVAREAKLSARNLLODPDOEIN-----GE 749
Db 684 SDFCLDEKKELEKVKYAKRLSDERMLLODPNTSINKQDPFISTNEQSNFTSIHQSE 743
Qy 750 NGWTAAGIEVIGDALFKGRIYLPKGLAREIDTETPTLYQKVEEGLPYTYRRLRGF 809
Db 744 HGWGSENIITQEGNDVFNKENVYTLPGT---FNECYPTLYQKIGESLKAAYTRYQLRGY 800
Qy 810 VGSQGLIEFTIRHQTNRIVKQNP--DDLIP--DVSPNSDGSINRSCQKYVNSRLEVE 865
Db 801 IEDSQDLIEILIRYNAKHETLDVPGTESLWPLSVESPIGRGCEPNRCAPHFEMNPDLCDS 860
Qy 866 NRSGE-----AHEPSIPIDTGEIDYNENAGIWWGFKITDREGYATLGNLELVEGSLSGD 920
Db 861 CRDGEKCAHSHHPSLDDVCGCTDLHENLGVVWVFKITQEGHARLGNLEFIEBKPLUGE 920
Qy 921 ALERLQREBOQWKIOMTRREEDTDRRYMAKQAVDRLYADYQDQQLNPDPVEITDLTAQD 980
Db 921 ALSRVKAEKWRDKREKLOLETKRVVTEAKEADVALFVDSQYDLQADTWIGMHAADK 980
Qy 981 LIQSIPVYNEMPEIFPGMNTKTELTDLRQQAWSLYDQNAIPNGDFRNLGNWNAATP 1040
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Db 981 LVHREIRAYSELVPIGVNAEIPFEELEGHITAIISLYDARNVVKNGDFNNGLTCWNVK 1040
QY 1041 GVEVQOINHTSVLVIPNDEQVSOQFTVOPNORYVLRVYARKEGVNGVYSIRDOGNTE 1100
Db 1041 HVDVQOQSHRSDLVIPWEAEVSQAVRVCPCGGYILRVYARKEGVNGCVTHIEHNWD 1100
QY 1101 TLTFASDYDNTGNTQVSTNGTNTNAYNTQASSTNGYNANNMNTQASNTNGYNTN 1160
Db 1101 ELKE--KNREBEVPTDGTGCDYTAHQGTAGCADCACNSRAGYEDAYEDVTTASVNYK 1158
QY 1161 SVYNDOT-----GYITKVTFTPYTDOMIEMSETEGTPI 1196
Db 1159 PTVEEYTYDVRDNHCEYDRGVNYPVPAGYVTKLEYFPTDVTWIEIGTEGKPIV 1218
QY 1197 ESVELIV 1203
Db 1219 DSVLELL 1225

RESULT 4
ID Q9L877 PRELIMINARY; PRT; 1189 AA.
AC Q9L877;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Toxin Cry1Ca6.
GN CRY1CA6.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A2-F;
RA Yu J., Pang Y., Li J.;
RT "Cloning and sequence analysis of the cry1Ca6 gene from Bacillus
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF215647; AAF37224.1; -.
DR HSP; P02965; IC1Y.
DR InterPro; IPR001178; Endotoxin.
DR Pfam; PF00555; endotoxin; 1.
SQ SEQUENCE 1189 AA; 134685 MW; 98F8C1D978DF9451 CRC64;

Query Match 34.5%; Score 2184.5; DB 2; Length 1189;
Best Local Similarity 40.1%; Pred. No. 3.7e-117;
Matches 505; Conservative 190; Mismatches 435; Indels 129; Gaps 31;

QY 1 MSPNNQNEYEIIATPSTSVSNDNSRYPFAPEPTNALQNMDDYKDYLRMSAGNASYPGSP 60
Db 1 MEENNQOC-----IPYNCLSNPE----- 19
QY 61 EVLYSGQ--DAAKAAIDIVGLSLGLVFPVGVPSLVLTQILDLWPSEKSKOWEIFMEQ 118
Db 20 EVLDGGERISTGNSSIDLSLVQFLVSNFY--PGGGFLVGLDIFDFWGVGVGSDAPLVQ 78
QY 119 VBEELINOKIAYARKALSEGLEGNVQLYLTALAEENPENGSRALRDYENRPEILDS 178
Db 79 IEQLINERIAEFARNAALANLEGLGNFNIVVEAFKEWEEEDNNPATRVIDRFLDGG 138
QY 179 LFTQYMPSPFRVNTPEVPLTVYMAANLHLLLLKDAIFGSEWGSSTTTINNYDROMKL 238
Db 139 LLERDIPSFRISEGEVPLSVYAQAANLHLAIRDVSIFGERGWGVTINVENYNNLRH 198
QY 239 TAEYSDDHCVKVYETGLAKIKTSAKQWVDVNOQFREMILAVLDVVVALPNTDTRYPMET 298
Db 199 IDEYADHCANTYRNLNLPKSTYQDMTYTNRRLRDLTLVLDIAAFPFNNRNPYIQP 258
QY 299 KAQLTREYVYDPLGANVYSSIGSWDKAPSGVIESSVIRPPHVDYLTGLTVYVTSRSI 358
Db 259 VGQLTREYVYDPL--INFNPOLQSVLAQLPTFNWMESSAIRNPHLPDILNLTIFTDWF 316

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QY 359 SSARYIRHWAGHOISYHRVSRGSLNQMGYNTQNQLHSTSTFDFTNYDIYKTLSDAV-LL 417
Db 317 GRNFI---WGHREVISLIGGNIITSPIYKEANQEPSPSFTF--NGPVFTLSNPTLRLL 372
QY 418 DIVVPGTYIIFPGMPEVEFPFVWNLNTRTKLNPNVSKDIIIASTRDSELELPETSQOP 477
Db 373 QQMPAPPPNLRGVGEYEP-----STPTNSFTYRG-----RGTVDSLTELPPEDNSVP 420
QY 478 NYESYSHRLCHITSIPATGN---TTGLVPVFSWTHRSADLNNTIYSOKITQIPAVKWDN 534
Db 421 PREGYSHRLCHATFVQBSGTFPLTTGV--VFSWTHRSATLTNTIDPERINQIPLVKGFV 478
QY 535 LPFPVVKPGCHTGGDILQYNRSTGSGVTLLFARYGLALEKAGKYRVRLYAT--DADIV 592
Db 479 WGGTSVITGPGFTGGDILRN---TFGDFVSLQVWINSPIQRYLRFRVYASSRDARVI 534
QY 593 LHVDA-----QIOMP---KTNWPGEDITSKTFKVADAITLTNLATDSSLAKHNLGE 642
Db 535 VLTGAASTGVGGQVSNMPLQKTMIEIGENTSRFTYTFDSNPFSPFRANPDII---GISE 591
QY 643 DP-----NSTLSGIVVDRIEFIPVDETYEABQDLAAKAVNALFTNTKO--GLRPGVTDY 697
Db 592 RPLFGAGSISGELYIDKIELIILADATPEABSDLERAKAVNALFTSSNQIGLKTVDY 651
QY 698 EYVQAANLVECLSDLYPNBKRLLFDVAREAKRLSEARNLLQDPDFQFIN--GENGWAS 755
Db 652 HIDQVSNLVDCLSDDFCLDEKRELSEKVKAKRLSDERNLLQDPNFRGINRQPDGRWRS 711
QY 756 TGIEVIEGDALFKGYRLRPGAREIDTETPTVLYQKVEGVLPKYTRYRLRGVGSQ 815
Db 712 TDITIQGGDDVFKEHYVTLFTG--VD--ECPYTYLYQKIDESKLKAYTRYELRGYIESQD 768
QY 816 LEIFTIRHOTNRIVGNVDDP---LLPDVSPVNSDGSINRCSEKQKYNYSRLEVENRSGE- 870
Db 769 LEIYLIRYNKAEIVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHEWNPDDCSCRDGEK 828
QY 871 ----AHEPSIPIDTGEIDYNENAGIIVGPKITDPPEGVATLGNLELVEEGLSGDALRELQ 926
Db 829 CAHSHHFTLIDIVGCTDLNEDLGWVIFKIQDQGHARLGNLELVEEGLKPLGALARKV 888
QY 927 REEQWIKIQTREEREDRYMASQAVDLYADYQQQLNPDEIETDLTAAQDLIOSIP 986
Db 889 RAEKKWRDKREKLEQLETNIVYKEAKESVDALFVNSQYDRLQVDTNIAHIAADKRVHRIR 948
QY 987 VYVNEPPEIPGMNYTKFTLTDLQQAWSLYDORNAI PNGDFRGLSNMNAIPGVV-Q 1045
Db 949 EAYLPELSVIGVNAALPELEGRIFTAYSLYDARNVIRKNGDFNNGLLCNWVKGHVDEE 1008
QY 1046 QINHTSVLVIPNNDQVSOQFTVOPNORYVLRVYARKEGVNGVYSIRDOGNQOTETLFS 1105
Db 1009 QNNHRSVLVPEWEAEVSQVVRVCPGRGYILRVYARKEGVGEGCVTHIEIEDNTDELKFS 1068
QY 1106 ASDYDTNGMTATQVSWNTGNTNAY--NTQASSTNGYN---ANN-----MTN----- 1148
Db 1069 -NCVEEYVYNNVTTCNNYTGTEEGYTSRNRQGYDEAFGNPNPSVPADYASYBSEKSY 1127
QY 1149 TQASNTGNTNSVYNDOT---GYITKVTFTPYTDOMIEMSETEGTFTYBSVELIV 1203
Db 1128 TDGRENPCSNRGYGYTTPLPAGYVTKDLEYFPETDKVMIEIGETEGTFTVIDSVLVL 1186

RESULT 5
ID Q9S5V8 PRELIMINARY; PRT; 1180 AA.
AC Q9S5V8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Bt84a1 crystal protein.
GN Bt84a1.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.

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OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=T84A1;
RA Nagamatsu Y.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=T84A1;
RA Ogo M., Yamada S., Kobayashi Y., Shibata J., Nagamatsu Y.;
RT "Nucleotide Sequence of the Lepidoptera-toxic Protein Gene of Bacillus
thuringiensis subsp. dendrolimus T84A1.";
RL J. Fac. Appl. Biol. Sci. Hiroshima Univ. 29:95-107(1990).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=T84A1;
RA Nagamatsu Y., Itai Y., Hatanaka C., Funatsu G., Hayashi K.;
RT "A Toxic Fragment from the Entomocidal Crystal Protein of Bacillus
thuringiensis.";
RL Agric. Biol. Chem. 48:611-619(1984).
DR EMBL; AB026261; BAA77213.1; -.
DR HSSP; P02965; 1CIY.
DR InterPro; IPR001178; Endotoxin.
DR Pfam; PF00555; endotoxin; 1.
SQ SEQUENCE 1180 AA; 133489 MW; 1199E4A6D1DC62D CRC64;

Query Match 32.8%; Score 2075.5; DB 2; Length 1180;
Best Local Similarity 39.6%; Pred. No. 7e-111;
Matches 493; Conservative 179; Mismatches 441; Indels 131; Gaps 33;

QY 23 DSNRYPPANE--PTNALQNMDDYKDYLMKMSAGNASEYFGSPPEVLVSGQDAAKA---IDIV 77
DB 2 DNN--PNINECIPYCNLSN-----PEVVLGGRIETGVTYPIDIS 39

QY 78 GKLLSGLVPGVPIVSLYLTOLIDILPSPGKESOWEIPMEQVEHELINOKIAEYARNKALS 137
DB 40 LSTQFLLESEV-FCAGFVLVGLIINGIFGSPQWDAPLVQIEQLINQRIEEPARNOAIS 98

QY 138 ELEGLGNYYQLYLTALEWEENPNPGRALDRNRKFEILDLSFTQYMPSPRTNPFVPEFL 197
DB 99 RLGLSLNLYQIYAESFREWEDPTNPALREBEMRIQFNDMSALITATPLFAVQYQVPLL 158

QY 198 TVYMAANLHLKDKASIFGEEGWSTTTINYYDROMKLTABYSCHVCWKYETGLAKL 257
DB 159 SVTYQAANLHLVLRDVSFQGRGPDAAATINSRYNDLTRIGNYTDVAVRWYNTGLERV 218

QY 258 KGTSAKQWVDYQNRREMTLAVLDVVALFPNYDRTTYPMETKAQLTRREYVTDPLGANNVS 317
DB 219 WGPDSRDWRYNQPRRELTTLVLDIVLAFSNYDSRRYPRTVSQLTRREIYTNP---VLEN 275

QY 318 SIGSWYDKAPSGFVIESVIRPPHVDYITGLTVYVTSQSRSSARYIRHWAGHOISYHRV 377
DB 276 FDGSGFRGAQR---IEQN-IKQPHMDILNRITTYDVH-----RGFNWGHGQITASPV 326

QY 378 --SRGSLQOQMYGNQNLHSTSTFDFTNYDIYKTLSDKAVLLDVIYPGTYTIFPG----- 430
DB 327 GFSGPEPAFLPGNAGNAAPPVLVSLTGLGIFRTLS-----PLYRRIILSGGN 377

QY 431 -----MPEVEFMVQNLNTRKTKYNPVSKDIIASTRDSLELPPTSDQDPNTYESYHR 485
DB 378 QELFVLGDTEFSPASLTNLPSTI-YRQ-----RGTVDSLDVIPPQDQNSVPPRAGFSHR 430

QY 486 LCHTSTPATGNT--TGLVPVPSVTHRSADLNNTYSKTIQIPAVKCDNLPFPVPVVKG 543
DB 431 LSHVTMLSQAGAVYTLRAPFTSWQHSABFNIIIPSSQITQIPLTKSTNLGSGTSVVKG 490

QY 544 PGHTGGDLQVNRSTGVTFLFARYGLALEKAGKRYRLRAYATDADIVLHVN-DA----- 598
DB 491 PGFTGGDILR-RTSPGQISTL---RVNITAPLSQRYRVRIRYASTNQLQFHTSIDGRPIN 546

QY 599 QIQMPKTNMPGEDITSKTFKVAADAITTLNLTADGSL-----ALKNLGSDPNSTLSGIYVV 654
DB 547 QGNFSATMSSGSLQSGSFRTVGTTPFPNFSNGSVFTLSARVNSGNE-----VYI 598
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QY 655 DRIEPIVDVETYEAEQDLAAKAVNALFTNTKD-GLRPGVTDYEVNQANLVCELSDDL 713
DB 599 DRIEFPVAEVTPEAYDLERAQKAVNELFTSSNQIGLTKDVTDTYHIDVSNLVCELSDEF 658
QY 714 YPNEKLLFDVAEREAKRLSEARNLLQDPDFQIEING--ENGWTASTGIEVIEGALPKGRY 771
DB 659 CLDEKQELSEKVKHAKRLSDERNLLQDPNFRGINRQDRGWRGSTDTITIQGGDDVPKENV 718
QY 772 LRPLPGAREIDTETPYLVYQKVEEGLVKPYRVRRLGFGVSSQGLLEIFTIRHQTNRIVKN 831
DB 719 VTLLGTDF---ECYPTLVYQKIDESKLKAYRYQLRGYTEDSODLEIYLYRYNAKHETVN 775
QY 832 VPDD-----LLPOVSPVNSDGSINRCSEQKYVNSRLVENRSGE-----AHEFSIPIDTGE 882
DB 776 VPGTGLWPLSAQSPICKGCEPNKCAPHLEWNPDLDCSCRDGKCAHSHHSLDIDVGC 835
QY 883 IDYNEAGIWWGKIYDTPGAYATLGNLELVESGPLSGDALERLQREBEOQWKIQWTRREE 942
DB 836 TDLNEDLGWVVIKIKITQDGHARLGNLEFLLEKPLVGEALARKVRAKKWRDKREKLEWE 895
QY 943 TDRRYMASKQAVRLYADYQDQOLNPDPVEITDLTAQDLIQSIPIYVYNEMFPPIPGHNYT 1002
DB 896 TNIVYEAKESVDALFVNSQYDRLOQADTNIAHRAADKRVHSIREAYLPELSVIPGVNAA 955
QY 1003 KFTELTDLRQQAWSLYDQRNAIPNGDFRNGLSNNNATPGVEV--QGINHTSVLVIPNWDQ 1061
DB 956 IFEELEGRIPTASLYDARNVKNKGDFNGLSCWNVKGVHDVEEQNNHRSVLVVPWEAE 1015
QY 1062 VSQQTVPQNRQVRLVARTAKGEGVGVISIRGGNQGTETLTFSS-----AS 1107
DB 1016 VSQEVRCPCRGYILRTVATYKGEVGEQVTHIEINNTDELKFSNCVBESEVYNNVTVCN 1075
QY 1108 DYD-TNGMY-NTQVSNVTNGYNTNAYNTQASSTNGYNA--NNMYNTQASNTGNTNTSVY 1163
DB 1076 DYTATOEYEGTTSNRGY--DCAYESNSVADYASAYEEKAYTDGRDRDNPCESNRGY 1133
QY 1164 NDQT---GYITKTVPIPTDQMWIEMSETEGTFVIESVELIV 1203
DB 1134 GDYTPLAGVITKLEYFPETDKVWIEIGETGTFIVDSVELLL 1177

RESULT 6
Q45736 PRELIMINARY; PRT; 1176 AA.
AC Q45736;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
DE Insecticidal crystal protein.
GN CRYIA(A).
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FU-2-7;
RA Kondo S., Tamura N., Kunitate A., Hattori M., Akashi A., Ohmori I.;
RT "Cloning and nucleotide sequencing of two insecticidal delta-endotoxin
genes from Bacillus thuringiensis var. kurstaki HD-1 DNA.";
RL Agric. Biol. Chem. 51:455-463(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FU-2-7;
RA MEDLINE=94289859; PubMed=7764972;
RA Udayasuriyan V., Nakamura A., Mori H., Masaki H., Uozumi T.;
RT "Cloning of a new cryIA(a) gene from Bacillus thuringiensis strain
FU-2-7 and analysis of chimaeric CryIA(a) proteins for toxicity.";
RL Biosci. Biotechnol. Biochem. 58:830-835(1994).
DR EMBL; D17518; BAA04468.1; -.
DR HSSP; P02965; 1CIY.
DR InterPro; IPR001178; Endotoxin.
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DR Pfam; PF00555; endotoxin; 1.
FT CONFLICT 77 77 L -> P (IN REF. 1).
FT CONFLICT 965 965 S -> F (IN REF. 1).
SQ SEQUENCE 1176 AA; 133075 MW; AA4135B49A289F85 CRC64;

Query Match 32.7%; Score 2070.5; DB 2; Length 1176;
Best Local Similarity 39.4%; Pred. No. 1.4e-110;
Matches 492; Conservative 176; Mismatches 440; Indels 137; Gaps 33;

QY 23 DSNRYPPANE--PINALQNDYKDYLMKMSAGNASEYPGSPVLYSGQDAKAA---DIDV 77
DB 2 DNN--PINEICPNCLSN-----PEVEVLGGERIETGTPIDIS 39

QY 78 GKLLSGLVGPEVGVISLYTOLIDILMPGSGKQWEIFMEQVEBELINOKIAEYARNKALS 137
DB 40 LSLTQFLSERV-PGAGFVLGLVDIIWGIFGPSQWDAPLQIEQLINQRIEFARNQAS 98

QY 138 ELEGNNYQIYLTALBEBEENPGSRALRDVRNRFELDSLFTQYMPSPFVTPVPEPFL 197
DB 99 RLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMSALATTAIPLLAVQNYQVPL 158

QY 198 TVYMAANLHLLKADSIQEEGWSMTTINNYDROMKLTAEYSDHCVKWYETGLAKL 257
DB 159 SVYVQAANLHLSVLRDVSFGQRGWGFDAATINSYNDLTRLIGNYTDYAVRWYNTGLERV 218

QY 258 KGTSAKQWVDYNQRRMTLAVLDVALFPNYDTRTPMETKAQLTREVTDPILGAVNVS 317
DB 219 WGPDSRDWRVYNQRRRLTLVLDIVAFSNYDSRRPIRVSQLTRITVNP---VLEN 275

QY 318 SIGSWYDKAPSGFVIESVIRPPHFVDYITGLTVYTSQSRISARYIRHWAGHQISYHRV 377
DB 276 FDGSGFRGAQR---IQN-IRQPHLMDILNSITVTVH-----RGFNWYSGHQITASP 326

QY 378 --SRGSLNQMYGTNQLHSTSTFDNYDIYKTLKSDAVLLDIVPGYTIFFG----- 430
DB 327 GFSGPEFAPPLFGNAGNAAPVLSLTGLGIFRTLS-----PLYRRILILGSGPNN 377

QY 431 ----MPEVEFFMYNQLNTRKTLKYNPVSKDIIASTRDSLELPPETSQDPNYESYSHR 485
DB 378 QELFVLDTGTEFSPASLTNLNPSIT-YRQ-----RGTVSDLDVIPPQDQNSVPPRAGFSHR 430

QY 486 LCHITSIPATGNT--TGLVPVFSWTHSADLNNTIYSDKITQIPAVKCDNLPPFVVKVG 543
DB 431 LSHVTMLSQAGAVYTLRAPTFSGHRSAPFNIIIPSSQITQIPLTKSTNLGSGTSVYKG 490

QY 544 PGHTGGDLQVNRSTGVTGLFLARYGLALEKAGYRVLAYATDADIVLVN-DA----- 598
DB 491 PGFTGGDILR-RTSPGOISTL---RVNITAPLSQRYRVRIRYASTTNLQFHTSIDGRPIN 546

QY 599 QIQMPKTMNPGEDLTSKTFKVADAITTLNLTDSLSL---ALKENLGEDPNSTLSGIYV 654
DB 547 QGNFSATWSSGNSNLOSGSPRTVGTTPFNFSNGSVFTLSAHVNSGNE-----VYI 598

QY 655 DRIFIPVDETYEAOBLEAKAVNALFTNTKD-GLRPGVTDYEVNQANLVECLSDDL 713
DB 599 DRIFVPAEVTFEAYDLERAQKAVNELFTSSNQIGLKTVDTHIDQVSNLVECLSDPE 658

QY 714 YPNEKRLFLDAVREKRLSEARNLLOPDQFOENG--ENGWASTGIEVIEGDALPKRY 771
DB 659 CLDEKQELSEKVKHAKLSDBENLLODPNFRGINRQRLDRGRWGSTDTIQGGDDVFKENY 718

QY 772 LRLPGAREIDTETPTLYLYQKVEGVLLKPYTRYRLRGVPGSSQGLEIFTIRHOTNRIVKN 831
DB 719 VTLTGTFD---ECYPTLYQXIDESKUKAYTRYQLRGVIEDSQLEIYLIRYNKHTVN 775

QY 832 VPDD-----LLPDSVPVNSDGSINRCSEQKYNSRLEVENRSGE-----AHFSPIDTGE 882
DB 776 VPGTGLWPLSAQSPFGKGBEPNRCAPHEWNPDLDCSDRGKCAHSHHFLSDIDVGC 835

QY 883 IDYVENAGIWWGFKITDPEGVATIGNELVEEGPLSGDALRRLQREBOQWKIQWTRREE 942
DB 836 TDLNEDLGWVWIFKIQDQGHARLGNLEFLKEKPLVGLGALARVKRAEKKWRDKEKLEWE 895

QY 943 TDRRYMASKQAVDLRYADYQDQOQLNPDVBITDLTAADLIQISPIYVYNNEMFPPIGNNYT 1002
DB 896 TNIVYKEAKESVDALFVNSYDQLQADTNLAMIHAADKRVHSIRREAYLPSELSVIPGNAA 955

QY 1003 KFTFELDRLOQASWLYDQRNAIPNGDFRGLSNWNTAPGVEV--QQINHTSVLVIPNWDQ 1061
DB 956 IFBELEGRISTAFSLYDARNVIKNGDFNGLSCWNYKGVHDVEEQNNQSRVLPVPEWEAE 1015

QY 1062 VSOQFTVQPNQRYVLRVARTAKKGVNGYVIRDDGNGOTETLTES-----AS 1107
DB 1016 VSOEVRVCPGRGILRLYATYKEGEGGCVTIHEIENNTDELKFCVCEBIEIYNNVTTCN 1075

QY 1108 DYDTN-----GMTNTQVNTNGYNTNAYNTQASSTNGYNNANNMYNTQASNTNGYNTNSV 1162
DB 1076 DYTQNEEYGGAY--TSRNRGI--NEAPSVADYASVYEKSY--TDGRRNPCEBNRG 1128

QY 1163 YNDQT-----GYITKTVTFPIPYTQOMIEMSETEGTFFYIESVELIV 1203
DB 1129 YRDYTPLPVGVYVTKLEYFPETDKWIEIGETGTFIVDSVELLL 1173

RESULT 7
Q93TF9 PRELIMINARY; PRI; 1160 AA.
AC Q93TF9;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMELrel. 20, Last annotation update)
DE Insecticidal crystal protein.
GN CRYIDB.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_taxid=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B-PR-88;
RA Li C., Zhang J., Huang D., Li G.;
RT "A crystal endotoxin from Bt strain B-Pr-88";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF358662; AAK48937.1; -
DR InterPro; IPR001178; Endotoxin.
DR Pfam; PF00555; endotoxin; 1.
SQ SEQUENCE 1160 AA; 130952 MW; B18B04193D87695E CRC64;

Query Match 32.7%; Score 2068; DB 2; Length 1160;
Best Local Similarity 39.4%; Pred. No. 1.8e-110;
Matches 482; Conservative 189; Mismatches 425; Indels 126; Gaps 29;

QY 33 PTNALQNDYKDYLMKMSAGNASEYPGSPVLYSGQDAKAAIDIVGKLLSGLVPPVGP 92
DB 11 PYNCLN--PDAILIDA-----ERLETGNTVADISUGLINFLYNSP-VPGGGPI 56

QY 93 VSLYTOLIDILMPGSGKQWEIFMEQVEBELINOKIAEYARNKALSLEGLNNYQIYLT 152
DB 57 VG---LLELGVGVPQWEIPLAQIEQLISQRIEFARNQASIRLEGLSNYIYET 112

QY 153 LEEWENPGSRALRDVRNRFELDSLFTQYMPSPFVTPVPEPFLTYMAANLHLLK 212
DB 113 FRAMEKDPSPALREEMRTQFNWMSALIAAIPLLVRNVEVALLSVYQAANLHLSVL 172

QY 213 DASIFGEWGSMTTINNYDROMKLTAEYSDHCVKWYETGLAKGTSAKQVYNOFR 272
DB 173 DVSIVQRMGDFPATVNSRYSDDLRIHVITDCHVDYNDGLKNLEGRISDWWVYNNR 232

QY 273 REMTLAVLDVALFPNYDTRTPMETKAQLTREVTDPILGAVNVSISGWDKAPSGV 331
DB 233 RLITISVLDIILAFPNYDIENYPIQTASQLTREVLDPVNETLSPASV----PTFSA 298

QY 332 IESVIRPPHFVDYITGLTVYTSQSRISARYIRHWAGHQISYHRVSRGSL--QQMYGT 389
DB 289 AESAIRSPHLVDFLNSFTIYTD--SLASVAY--NGGHLVNSFRGTGTTNLTIRSPLYGR 343


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QY 390 NQNLHSTSTPFT--NYDIYKTLKDAVLLDIVYGYTYTFF-----GMPEVEFFM 438
DB 344 EGTERPVTISASPSVPIFTLS-----YFTGLNNNPVAGIBGEV-- 385
QY 439 VQNLNTRKTLKYNPVSKDIIASTR--DSELELPETSDQPNYESYSHRLCHITISIPATG 496
DB 386 -----QNTISRSYRKSGBPDSFSELPQDVSVSPAIGYSHRLCHATFLERIS 433
QY 497 NTTGLVPFVSWTHRSADLNNTIYSDKITQIPAVKWCNDLPPVPVKGPGHGTGGDLQYNR 556
DB 434 GPRIAGTVFVSWTHRSASPIVSEPSRITQIPWKAHTLASCASVKGPGGTGGDLTRN- 492
QY 557 STGSVGLFLIARYGLALEKAGKYRRLRYATDADIVLHVNDQA-----IQMPKTMNPGED 611
DB 493 SMGDLGALRVTFTRGLPQ---SYVIRFYASVANRSCTFRYSQPPSYGISFPKTMADAGEA 549
QY 612 LTSKTFKVADAITTLNLTADSSIALKKNLGEDPNSTLSGIYVYDRIRFIPVDETYEABQD 671
DB 550 LTRSRP-----AHTTLFTPIFTSRA-----QEEFDLYIQSGVYIDRIEPIFVDATFESEIN 600
QY 672 LEAAKAVNALFTNTKD--GLRPGVTDYEVNOANLVECLSDLLYPNEKRLLEDAVREAKR 730
DB 601 LERAQAVNALFTSTNQLGKLTVDTHIDQVSNLVECLSDPECLDEKRELSEKVRHAKR 660
QY 731 LSEARNLLODPDFOEIN--GENGWTAFTGIEVIEGDALFKRVLRLPFGAREIDTETPTY 788
DB 661 LSDERNLLODPNFRGINRQPDGRWGRTDITIQQGDDVFKENVTLTGTFD---ECYPTY 717
QY 789 LYQKVEGLVKPTRYRLRGFRVSSQGLEIFPTRHQNTRIVKQNVDD-----LLPDVSPVN 844
DB 718 LYQKIDESKLYKATRYOLRGYIEDSOBLEIYLIRYNKAKHEIVNVPGTGSLWPLSVQSPIG 777
QY 845 SDGSINRCRQKTVNSRLEVENSGE-----AHEFSIPIDTGEIDYNNENAGIWWGPKITD 899
DB 778 KCGEPRNCAPHEWNPDLDCSDEEKCASHHSHFSLDIDVCTDLNEDLWGVIFIKT 837
QY 900 PEGYATLGNLEVEGLSDGALERLQREQOWKIQWTRREETDRRYMASKQAVDELYA 959
DB 838 QDGHARLGNLEFLEKPLVGEALARVKAERKWRDKREKLELTNIIVYKEAKESVDALFV 897
QY 960 DYQDQQLNPVVEITDLTAAQDLTQSIPIYVNVEMPPETPGMNYTKFTLRLORLOQMSLYD 1019
DB 898 NSQYDQLQADTNTAMTHAADKRVHSIREAYLPELSVIFPGVNAIGFEBLEGRIFTAVSLYD 957
QY 1020 QRNAIPNGDFRNLGNWNAFPGEV--QIINHSTVLVLPNDDEQVSOQFTQPNQRYVLR 1078
DB 958 ARNVIKNGDFNGLGSCNVKGVHDVBEQNHRSVLVVPWEAEVSQBRVCPGGRGYTLRV 1017
QY 1079 TARKEGVGVYIRIDGNGQNTETLTFSASDYDNGMTNTQVSNNTNGNNTNAYNTQASST 1138
DB 1018 TAYKEGVGECVTHIEVDNNTDELK--SNCEKEQVYPGNTVACNDYKXKHGANACSSRN 1075
QY 1139 NGYNANNMNT-----QASNTNGYNTN--SVYND-----QTYITKTVTFPIPTD 1181
DB 1076 RGYDESYESNSSIPADYAPYIEBEAYTDGQGNPSEFNRGHTPLPAGYVTAELIYEPETD 1135
QY 1182 QMIEMSETEGTFYIESVELIV 1203
DB 1136 TWVVEIGETGTFIVDSVELLL 1157

RESULT 8
Q9RC30
ID Q9RC30 PRELIMINARY; PRT; 1176 AA.
AC Q9RC30;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE 135 kDa insecticidal protein.
OS Bacillus thuringiensis (subsp. kurstaki).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=29339;
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[1]
RN SEQUENCE FROM N.A.
RP STRAIN=HD-1-02;
RA Hou B.K., Chen Z.H.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF154676; RAD5382.1; -
DR HSSP; P02965; 1CIY.
DR InterPro; IPR001178; Endotoxin.
DR Pfam; PF00555; endotoxin; 1
SQ SEQUENCE 1176 AA; 133010 MW; FCEE069D0B81D8C4 CRC64;

Query Match 32.5%; Score 2055.5; DB 2; Length 1176;
Best Local Similarity 39.4%; Pred. No. 9.9e-110;
Matches 491; Conservative 175; Mismatches 442; Indels 137; Gaps 33;

QY 23 DSNRYFANE--PTNALQWMDYKDYLMASAGNASEYPGSPVVLVSGQ---DAAKAAIDIV 77
DB 2 DNN--ENINECIPYNCLN-----PEVEVGGRJETGYTPIDIS 39
QY 78 GKLLSGLVPPFVGPVIVSLYTLQDILILPSPGSEKQWEIFMEQVEELINOKIAEYARNKALS 137
DB 40 LSTQFLLSEFV--PGAGFVLGLVDIIIGFSGQWDTFLVQIEQLINORIEEFARNOAIS 98
QY 138 ELEGLGNNTQLYLTALEEWENPENGSRALRDVNRNRFIILDSLFTQYMPSPRVNFEVPFL 197
DB 99 RLGLSLNLIQIYAESFREWEADPTNPALEEMRIQFNDAWSALTALPLAVQNYQVPLL 158
QY 198 TVYMAANLHLLLLKQASIFGEWGSTTTNNYDRQMKLTAEYSDCHCVKWTETGLAKL 257
DB 159 SVYVQANLHLSLRVDSVFGQWGPDAATINSRYNDLTRLIGNYTDYAVRWNTGLERV 218
QY 258 KGTSAQWVDYQNPFRREMTLAVLDVVALPNDYTRYPMETKAQLTRVYVTDPLGAVNVUS 317
DB 219 WGDPSRDWRYNQFRRELTLTVDIVALFSNDSRRYPITVSQLTREIYTNP---VLEN 275
QY 318 SIGSWDKAPSEFVIBSSVIRPPHVFYITGLTYTQSRSSISSARYIRHWAGHQISVHRV 377
DB 276 FDGSPRGAQR---ISQN--IRPQLMDILNSTIYTDVH-----RGPNYWSGHQITASPV 326
QY 378 --SRGNLQOMGTNQNHLSTSTFDFTNVDIYKTLKDAVLLDIVYGYTYTFFG----- 430
DB 327 GFSGPFAFPFLFNGAGNAAPPVLVSLTGLGIFRTLSS-----FLYRRIILGSGPNN 377
QY 431 -----MPEVEFFMVNQLNTRKTLKYNPVSKOIIASTRSELELPETSDQPNYESVSHR 485
DB 378 QELFVLDGTGTFSPASUTLNLPSIT--YRQ-----RGTVDSLDVIPPQDMSVPPRAGFSHR 430
QY 486 LCHITISIPATGNT--TGLVPFVSWTHRSADLNNTIYSDKITQIPAVKWCNDLPPVPVKG 543
DB 431 LGHVWLSQAAGAVYTLRAPTFESQWHRSAEFNNIIPSSQITQIPLTKSNLGSSTSVKG 490
QY 544 PGHTGDLLOYNRSTGSGVTFLIARYGLALEKAGKYRRLRYATDADIVLHVNDQA----- 598
DB 491 PGFTGDLIR--RTSPQIISTL---RVNITAPLSQRYVRIRVYASTTNLQPHSTSIDGRPIN 546
QY 599 QIQMPKTMNPGEDLTSKTFKVADAITTLNLTADSSL-----ALKHNLGEDPNSTLSGIYV 654
DB 547 QGNFSAIATSGSNLQSGSFRTGTFPPFNSGSSVFTLSAHVFNSGNE-----VYI 598
QY 655 DRIEFIPDVEYAEQDLEAAKAVNALFTNTKD--GLRPGVTDYEVNOANLVECLSDLL 713
DB 599 DRIEFVPAEVTPEAEYDLERAQKAVNELFTSSNQIGLKTVDTHIDQVSNLVECLSDDEF 658
QY 714 YNEKELLFPDAVREAKRLSEARNLLODPDFOEIN--ENGWTAFTGIEVIEGALPKGRY 771
DB 659 CLDEKQELSEKVKHAKRLSDERNLLODPNFRGINRQLDGRWGRTDITIQQGDDVFKENV 718
QY 772 LRLPGAREIDTETPTYLYQKVEGLVKPTRYRLRGFRVSSQGLEIFPTRHQNTRIVKQ 831
DB 719 VTLGLTFD---ECYPTYLYQKIDESKLYKATRYOLRGYIEDSOBLEIYLIRYNKAKHETVN 775
QY 832 VPDD-----LLPDVSPVNSDGSINRCRQKTVNSRLEVENSGE-----AHEFSIPIDTGE 882
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Db 776 VFGTGLWPLSAQSPFGKIGKGEPRNRCAPHLEWNPDLDCSDGCEKCAHHSHHFLSDIDVGC 835
Qy 883 IDYNENAGIWWGFKITDPGKYATLGNLEVEEGPLSGDALERLOREEQOWKIOMTFRREE 942
Db 836 TDLNEDLGWVIFKIKTQDCHARLGNLEFLEKPLVGEALARKVIAKRWDRKRELEWE 895
Qy 943 TDRRYMASKQAVDRLYADYQDQOLPNVDVITDLTAAQDLIQSIPIVYNEMFPEIGMNYT 1002
Db 896 TNIUVYKEAKESVDALFVNSQYDQLOADTNIAIMIHAADKRVHSIREAYLPELSVPGVNA 955
Qy 1003 KTELTDRLQOAWSLYDQNAIPNGDFRGLSNWNTATPGVEV-QQINHTSVLVIWPDQ 1061
Db 956 IPEELEGRIFTAFSLYDARNVIRKNGDFNGLSCWNYKHVDVEEQNNQSRSLVWPEWEAE 1015
Qy 1062 VSQQFTVQPNQRYVLRVARTARKEGVNGYVSIIRDGNQOTLTFS-----AS 1107
Db 1016 VSQEVVPCRGYILRVATYKGGYEGCVTHIEIENNTDELKFSNCVEBEIYNNVTVCN 1075
Qy 1108 DYDTN-----GMNTQVSNNGYNTNAYNTQASSTNGYNANNMNTQASNTNGYNTNSV 1162
Db 1076 DYTVAQEEYGGAY---TSNRNGY--NEAPSVPADYASVVEEKSY--TDGRRENPCFNRG 1128
Qy 1163 YNDQT-----GYTKVTFTPYTDQMIEMSETEGTPYIESVELIV 1203
Db 1129 YRDYTFPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLL 1173

RESULT 9
ID O06894 PRELIMINARY; PRT; 1171 AA.
AC O06894;
AT 01-JUL-1997 (TremBrel. 04, Created)
DT 01-JUL-1997 (TremBrel. 04, Last sequence update)
DT 01-DEC-2001 (TremBrel. 19, Last annotation update)
DE CryEa4.
GN CryEa4.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LBIT-147;
RA Barboza-Corona J.E., Lopez-Meza J.E., Ibarra J.E.;
RT "Cloning and expression of the cryIEa4 gene of Bacillus thuringiensis
RL and the comparative toxicity of its gene product.";
RL World J. Microbiol. Biotechnol. 14:437-441(1998).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=LBIT-147;
RC Ibarra J.E., Barboza-Corona J.E.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U94323; AA004732.1; -.
DR HSSP; P02965; 1CIY.
DR InterPro; IPR001178; Endotoxin.
DR Pfam; PF00555; endotoxin; 1.
DR PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN 1.
SQ SEQUENCE 1171 AA; 133310 MW; 333603A1A782523A CRC64;

Query Match 32.4%; Score 2054.5; DB 2; Length 1171;
Best Local Similarity 38.9%; Pred. No. 11e-109;
Matches 483; Conservative 193; Mismatches 433; Indels 135; Gaps 33;

Qy 20 VSNDNRNPFANEPTNALQNDYDKYLKMSAGNAGSPEVLSVGGDAKAAADIVGK 79
Db 4 VNNQOCVPY-----NCLNPE-NEILDERSNSTV-----ATNIALEISRL 44

Qy 80 LLSGLGVFVGIVSLYTLIDILPSPGSKSQWEIFMEQVEBLINQKIAEYARNKALSEL 139
Db 45 LASAT-----PIGGILLGLFDIAIGSIPGSQWDLFLQIEILLIDKIEFARNQAISRL 98

Qy 140 EGLGNNYQLYLTALEWEENPNGRALRDVRNRFELDLSLFTQYMPFSFVTFVFPFLTV 199
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Db -99 EGISLYGIYEAFAREWADPTNPALKEEMRTQFNDMNSILVTAIPLFSVQYQVPLSV 158
Qy 200 YAMRANLHLLLKDASIPGEWGHSTTTINNYDROMKLTAEYSDHCYKWTETGLAKG 259
Db 159 YVOAANLHSLVRDVSFQWAGFDIATINSYRNDLTRILPIYTDYAVRWNTYGLDLPLR 218
Qy 260 TSA-KQWYDYNQFRREMTLAVLDVVVALFPNPDYRTYPMETKAQLTREYVTPPLGAVNVSS 318
Db 219 TGGLENWARFNQFRELTISVLDIISFRNVDLSRPIPTSSQLTREYVTPDV--INTD 276
Qy 319 IGSWYDKAPSGVIESSVIRPPHVDYITGLVYVYQSRSSISARYIRHWAGHQISYHRVS 378
Db 277 ---YRVGSPENIENSARSPLHMLFNLNLTIDT-----DLIRGVHWAGHRVTSH--F 325
Qy 379 RGSN---LQWQYNTGNLH-----STSTPDTNYDIYKTLSDAVLLDIVPGYIYIFG 430
Db 326 TGSQVITTPQYGNQNAEPRTIAPSTFGLNL-FYRTLSNP-----FPR 370
Qy 431 MPEVEFFWVNLNTRKTLKYN-----PVSKDIIASTR---DSELELPPETSDQPN 478
Db 371 RSE-----NITPLGINVVGVGFIQPNNAEVLIRSGRTVDSLNELP--IDGENS 418
Qy 479 YESXSHRLCHITSPATGNT--TGLVPVFSWTHRSADLNNTIYSDKITQIPAVKCDNLP 536
Db 419 LVGYSHRLSHVLTLSLNTNITSL-PTFWTHSATNTNINPDIITQIPLVKGFRGG 477
Qy 537 FVPVVGPGHGTGDDLQVNRSTGVTGLFLARYGLALEKAGKYRVRLRYAT--DADIYH 594
Db 478 GTSVIKSGPGTGGDILRRN---TIGEFVSLQVNSPITQRYRLRFRYASSRDARITVA 533
Qy 595 VND---AQIQMPKMNPGEDLTSTKFKVADAITNLNLTATDSSLAKKNLGEDPNSTLSGI 651
Db 534 IGGQIRVDMTLEKTEWIGESLTSRTFSYTNFSPFRANPDII---RIABE-LPIRGGE 589
Qy 652 VYDRIEIPVDETVEARQDLAAKAVNALFTNTKD-GLRPGVTYDVNQAANLVECLS 710
Db 590 LYIDKIELILADATFEEYDLERAQKAVNALFTSTNQLGKTDVTDHIDQVSNLVECLS 649
Qy 711 DDLFPNEKRLLPDAREKRLSEARNLLQDPDPQRI--GENGWASTAGIEVIEGDAIFK 768
Db 650 DEFCLDEKRELSEKVKHAKLSDBERNLLIQDPFRGINRQDPDRGWRGSTDITIQGGDDVFK 709
Qy 769 GRYLRLPCAREIDETETPYLYQKVEGVLPKPYRYLRGVGSSQGLEIETIRHQTWRI 828
Db 710 ENYVTLPGTFD---ECYPTIYQKIDSKLKAYTRYELRGYIEDSQDLEIYLRNAXHE 766
Qy 829 VKNVPDD---LLPDVSPVNSDGSINRCSEQKYNSRLSEVENRSGE-----AHPFSIPID 879
Db 767 TVNVPGTGSLWPLSAQSPFGKIGKGEPRNRCAPHLEWNPDLDCSDGCEKCAHHSHHFLSDID 826
Qy 880 TGEIDYNNAGIWWGFKITDPGKYATLGNLEVEEGPLSGDALERLOREEQOWKIOMTFR 939
Db 827 VGCTDLNEDLGWVIFKIKTQDGVARLGNLEFLEKPLVGEALARKVIAKRWDRKRELE 886
Qy 940 REETDRRYMASKQAVDRLYADYQDQOLPNVDVITDLTAAQDLIQSIPIVYNEMFPEIGM 999
Db 887 EWETNIVYKEAKESVDALFVNSQYDRLQADTNIAIMIHAADKRVHSIREAYLPELSVPGV 946
Qy 1000 NYTKFTLTDLRQOAWSLYDQNAIPNGDFRGLSNWNTATPGVEV-QQINHTSVLVIWPDQ 1058
Db 947 NAAIFEELEGRIFTAFSLYDARNVIRKNGDFNGLSCWNYKHVDVEEQNNHRSVLVWPEW 1006
Qy 1059 DEQVSQQTVPQPNQRYVLRVARTARKEGVNGYVSIIRDGNQOTLTFS-----ASDY 1109
Db 1007 EAEVSQEVVPCRGYILRVATYKGGYEGCVTHIEIENNTDELKFSNCVEBEIYNNVT 1066
Qy 1110 DTNGHYNTQVSNNGYNTNAYNTQASSTNGYNANNMNTQASNTNGYNTNSVND 1165
Db 1067 TCNNYATQEEHEGTYTSRNRGYDEAYESNSVHASVVEEKSYTDRRENPCSNRGYGD 1126
Qy 1166 QT----GYTKVTFTPYTDQMIEMSETEGTFVIESVELIV 1203
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Db 1127 YTPLPAGYVTKLEYFPETDKWIBIGETGTGTFIVDSVELLL 1168

RESULT 10

Q9F296 PRELIMINARY; PRT; 1155 AA.

AC Q9F296; 01-MAR-2001 (TREMELrel. 16, Created)

DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)

DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)

DE Delta endotoxin.

OS Bacillus thuringiensis.

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;

OC Bacillaceae; Bacillus.

OX NCBI_TaxID=1428;

RN [1]_SEQUENCE FROM N.A.

RP MEZA-BASSO L.A., Theodoroz C.; "Cloning and expression of a delta endotoxin gene from a Chilean native Bacillus thuringiensis strain.";

RT Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; U94191; AAG16877.1; --

DR HSSP; P02965; ICY.

DR InterPro; IPR001178; Endotoxin.

DR Pfam; PF00555; endotoxin; 1.

SQ SEQUENCE 1155 AA; 130557 MW; 5D69E3E2F527749D CRC64;

Query Match 32.3%; Score 2048; DB 2; Length 1155;

Best Local Similarity 38.9%; Pred. No. 2.6e-109;

Matches 480; Conservative 192; Mismatches 426; Indels 136; Gaps 32;

QY 23 DSNRYPFANE--PTNALQNMNDYKDYLMKMSAGNASEVPGSPVSLVSGODAAKAA--IDIV 77

Db 2 DNN--PINECIPTNCLN-----PEVEVLGGERIETGYTIDIS 39

QY 78 GKLLSLGLGVFPVPGPIVSLYQLDILIMPSEKQWEIPEQVBEINQKIAEYARNKALS 137

Db 40 LSLTQFLSEFV--PGAGFVLGLVDIIWIFGPSQWDAFLVQIQLINQRIEAFARNAQIS 98

QY 138 ELEGNNYQLYLTALAEENENPNSGRALDVRNRBELDSLQTQYPSRVNFEVPEL 197

Db 99 RLEGSLNYQIYAESPFEWDEPTNPALEEMRIQFNDMNSALTATPLFAVQNYQVPLL 158

QY 198 TVYMAANLHLLKDAISIFGEWGSSTTINNYDRQMKLTAEYSDHCVKWYETGLAKL 257

Db 159 SVTVQANLHLVLRDVSVPQGRGDAATINSRYNDLTRIGNYTHAVRWNTGLERV 218

QY 258 KGTSAQWVDYNOFRREMTLAVLDVVALFPNYDTRTYPMETKLAQLTRVYTDPL-----G 312

Db 219 WGPDSRDWIRYNOFRRELTTLVLDVSLFPNYSRTYPIRTVSQLTRIEYTNVPLENFDG 278

QY 313 ANNVSSIGSWYDKAPSGFVIESSVIRPPHVDYITGLTVTQSRSSSARYIRHWAGHOI 372

Db 279 SFRGSAGQ-----IEGS--IRSPHMDILNSTIYTDH-----RGEYWSGHQI 321

QY 373 SYHRV--SRGSNLQOMYGTQNLHSTF--DFTNYDIYKTLSDKDAVLDDIVPGYTVIP-- 428

Db 322 MASPVGSGPEFTFPLVGTGMNAPQORIVAQLGGYVRLSSTL-----YRPPN 372

QY 429 FGMPEVEFPFVMVQNLNTRKTLKYNVSKDIIASTRDSLELPPETSQPNYESYHRLCH 488

Db 373 IGINNQSLVDCTEAYGTSNNLPSAVYKSGVTDSLDSDIPEQNNVPPRQGFSLHLSH 432

QY 489 ITSIPATNTGL-----VPVFSWTHRSADLNTIYSKTIQIPAVKCDNLPPFVVKGP 544

Db 433 VSMFRSGFSNVSIIIRAPMFSWIHRSABFNIIIPSSQITQIPLTKSTNLGSGTSVVKGP 492

QY 545 GHTGGDLQYNRSTGSGTLFLARYGLALEKAGKYRVLRYATDADIVLVN--DA-----Q 599

Db 493 GFTGGDILR--RTSPGOISTL---RVNITAPLSQRYRIRIYASTNLPQFTSIDGRPINQ 548

QY 600 IQMPKTNWPCEDLTSKTFKVADAITLNLATDSSL-----ALKENLGDPNSTLSGIVYVD 655

RESULT 11

Q45735 PRELIMINARY; PRT; 1177 AA.

AC Q45735; 01-NOV-1996 (TREMELrel. 01, Created)

DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)

DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)

DE Delta-endotoxin.

OS Bacillus thuringiensis.

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;

OC Bacillaceae; Bacillus.

OX NCBI_TaxID=1428;

RN [1]_SEQUENCE FROM N.A.

RP MEDLINE=91197102; PubMed=2014985;

RA Von Tersch M.J., Robbins H.L., Jany C.S., Johnson T.B.;

RT "Insecticidal toxins from Bacillus thuringiensis subsp. kenya: Gene cloning and characterization and comparison with B. thuringiensis subsp. kurataki CryIA(c) toxins.";

RL Appl. Environ. Microbiol. 57:349-358 (1991).

DR EMBL; M35524; AAA22338.1; --

DR HSSP; P02965; ICY.

DR InterPro; IPR001178; Endotoxin.

DR Pfam; PF00555; endotoxin; 1.

SQ SEQUENCE 1177 AA; 133114 MW; C81F76D03F3BCCB5 CRC64;

Query Match 32.0%; Score 2027; DB 2; Length 1177;

Best Local Similarity 39.4%; Pred. No. 4.4e-108;

Matches 494; Conservative 186; Mismatches 419; Indels 156; Gaps 37;

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Qy 23 DSNRYPFANE--PTNALQNDYKDYLMKMSAGNASSEYPGSPVLVSGQDAKAA---IDIV 77
Db 2 DNN--PNINECIPYNCLSN-----PEVEVLGGERIETGYTPIDIS 39

Qy 78 GKLLSGLGVFPVGPVIVSYLTQILDLWPSEKESQWEIFMEQVEELINOKIAEYARKALS 137
Db 40 LSLTOFLLSSEFV-PGAGFVLGLVDIWIIGFPGSQWDAFLVQIEQLINQRIEFAFNQAIS 98

Qy 138 ELEGGLNNYQLYLTALBEEWENPNSRALRDVRNRFEILDSLFTQYMPSPRVNFEVPL 197
Db 99 RLEGSLNLYQIYAESFREWEADPTNPALREVRQFNDMNSALTATPPLAVQNVPL 158

Qy 198 TVYAMAANLHLLKLDASIFGEEGWSMTTNNYDROMKLTAEYSDHCVKWYETGLAKL 257
Db 159 SVYVQAANLHLSVLDRVSVFGQWGFDAATINSRYNDLTRIGNYTDHVRWYNTGLERV 218

Qy 258 KTSKQWVDVNOQPREMTLAVLDVVALFPNYDRTYTPMETKQAQLTRVYTDPL-----G 312
Db 219 WGPDSRDWRYNQFRELTLTVLDIVALEFPNYSRRYPRTVSQLTRTYTPNVLNFDG 278

Qy 313 AVNVSSIGSWYDKAPSGFVIESSVIRPPHVDYITGLTVYTOSRSISSARYIRHWAGHOI 372
Db 279 SFRGSAQG-----IEGS-IRSPHMDILNSITTYDAH-----RGYYWSGHQI 321

Qy 373 SYHRV--SRGSNLOQMYGTNQNLHSTSTF-DFTNYDIYKTLSDKDAVLDDIVPGYTYIF 429
Db 322 MASPVGSGPEFTFLYGTMGNAAPQORIVAQLGQGVYRTLSL-----YRRFPN 372

Qy 429 FGMPVEFFMNQNLNRTKLYKNPVSKDIIASTRDSLELPPEPSTSDPNTESYSHRLCH 488
Db 373 IGINNQQLSVLDGTFAGYGTSSNLPASVYRKSGTVSDSDEIPQNNNPPRQGFPHRLSH 432

Qy 23 DSNRYPFANE--PTNALQNDYKDYLMKMSAGNASSEYPGSPVLVSGQDAKAA---IDIV 77
Db 2 DNN--PNINECIPYNCLSN-----PEVEVLGGERIETGYTPIDIS 39

Qy 78 GKLLSGLGVFPVGPVIVSYLTQILDLWPSEKESQWEIFMEQVEELINOKIAEYARKALS 137
Db 40 LSLTOFLLSSEFV-PGAGFVLGLVDIWIIGFPGSQWDAFLVQIEQLINQRIEFAFNQAIS 98

Qy 138 ELEGGLNNYQLYLTALBEEWENPNSRALRDVRNRFEILDSLFTQYMPSPRVNFEVPL 197
Db 99 RLEGSLNLYQIYAESFREWEADPTNPALREVRQFNDMNSALTATPPLAVQNVPL 158

Qy 198 TVYAMAANLHLLKLDASIFGEEGWSMTTNNYDROMKLTAEYSDHCVKWYETGLAKL 257
Db 159 SVYVQAANLHLSVLDRVSVFGQWGFDAATINSRYNDLTRIGNYTDHVRWYNTGLERV 218

Qy 258 KTSKQWVDVNOQPREMTLAVLDVVALFPNYDRTYTPMETKQAQLTRVYTDPL-----G 312
Db 219 WGPDSRDWRYNQFRELTLTVLDIVALEFPNYSRRYPRTVSQLTRTYTPNVLNFDG 278

Qy 313 AVNVSSIGSWYDKAPSGFVIESSVIRPPHVDYITGLTVYTOSRSISSARYIRHWAGHOI 372
Db 279 SFRGSAQG-----IEGS-IRSPHMDILNSITTYDAH-----RGYYWSGHQI 321

Qy 373 SYHRV--SRGSNLOQMYGTNQNLHSTSTF-DFTNYDIYKTLSDKDAVLDDIVPGYTYIF 429
Db 322 MASPVGSGPEFTFLYGTMGNAAPQORIVAQLGQGVYRTLSL-----YRRFPN 372

Qy 429 FGMPVEFFMNQNLNRTKLYKNPVSKDIIASTRDSLELPPEPSTSDPNTESYSHRLCH 488
Db 373 IGINNQQLSVLDGTFAGYGTSSNLPASVYRKSGTVSDSDEIPQNNNPPRQGFPHRLSH 432
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Db 1007 VLVVPEWEAEVQSVRVCPGRGYILRVYAYEGYCEGCVTHIEINNTDELKFSNCVBE 1066
Qy 1106 -----ASDYDTN-----GMYNTQVSTNGYNTNAYNTQASSTNGYNNANNMTQAS 1152
Db 1067 IYPNNVTVCNDYTNQBEYGGAY---TSNRNGY--NEAPSPADYASVEKSY--TGR 1119
Qy 1153 NTNGYNTSVVNDQT---GYITKVTPIPTDQMWIEMSETEGTFYIESVELIV 1203
Db 1120 RENPCEFNRGYRDYTPLPVGIVTKLEYFPETDKWIEIGETGTFIVDSVELLL 1174

RESULT 12
Q93T21 PRELIMINARY; PRT; 1155 AA.
AC Q93T21,
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Crystal protein CryIAb16.
GN CRYIAB16.
OS Bacillus thuringiensis (subsp. israelensis).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OC NCBI_TaxID=1430;
RN 1)
RP SEQUENCE FROM N.A.
RC STRAIN=407;
RA Yu J., Tan L., Wu D., Pang Y.;
RT "Molecular characterization of a silent gene encoding a 130-kilodalton
RT crystal protein from Bacillus thuringiensis subsp. israelensis.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF3755608; AAK55546.1; -.
DR InterPro; IPR001178; Endotoxin.
DR Pfam; PF00555; endotoxin; 1.
SQ SEQUENCE 1155 AA; 130747 MW; 7F0C98E0100C7698 CRC64;
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Query Match 32.0%; Score 2024; DB 2; Length 1155;
Best Local Similarity 38.6%; Pred. No. 6.3e-108;
Matches 476; Conservative 193; Mismatches 429; Indels 136; Gaps 32;

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Qy 23 DSNRYPFANE--PTNALQNDYKDYLMKMSAGNASSEYPGSPVLVSGQDAKAA---IDIV 77
Db 2 DNN--PNINECIPYNCLSN-----PEVEVLGGERIETGYTPIDIS 39

Qy 78 GKLLSGLGVFPVGPVIVSYLTQILDLWPSEKESQWEIFMEQVEELINOKIAEYARKALS 137
Db 40 LSLTOFLLSSEFV-PGAGFVLGLVDIWIIGFPGSQWDAFLVQIEQLINQRIEFAFNQAIS 98

Qy 138 ELEGGLNNYQLYLTALBEEWENPNSRALRDVRNRFEILDSLFTQYMPSPRVNFEVPL 197
Db 99 RLEGSLNLYQIYAESFREWEADPTNPALREVRQFNDMNSALTATPPLAVQNVPL 158

Qy 198 TVYAMAANLHLLKLDASIFGEEGWSMTTNNYDROMKLTAEYSDHCVKWYETGLAKL 257
Db 159 SVYVQAANLHLSVLDRVSVFGQWGFDAATINSRYNDLTRIGNYTDHVRWYNTGLERV 218

Qy 258 KTSKQWVDVNOQPREMTLAVLDVVALFPNYDRTYTPMETKQAQLTRVYTDPL-----G 312
Db 219 WGPDSRDWRYNQFRELTLTVLDIVALEFPNYSRRYPRTVSQLTRTYTPNVLNFDG 278

Qy 313 AVNVSSIGSWYDKAPSGFVIESSVIRPPHVDYITGLTVYTOSRSISSARYIRHWAGHOI 372
Db 279 SFRGSAQG-----IEGS-IRSPHMDILNSITTYDAH-----RGYYWSGHQI 321

Qy 373 SYHRV--SRGSNLOQMYGTNQNLHSTSTF-DFTNYDIYKTLSDKDAVLDDIVPGYTYIF 428
Db 322 MASPVGSGPEFTFLYGTMGNAAPQORIVAQLGQGVYRTLSL-----YRRFPN 372

Qy 429 FGMPVEFFMNQNLNRTKLYKNPVSKDIIASTRDSLELPPEPSTSDPNTESYSHRLCH 488
Db 373 IGINNQQLSVLDGTFAGYGTSSNLPASVYRKSGTVSDSDEIPQNNNPPRQGFPHRLSH 432
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QY 489 ITSIPATGNTTGL-----VPVFSWTHRSADLANNTIYSKTIQIPAVKCDNLPFPVVKGP 544
DB 433 VSMFRSGFSNSVSIIRAPMFSWTHRSAEFNNIIPSSQIQTIPLTSTKSTNLSGSGTSVKGP 492
QY 545 GHTGGDLQYNRSVSGVTLFLARYGLALEKAGKVRRLRYATDADIVLHN-DA-----Q 599
DB 493 GFTGGDLRL-RTSPQISTL---RVNITAPUSQRYRIRYASTNIOFTSIDGRFINQ 548
QY 600 IOMPKNWPGEDLTSKTFKVAADATITNLATDSSL---ALKHNLGSDPNSTLSGIVVVD 655
DB 549 GNFSATWSGSLGSGFRVFTPTPNFSGNSGVFTLSAHVPSGNE-----VVID 600
QY 656 RIFPIVDETYEAEQDLAEAKAVNALFTNYD-GLRPGVTDYVNVQANALVECLSDLY 714
DB 601 RIFVPAEVTFAEAYDLERAQKAVNELFTSSNOIGLKTVDVTDYHIDQVSNLVECLSDBFC 660
QY 715 PNEKRLIPDAREAKRLSEARNLQDPPQIRING-ENGWTAFTSGIEVIEDALPKGYL 772
DB 661 LDEKELSEKVKHAKRLSDERNLLQDPNFRGINQLORQWRGSTDTITQGGDDVFKENV 720
QY 773 RLPGARIDTETTYLYQKVEGVLPKYTRYRLRGFVGGSQGLEIFIRHQTNRIVKQV 832
DB 721 TLLGTDP---ECYFYLYQKIDESKLKAYTRYQLRGYIEDSQDLEIYLIRYNAKHETNV 777
QY 833 PDDLPLDVSPVNSDGSINRCSEQKYVNSRLEVENRSGEAEHFSIPIDTGETIDYNNAGIW 892
DB 778 PG--TGLMPLSAPSPIGKCAH-----HSHFSLDIDVGCTDINEDLGW 820
QY 893 VGFKITDPGATVATGNLVEBEGPLSGDALERLOREQWKIOMTRRRRETDTRYMASKQ 952
DB 821 VIFKIKTQDGHARLGNLEFLEKEPLVSGALARVKAERKWRDKLEWETNIVYKEAKE 880
QY 953 AVRLYADYDQDLNPOVEITDLTAADLIQSIPTVYNEPELPGNYTKFTLTORLQ 1012
DB 881 SVDAVNSQDRLQADNTNIMIAHAKRVHSIREAYLPESLVIPGVNAALFELEGRI 940
QY 1013 QAWSLYDORNAIPNGDFRNLGNNAATPGVEV-QQINHTSVLVIIPNWDQVSOQFTVQPN 1071
DB 941 TAFSLYDARVINKGVNGDFNGLSCNVKGVHDVEBQNNHRSVLVPEAEVSVQVRCPG 1000
QY 1072 QRYVLRVTAKEGVNGVSVTRDGGNOTETLTPS-----ASDYD-TNGMY- 1115
DB 1001 RGXYLRVTAKEEYEGECVTHIEINNTAELKFSNVEEYVNNVTYCNDYATQBEYE 1060
QY 1116 NTQVSNNGYNTNNAKYNTQASSTNGYNA--NNMYNTQASNTNGYNSVNDQY----GY 1169
DB 1061 GTYTSRNGY--DGAYESNSVPADYASABEAYTDGRRDNPCESTRNGYGDYTPLPAGY 1118
QY 1170 ITKVTPTPYTDQWIMSETEGTFYIESVELIV 1203
DB 1119 VTRELYFPETDKWIEIGETEGTFIVDSVELLL 1152
RESULT 13
Q03743 ID Q03743 PRELIMINARY; PRT; 1177 AA.
AC Q03743;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE 135 kDa CRYSTAL protein (Delta endotoxin) (CRYSTALLINE ENTOMOCIDAL
DE protoxin).
GN CRYIA(C)3.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA Feitelson J.S.;
RL Submitted (XXX-1991) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
EPITHELIAL CELLS OF INSECTS.
```

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CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART OF
THE SPORE COAT.
-!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-
TERMINUS.
EMBL; M73248; AAA22339.1; -.
DR HSSP; P02965; ICYI.
DR InterPro; IPR001178; Endotoxin.
DR Pfam; PF00555; endotoxin; 1.
KW Toxin; Sporulation.
SQ SEQUENCE 1177 AA; 133156 MW; FDB2B6C1BB909DAF CRC64;

Query Match 31.9%; Score 2021; DB 2; Length 1177;
Best Local Similarity 39.3%; Pred. No. 9.7e-108;
Matches 493; Conservative 187; Mismatches 419; Indels 156; Gaps 37;

QY 23 DSNRYPFANE--PTNALQNMVDYKYLKMSAGNASEYPGSEVLVSGODAKAA--IDIV 77
DB 2 DNN--PNINECIPNCLSN-----PEVVLGGERIETGYTPIDIS 39
QY 78 GKLLSGLVGVPFVGPVIVSLYTLQILIDILWPGEKQWEIFMEQVEELINQKIAEYARNKALS 137
DB 40 LSTQFLLSEFV-PGAGFVLGLVDIIINGIFGPSQWDAFLVQIEQLINQRIEEFARNQAIS 98
QY 138 ELBGLGNYYQLYLTALEEENPNRGRALRDVNRREIFLDSLFQYMPSPRVTNFVFPFL 197
DB 99 RLEGLSNLYQIYAESFREWEDPTNPALREEMRIQFNDMNSALTTPAILLAVQNYQVPLL 158
QY 198 TVYAMAANLHLLKDAISFGEWGWSTTTINNYDROMKLTAEYSDHCVKWYETGLAKL 257
DB 159 SVTVQANLHLSVLRDVSFVGQWGFDAATINSRYNDLTRGLIGNYTDYAVRWYNTGLERV 218
QY 258 KGTSAQWVDYNOFRREMTLAVDVALPNYDTRYTPMETKAQLTREVTYDPL---G 312
DB 219 WGPDSRDWRVNGYFRRELTUTVLDIIVALFPNYSRRYPITVSQLTREITNPNVLEFDG 278
QY 313 AVNVSSIGSYDKAPSGFVIESVIRPPHVDYITGLTVYTSQSRSSSARYIRHWAGHAI 372
DB 279 SPRGSAG-----IERS-IRSPHLMIDILNSTIITDAH-----RGYYWWSGHQI 321
QY 373 SYHRV--SRGSNLQMGYNTQNLHSTSTF-DFTNYDIYKTLSDKDALVLDIVPGYTIFF 429
DB 322 MASPVGSGPEPTFPPLYGTMGNAAPQORIIVAQLGGQGYRTLS-----TFY 367
QY 430 GMEVEFPMVQNLNTR-----KTLKYNPVSQDIIASTRDSELELPPETSQPN 478
DB 368 RRP-----FNIG-INNQSLVDGTGTFAYGTSNLPASVYKSGTVDSLDIPQNNVPP 422
QY 479 YESYSHRLCHITSIPATGNTTGL---VPVFSWTHRSADLANNTIYSKTIQIPAVKCDN 534
DB 423 RQGFSHLSHV-SMFRSGSSSVSIIRAPMFSWTHRSAEFNNIIASDSITQIPAVK--GN 479
QY 535 LPP-VPVVKPGHTGGDLLOYNRSTGVTLFLARYGLALEKAG-KYRVLRLRYATDADIV 592
DB 480 FLFNGSVISGFGTGGDLVRLNSGNNIQNRGYIEVDIHFPESTSTRYRVRVYASVTFIH 539
QY 593 LHVN--DAQI---QMPKTMNPGEDLTSKT---FKVDAITLNLATDSSLAKHNLCEDP 644
DB 540 LNVNMGNSIFSNVTNPATATSLNLOSDFGYFESANAFTS-----SLGNIVGVN 590
QY 645 NSTLSGVYVYDRIEFIPVDETYEAEQDLAEAKAVNALFTNTKD-GLRPGVTDYEVNQAA 703
DB 591 FSGTAGVI-IDREFIPVTATLEAYNLERAQKAVNALFTSTNQLGLKTNVTDHIDQVS 649
QY 704 NLVECLSDDLYPNEKRLLPDAVEAKELSPARNLLOPDPQIRIN--GENGWTAFTSGIEVI 761
DB 650 NLVTLSDEFCLDEKRELSSEKVKHAKELSDERNLLQDSNFKDINRQPERGWSGTGITI 709
QY 762 EGDALPKGYRLRLPGAREIDTETTYLYQKVEGVLPKYTRYELRGLFVSGSQGLEIFTI 821
DB 710 GGDVDFKENVYTLSTGTFD---ECYFYLYQKIDESKLKAFTRYQLRGYIEDSQDLEIYL 766
QY 822 RHQTNRIYKGVNPD-----LLPDVSPVNSDGSINRCSEQKYVNSRLEVENRSGE-----AH 872
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01-DEC-2001 (TreeBLrel. 19, Last annotation update)
DE Gene, complete cds.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RW [1]
RP SEQUENCE FROM N.A.
RA STRAIN=PS85A1;
RC Feitelson J.S.;
RL Submitted (JUL-1991) to the EMBL/GenBank/DBJ databases.
DR EMBL; N73249; AA73077.1; --
DR HSRF; F02965; ICYI.
DR InterPro; IPR001178; Endotoxin.
DR Pfam; PF00555; endotoxin; 1.
SQ SEQUENCE 1178 AA; 133296 MW; 1336524F410E8863 CRC64;

Query Match 31.9%; Score 2017.5; DB.2; Length 1178;
Best Local Similarity 39.3%; Pred. No. 1.5e-107;
Matches 489; Conservative 187; Mismatches 434; Indels 135; Gaps 34;

QY 23 DGNRYPFANE--PTNALQNDYKDYLNKMSAGNASEYPGSEVLVSQDAKAA---IDIV 77
DB 2 DNN--PINECPYCLSN-----PEVLGGERIETGYTIDIS 39
QY 78 GKLSGLGVFPVGPVLSYLTQIDILWPGEKSKQWIFMEQVEELINQIAEYARNKALS 137
DB 40 LSLTQFLLEFV--PGAGFVLGVDIIWGIFGPGQWDAFLVQIQELINQRIEFAFNQALS 98
QY 138 ELEGNNYQLYLTALAEHEENPNNGRALRDVNRREILDSLTQYMPFRVNFVPL 197
DB 99 RLEGLSNLYQIYAESPREWEADPTNPALEEMRIQFNDMNSALTTPAILLAQVQYVPLL 158
QY 198 TVYAAANLHLLLLKDAISIFGREGWSTTTINNYDROMKLTAEYSDHCXVYETGLAKL 257
DB 159 SVYQAANLHLSVLRDVSFVGQWGDAAATINSRYNDLIRLIGNYDYAVRWYNTGLERV 218
QY 258 KGTSAKQVYDQFREMFLAVLDVVVALFPNYDTRYPYMETRAQLTREVYDPL-----G 312
DB 219 WGPDSRDVRYNQFREELTLVDLVALFPNYDSRYPIRTVYQSLTREIYTNPVLENFDG 278
QY 313 AVNVSIGSWYDKAPSGFVIESVIRPPHVDYITGLTVYQSRSSISARYIHHWAGHQI 372
DB 279 SFRGSAQG-----IERS-IRSPHLMIDILNSITITDAH-----RGYYWSGHQI 321
QY 373 SYHRV--SRGSNLQMYGYNQNLHSTP--DFTNYDIYKLSKDAVLDDIVPGYIYP- 428
DB 322 MASPVGSGPEFTFPLYGTMGNAAPQORIVAQLGQGYRTLSSTL-----YRRPFN 372
QY 429 FGMPEVEFFPMQNLNTRKTLKYNPVSKDIIASTRDSLELPPETSDQPNYESYSHRLCH 488
DB 373 IGINNQQLSVLDGTEPAYGTSSNLPBAVYKSGTVDSLDLPIPNQNNVPPRQGFSHRLSH 432
QY 489 ITSIPATGNTTGL-----VPVFSWTHESADLNNTIYDKITQIPAVKCDNLPP--VPVVKG 543
DB 433 VSMFRSGFNSVSIIRAPMFSWIHESABENIIASDSITQIPAVK--GNFLNGSVISG 490
QY 544 PGHTGGDLLOYNRSTGVTGLFLARYGLALEKAG--KYRVLRYATADIVLWV--DAQI 600
DB 491 PGFTGGDLVRLNSSGNINQNRGVEIPIHPPTSTRYRVRVRYAVTPPIHLNVNWNSSII 550
QY 601 ---QMPKTNWPGEDLTSKT---PKVADAITTLNATDSSLAKHNLGDPNSTLSGIVVV 654
DB 551 FSNTPVATATSLDNLQSSDFGFESANAFTS-----SLGNIVGVNRFSGTAGVI-I 600
QY 655 DRIEPIPDVDEAEQDLEAKAKAVNALPTNTKD--GLRPGVTDYEVNQANLVECLSDDL 713
DB 601 DRFEPIPVTTALEAYNLERAKAVNALPTSTNQLGKTNVTYDHIDQVSNLVYLSDEF 660
QY 714 YNPKELLFDVAKEAKRLSEARNLQDDPQIEIN--GENGWTAETASTGIEVIEGDLFKRY 771
DB 661 CLDEKELESEKVKHAKRLSDERNLQDSNPKDINRQPERGWGGSTGITIQGGDDVFKENY 720

QY 772 LRLPGAREIDTETVPTLYYQKVEGVLPKPYTRYLRGFRVGSQGLIEITIRHQTNRIVQN 831
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QY 832 VPDD-----LLPDVSPVNSDGSINRCSEQKYNSRLEVENRSGE-----AHBESIPIDTGE 882
DB 778 VEGTSLMPLSAQSPIGKGBFNRCAPHLEWNPDLDCSRDEKCAHSHHFSLDIDVGC 837
QY 883 IDYNENAGIWTGFKITDPPEGVATLGNLSELVEGPLSGDALERLQREEQWKIQTMRREE 942
DB 838 TDLNEDLGWITFKITQDGHARLGNLFLFEKPLVGEALARVKAEEKWRDKREKLEWE 897
QY 943 TDRRYNASKQAVDRLYADYQOQLNPDVEITDLTAQDLIOSIPYVYNEMFPEIPEGMNT 1002
DB 898 TNIVYKEAKESVDALFVNSQYDQLQADTNIAHIAADKRVHSIREAYLPESLVIQGVNAA 957
QY 1003 KPELTDLRLOQAWSLYDORNAIPNGDFRNLGNLNNWATPGVEV--QIINHTSVLVIWNWDEQ 1061
DB 958 IFEELGRIPTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVVEEQNNORSVLVVPWEAE 1017
QY 1062 VSQQTVPQPNORYLVRVTARKEGVNGVYSIRDGNQOTETLTFSS-----AS 1107
DB 1018 VSQEVYVCPGRGYILIRVTAYKEGYEGCVTHIEINNTDELKFSNCVEEIIYPNNVTTCN 1077
QY 1108 DYDTN-----GMYNTPQVSNNTNGYNTNAYNTQASSTNGYNANNMYNTQASNTNGYNTNSV 1162
DB 1078 DYTVAQEEYGGAY---TSRNRGY--NEAPSPVADYASVVEEKSY--TDCRRNPPCFENRG 1130
QY 1163 YNDQT-----GYITKVTPIPTDQMWIEMSETEGTFYIESVELIV 1203
DB 1131 YRDYTPLPVGYVTKELYPETDKWIBIGETEGTFIVDSVELLL 1175

Search completed: January 7, 2003, 05:16:23
Job time : 90 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 03:35:28 ; Search time 69 seconds
(without alignments)
2328.989 Million cell updates/sec

Title: US-10-032-717-2

Perfect score: 6332

Sequence: 1 MSPNNQNEYIIDATPSTSV.....MSETEGTYIHSVELVDVE 1206

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6332	100.0	1206	23	AAU99255
2	5673	89.6	1210	23	AAU99256
3	4959.5	78.3	1169	17	AAW06417
4	3951.5	62.4	1157	13	AAK28900
5	3950.5	62.4	1157	13	AAK28997
6	3950.5	62.4	1157	14	AAK33768
7	3950.5	62.4	1157	17	AAW06418
8	3943.5	62.3	1157	13	AAK27343
9	3940.5	62.2	1157	14	AAK44208
10	3511	55.4	669	23	AAU99259

11	3511	55.4	669	23	AAU99262	Bacillus thuringie
12	3502	55.3	667	23	AAU99257	Bacillus thuringie
13	3499	55.3	673	23	AAU99260	Bacillus thuringie
14	3499	55.3	673	23	AAU99265	Bacillus thuringie
15	3499	55.3	673	23	AAU99271	Bacillus thuringie
16	3485.5	55.0	670	23	AAU99266	Bacillus thuringie
17	3485.5	55.0	670	23	AAU99273	Bacillus thuringie
18	3246.5	51.3	1167	23	AAU0281	Bacillus thuringie
19	3229	51.0	616	23	AAU99264	Bacillus thuringie
20	3217	50.8	620	23	AAU99268	Bacillus thuringie
21	3217	50.8	620	23	AAU99269	Bacillus thuringie
22	3217	50.8	620	23	AAU99272	Bacillus thuringie
23	3203.5	50.6	617	23	AAU99270	Bacillus thuringie
24	3203.5	50.6	617	23	AAU99274	Bacillus thuringie
25	3021	47.7	1149	14	AAK32354	Coleoptera toxin f
26	3021	47.7	1149	15	AAK51692	B.thuringiensis se
27	2852	45.0	673	23	AAU99263	Bacillus thuringie
28	2821	44.6	667	23	AAU99258	Bacillus thuringie
29	2601.5	41.1	1157	20	AAW84585	Amino acid sequenc
30	2600.5	41.1	1157	20	AAW84586	Amino acid sequenc
31	2600.5	41.1	1157	20	AAW84576	Amino acid sequenc
32	2599.5	41.1	1157	20	AAW84582	Amino acid sequenc
33	2599.5	41.1	1157	20	AAW84567	Amino acid sequenc
34	2599.5	41.1	1157	20	AAW84569	Amino acid sequenc
35	2598.5	41.0	1157	20	AAW84584	Amino acid sequenc
36	2598.5	41.0	1157	20	AAW84572	Amino acid sequenc
37	2598.5	41.0	1157	20	AAW84575	Amino acid sequenc
38	2598.5	41.0	1157	20	AAW84577	Amino acid sequenc
39	2598.5	41.0	1157	20	AAW84578	Amino acid sequenc
40	2597.5	41.0	1157	20	AAW84592	Amino acid sequenc
41	2597.5	41.0	1157	20	AAW84573	Amino acid sequenc
42	2596.5	41.0	1157	20	AAW84586	Amino acid sequenc
43	2596.5	41.0	1157	20	AAW84579	Amino acid sequenc
44	2595.5	41.0	1157	15	AAK48678	Insecticidal proto
45	2595.5	41.0	1157	20	AAW84588	Amino acid sequenc

ALIGNMENTS

RESULT 1

AAU99255

ID AAU99255 standard; Protein; 1206 AA.

XX AC AAU99255;

XX DT 07-OCT-2002 (first entry)

XX DE Bacillus thuringiensis Cry1218-1 protein sequence.

XX KW Pesticidal; spraying; dusting; broadcasting; seed coating; insect pest;

XX KW Colorado potato beetle; western corn rootworm; southern corn rootworm;

XX insect target range; endotoxin; Cry1218.

XX OS Bacillus thuringiensis.

XX PN WO200234774-A2.

XX PD 02-MAY-2002.

XX PF 24-OCT-2001; 2001WO-US45468.

XX PR 24-OCT-2000; 2000US-242838P.

XX PR 23-OCT-2001; 2001US-0032717.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

XX PI Abad AR, Duck NB, Feng X, Flannagan RD, Kahn TW, Sims LE;

XX WPI; 2002-519178/55.

XX DR N-PSDB; ABK87234.

XX PT New isolated pesticidal polypeptide useful for impacting insect pest

e.g. Colorado potato beetle -

Claim 4; Page 96-98; 176pp; English.

The present invention relates to a new pesticidal polypeptide. The invention is useful for impacting an insect pest by applying the molecules of the invention to the environment of the insect pest by spraying, dusting, broadcasting, or seed coating, where the insect pest is selected from Colorado potato beetle, western corn rootworm or southern corn rootworm. The invention is also useful for increasing insect target range and for producing transgenic microorganisms and plants that express the pesticidal polypeptide. The invention is also useful for producing transformed plants and in transforming any organism to produce the pesticidal polypeptide of the invention. The present amino acid sequence represents a *Bacillus thuringiensis* wild-type Cry1218 endotoxin protein.

Sequence 1206 AA;

Query Match 100.0%; Score 6332; DB 23; Length 1206;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MSPNNQNEYIIDATPSTSVSNDRYPFANEPTNALQNDYKDYLMKMSAGNASEYPGSP 60
QY 61 EVLYSGQDAAKAAIDIVGKLISGLGVPGVPIVSLYTQILIDILWPSGKSWEIFMEQVE 120
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DB 181 TOYMPSFRVTNFEVFPFLTVYAMAANLHLLLDKASIFGEEWGSTTTNNYIDRQMKLTA 240
QY 241 EYSDHCVKWYETGLAKLGTSAKQWVDYQNRREMTLAVLDVVALFPNYDRTYPMETKA 300
DB 241 EYSDHCVKWYETGLAKLGTSAKQWVDYQNRREMTLAVLDVVALFPNYDRTYPMETKA 300
QY 301 QLTREVYTDPLGAVNVSSIGSWYDKAPSGFVIESVIRPPHVFYITGLTVYTOSRSISS 360
DB 301 QLTREVYTDPLGAVNVSSIGSWYDKAPSGFVIESVIRPPHVFYITGLTVYTOSRSISS 360
QY 361 ARYIRHWAGHQISYHRVSRGSLNQMYGTQNLHSTSTFTDFTNYDIYKTLKDAVLLDIV 420
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DB 421 YPGYTYIFFGMPVEFFPMVGNLNTRKTLKYNPYSKDIIASTRSELELPETSDQPNYE 480
QY 481 SYHRLCHITSIPATNTTGLVPFVSWTHRSADLNNTIYSDKITQIPAVKQWDLNLPFVPV 540
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QY 541 VKGPGHTGGDLLQNRSTSGVGTFLARYGLALEKAGYRVLRYATDADIVLHVNDQAI 600
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DB 601 QMPTWMPGEDLTSTKFKVADAITTLNATDSSIALKENLGEDPNSTLSGIVYVDRIEPI 660
QY 661 PVDETYEAOQLEAAKAVNALFTNTKDLRPGVTDYEVNQAAANLVECLSDLYPNEKRL 720
DB 661 PVDETYEAOQLEAAKAVNALFTNTKDLRPGVTDYEVNQAAANLVECLSDLYPNEKRL 720
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DB 721 LFDVAVREAKRLSEARNLLQDPDFQIEINGENGWTAETGIEVGDALEFKGRYLRLPGAREI 780
QY 781 DTETYPYLYQKVEEGLVDPYTRYLRGPFVSSQGLEIFTRHQTNRIVKXNVPDLDLPDV 840
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QY 841 SPVNSDGSINRCSEQKYNRSLRLEVENRSGEAHFFSIDTGEIDYNNAGIWWGFKITDP 900
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QY 901 EGVATLGNLVBEGPLSGDALRQREBOQWKIQMTRREEDTDRRYMASKQAVDRLYAD 960
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QY 1021 RNAIPNGDFRNLGSLNNWATPGVEVQIQNHSTSLVLPNWDQVSOQFTVQPNQRYVLRTA 1080
DB 1021 RNAIPNGDFRNLGSLNNWATPGVEVQIQNHSTSLVLPNWDQVSOQFTVQPNQRYVLRTA 1080
QY 1081 RKEGVNGYVSIIRDGGNQTETLTFSSADYDTNGMYNTQVNTNGYNTNNAINTOASSTNG 1140
DB 1081 RKEGVNGYVSIIRDGGNQTETLTFSSADYDTNGMYNTQVNTNGYNTNNAINTOASSTNG 1140
QY 1141 YNANNMYNTQASNTNGYNTNSVYNDQGYITKTFTPTPYTDQMWIEMSETEGTYYIESVE 1200
DB 1141 YNANNMYNTQASNTNGYNTNSVYNDQGYITKTFTPTPYTDQMWIEMSETEGTYYIESVE 1200
QY 1201 LIVDVE 1206
DB 1201 LIVDVE 1206
RESULT 2
AAU99256
ID AAU99256 standard; Protein; 1210 AA.
XX
AC AAU99256;
XX
DT 07-OCT-2002 (first entry)
XX
DE *Bacillus thuringiensis* Cry1218-2 protein sequence.
XX
KW Pesticidal; spraying; dusting; broadcasting; seed coating; insect pest;
KW Colorado potato beetle; western corn rootworm; southern corn rootworm;
XX insect target range; endotoxin; Cry1218.
OS *Bacillus thuringiensis*.
XX
PN WO200234774-A2.
XX
PD 02-MAY-2002.
XX
PF 24-OCT-2001; 2001WO-US45468.
XX
PR 24-OCT-2000; 2000US-242838P.
PR 23-OCT-2001; 2001US-0032717.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Abad AR, Duck NB, Feng X, Flannagan RD, Kahn TW, Sims LE;
XX WPI; 2002-519178/55.
DR N-PSDB; ABK87235.
XX
PT New isolated pesticidal polypeptide useful for impacting insect pest
PT e.g. Colorado potato beetle -
XX
PS Claim 4; Page 103-105; 176pp; English.
XX
CC The present invention relates to a new pesticidal polypeptide. The

invention is useful for impacting an insect pest by applying the molecules of the invention to the environment of the insect pest by spraying, dusting, broadcasting, or seed coating, where the insect pest is selected from Colorado potato beetle, western corn rootworm or southern corn rootworm. The invention is also useful for increasing insect target range and for producing transgenic microorganisms and plants that express the pesticidal polypeptide. The invention is also useful for producing transformed plants and in transforming any organism to produce the pesticidal polypeptide of the invention. The present amino acid sequence represents a *Bacillus thuringiensis* wild-type Cry1218 endotoxin protein.

Sequence 1210 AA;

Query Match 89.6%; Score 5673; DB 23; Length 1210;

Best Local Similarity 89.2%; Pred. No. 0;

Matches 1095; Conservative 33; Mismatches 61; Indels 38; Gaps 7;

QY 1 MSPNNQNEYEIIIDATPSTSVSDNSRNPYPANETNALQNDYKDYLMGAGNASEYPGSP 60
 DB 1 MSPNNQNEYEIIIDATPSTSVSDNSRNPYPANETNALQNDYKDYLMGAGNASEYPGSP 60
 QY 61 EYLVSGQDAKAAIDIVGKLLSGLVFPVGPPIVSLVTQLIDILMPGSEKQWEIEMEYVE 120
 DB 61 EYLVSGQDAKAAIDIVGKLLSGLVFPVGPPIVSLVTQLIDILMPGSEKQWEIEMEYVE 120
 QY 121 ELINQKIAFYARNKALSELEGLNNYQLYLTALEENPNPNSRALRDVRNRFELDSLIF 180
 DB 121 ELINQKIAFYARNKALSELEGLNNYQLYLTALEENPNPNSRALRDVRNRFELDSLIF 180
 QY 181 TOYMSPRVNTEFVPLTVYMAANLHLLLDKASIFGEWGSTTTINNYDROMKLTATA 240
 DB 181 TOYMSPRVNTEFVPLTVYMAANLHLLLDKASIFGEWGSTTTINNYDROMKLTATA 240
 QY 241 EYSDHCVKWYETGLAKIGTSKQWYDYNQPREMTLAVLDVVALFPNVDTRYPMETKA 300
 DB 241 EYSDHCVKWYETGLAKIGTSKQWYDYNQPREMTLAVLDVVALFPNVDTRYPMETKA 300
 QY 301 QLTREYTDPLGAVNVSSIGSYDKAPSGVIESVIRPPHVPDYITGLTVYTSQSRSS 360
 DB 301 QLTREYTDPLGAVNVSSIGSYDKAPSGVIESVIRPPHVPDYITGLTVYTSQSRSS 360
 QY 361 ARYIIRHWAGHOISYHRVSGSNLQMGYGNQNLHSTSTDFPDNYDIYKTLSDKAVLLDIV 420
 DB 361 ARYIIRHWAGHOISYHRVSGSNLQMGYGNQNLHSTSTDFPDNYDIYKTLSDKAVLLDIV 420
 QY 421 YPGYTYIPGMEVEFFPMYNQNLNNTKTLKYNPVSKDIIASTEDSELELPPTSDQPNYE 480
 DB 421 YPGYTYIPGMEVEFFPMYNQNLNNTKTLKYNPVSKDIIASTEDSELELPPTSDQPNYE 480
 QY 481 SYSHRLCHTISIPATGNTTGLVPVPSWTHRSADLNNTIYSDKITQIPAVKCDNLPFV-- 538
 DB 481 SYSHRLCHTISIPATGNTTGLVPVPSWTHRSADLNNTIYSDKITQIPAVKCDNLPFV-- 538
 QY 539 -----PVVKGPGHGTGDLQYNSRSTGSGTFLYARYGLALEKAGK-YRVLRYATADIVL 593
 DB 539 -----PVVKGPGHGTGDLQYNSRSTGSGTFLYARYGLALEKAGK-YRVLRYATADIVL 593
 QY 541 GPNNTVSGPGFTGGGIIRVIEI-----GVIIHMERVKISDINKEYSMRIRVASANTF 595
 DB 541 GPNNTVSGPGFTGGGIIRVIEI-----GVIIHMERVKISDINKEYSMRIRVASANTF 595
 QY 594 HYNDQIQIOM-----PKTMNPGEDLTSTKTKVADAITTLNLTADSSLALKNLGEDPNSTLS 649
 DB 594 HYNDQIQIOM-----PKTMNPGEDLTSTKTKVADAITTLNLTADSSLALKNLGEDPNSTLS 649
 QY 650 GI-----VYVDRIEFPVDETYEARQDLLEAKKAVNALFTNTKQGLRPGVTDYEV 699
 DB 650 GI-----VYVDRIEFPVDETYEARQDLLEAKKAVNALFTNTKQGLRPGVTDYEV 699
 QY 644 ALPEAEDFLGIEAYIDRIEFPVDETYEARQDLLEAKKAVNALFTNTKQGLRPGVTDYEV 703
 DB 644 ALPEAEDFLGIEAYIDRIEFPVDETYEARQDLLEAKKAVNALFTNTKQGLRPGVTDYEV 703
 QY 700 NOAANLVECLSDLLYPNEKRLFLDFAVREAKRLSEARNLLQDPDFQINGENGWGTASTGIE 759
 DB 700 NOAANLVECLSDLLYPNEKRLFLDFAVREAKRLSEARNLLQDPDFQINGENGWGTASTGIE 759
 QY 704 NOAANLVECLSDLLYPNEKRLFLDFAVREAKRLSEARNLLQDPDFQINGENGWGTASTGIE 763
 DB 704 NOAANLVECLSDLLYPNEKRLFLDFAVREAKRLSEARNLLQDPDFQINGENGWGTASTGIE 763
 QY 760 VIEGDALFKGRVLRLEPCAREIDTETPTVLYQKVEGVLPKPYTRYRLRFGVSSQGLEIF 819
 DB 760 VIEGDALFKGRVLRLEPCAREIDTETPTVLYQKVEGVLPKPYTRYRLRFGVSSQGLEIF 819
 QY 764 VIEGDALFKGRVLRLEPCAREIDTETPTVLYQKVEGVLPKPYTRYRLRFGVSSQGLEIF 823
 DB 764 VIEGDALFKGRVLRLEPCAREIDTETPTVLYQKVEGVLPKPYTRYRLRFGVSSQGLEIF 823

QY 820 TIRHQTNRIVKNVPDDLLPDVSPVNSDGSINRCSPQKYNLSRLEVENRSGEAHEFSIPID 879
 DB 820 TIRHQTNRIVKNVPDDLLPDVSPVNSDGSINRCSPQKYNLSRLEVENRSGEAHEFSIPID 883
 QY 880 TGEIDYNNENAGTWGPKITDPEGYATLGNLELVEGPGPLSGDALERLQREEQQWKIQTMR 939
 DB 880 TGEIDYNNENAGTWGPKITDPEGYATLGNLELVEGPGPLSGDALERLQREEQQWKIQTMR 943
 QY 940 REETDRRYWASKQAVDRLYADYQDQQLNPVDVEITDITAAQDLIQSIPIVYNNEMFPEIPGM 999
 DB 940 REETDRRYWASKQAVDRLYADYQDQQLNPVDVEITDITAAQDLIQSIPIVYNNEMFPEIPGM 1003
 QY 1000 NYTKETELTDLRQQAWSLYDQRNAPNGDFRNLGNLSNWNATPGVEVQQINHTSVLIPNWD 1059
 DB 1000 NYTKETELTDLRQQAWSLYDQRNAPNGDFRNLGNLSNWNATPGVEVQQINHTSVLIPNWD 1063
 QY 1060 EQVSQOFTVQPNQRYVLTARKEGVNGYVIRGGNQGTETLTFSASDYDTNGMYNTQV 1119
 DB 1060 EQVSQOFTVQPNQRYVLTARKEGVNGYVIRGGNQGTETLTFSASDYDTNGMYNTQV 1123
 QY 1120 SNTNGYNTNNAVTQASSTNGYNANNMYNTQASNTNGYNTNSVYNDQTYITKTVTFFPY 1179
 DB 1120 SNTNGYNTNNAVTQASSTNGYNANNMYNTQASNTNGYNTNSVYNDQTYITKTVTFFPY 1183
 QY 1180 TDQMMIEMSETEGTFYIESVELIVDVE 1206
 DB 1180 TDQMMIEMSETEGTFYIESVELIVDVE 1210
 RESULT 3
 AAW06417
 ID AAW06417 standard; Protein; 1169 AA.
 XX
 AC AAW06417;
 XX
 DT 28-JAN-1997 (first entry)
 XX
 DE Antiscarab pest toxin 50C(b).
 XX
 KW Toxin 50C(b); scarab pest; toxin; insect; scarabaeidae; pest control;
 KW larval stage insect; grain; tuberous crop; white grub; chafer grub;
 KW cyclocephala; popillia.
 XX
 OS *Bacillus thuringiensis* strain kumamotoensis.
 XX
 FN US5554534-A.
 XX
 PD 10-SEP-1996.
 XX
 PF 30-SEP-1994; 94US-0315468.
 XX
 PR 01-FEB-1993; 93US-0014941.
 PR 16-DEC-1991; 91US-0808316.
 PR 30-JAN-1992; 92US-0828430.
 PR 30-SEP-1994; 94US-0315468.
 XX
 PA (MYCO) MYCOGEN CORP.
 XX
 PI Foncerrada L, Michaels TE, Narva KE;
 XX
 DR WPI; 1996-424659/42.
 XX
 DR N-PSDB; AAT43221.
 PT New nucleic acid encoding *B. thuringiensis* toxin active against
 PT scarab(s) - also related toxin and transformed microbes, effective
 PT against adult pests and their larvae
 XX
 PS Claim 2; Column 29-36; 24pp; English.
 XX
 CC AAW06417-W06419 represent toxins that are active against scarab pests.
 CC The DNA encoding this sequence was isolated from the *Bacillus*
 CC *thuringiensis* strain kumamotoensis. Insects in the family Scarabaeidae

CC constitute a serious pest control problem, especially when destructive
 CC larval stage insects infest high value turf found in golf courses,
 CC playing fields and lawns. The larvae of many species also attack grains,
 CC tuberous crops, and ornamentals. The larvae are known as white grubs, or
 CC chafer grubs, and can be found in decaying organic matter, or in the soil
 CC where they consume plant roots. In Europe and the U.S. populations of
 CC these larvae and adults have developed resistance to chemical
 CC insecticides such as the organochlorines and DDT. These toxin sequences,
 CC and intact cells that are capable of expressing these proteins, can be
 CC used to control many pests of the family scarabaeidae, such as species of
 CC Cyclocephala, and Popillia. The toxins are active against larvae
 CC (present in soil) and against adults.
 CC
 xx

SQ Sequence 1169 AA;

Query Match 78.3%; Score 4959.5; DB 17; Length 1169;
 Best Local Similarity 79.8%; Pred. No. 0;
 Matches 967; Conservative 68; Mismatches 128; Indels 49; Gaps 8;

Qy 1 MSPNNQNEYEIIIDATPSTVSNDNSRYPFANEPTNALQNDYKDYLMKSGAGNASRYPGSP 60
 Db 1 MSPNNQNEYEIIIDATPSTVSNDNSRYPFANEPTNALQNDYKDYLMKSGAGNRYEYPSGP 60
 Qy 61 EVLVSGDAAKAIDIVGKLSGLGVPFVGPVIVSLYTQILIDILWPGSKSQWEIFMEQVE 120
 Db 61 EVLVSGDAAKAIDIVGKLSGLGVPFVGPVIVSLYTQILIDILWPGSKSQWEIFMEQVE 120
 Qy 121 ELINOKIAEYARKKALSEGLEGNVQVLYLTALKEEENPNSGRALRDVNRREIILDSLF 180
 Db 121 ELINOKIAEYARKKALSEGLEGNVQVLYLTALKEEENPNSGRALRDVNRREIILDSLF 180
 Qy 181 TOYMPSFRVTNEVPFLTYVMAANLHLLLDKASIFGEWGSTTNNYDROMKLTA 240
 Db 181 TOYMPSFRVTNEVPFLTYVMAANLHLLLDKASIFGEWGSTTNNYDROMKLTA 240
 Qy 241 EYSDHCWKYETGLAKLKGTSKQWVDYNOFRREMTLAVLDVVALPNDYTRTPMETKA 300
 Db 241 EYSDHCWKYETGLAKLKGTSKQWVDYNOFRREMTLAVLDVVALPNDYTRTPMETKA 300
 Qy 301 QLTREYVTDPLGAVNYSISGWSYDKAPSGVIESSVRPPHVPDYITGLVYQTSRIS 360
 Db 301 QLTREYVTDPLGAVNYSISGWSYDKAPSGVIESSVRPPHVPDYITGLVYQTSRIS 360
 Qy 361 ARYIRHWAGHOISYHRVSRGSLNQMYGTGNQNLHSTFDTNYDIYKTLSDKAVLLDIV 420
 Db 361 DRYMYWAGHOISYKHIGYSSTFTQMYGTGNQNLQSTSNEDFTNYDIYKTLSDKAVLLDIV 420
 Qy 421 YPGYTYVIFPGMEVEPFMVNQLNTRKTLKYNPVSOKIIASTRDSSELELPETSDQPNYE 480
 Db 421 YPGYTYVIFPGMEVEPFMVNQLNTRKTLKYNPVSOKIIASTRDSSELELPETSDQPNYE 480
 Qy 481 SYSHRLCHTISIPATGNTGLVPVSWTHRSADLNTIYSDKITQIPAVKCDNLPFPVPV 540
 Db 481 SYSHRLCHTIFYSSTST-YVPVSWTHRSADLNTIYSDKITQIPAVKCDNLPFPVPV 540
 Qy 541 VKPGHGTGDLQYNRSTGSGVTLFLARYGLALEKAGKVRVRYATDADIVLHV---N 596
 Db 541 IKRGYVTDGLVALTDRIQS-----CEQMIPEQORFIRIRYASNETSYISLYGLNQ 593
 Qy 597 DAQIQMPKT-MNPGE-DLTSKTPKVAADAITLNLATDSSLALKKHNGEDPNSTLSGIVYV 654
 Db 597 DAQIQMPKT-MNPGE-DLTSKTPKVAADAITLNLATDSSLALKKHNGEDPNSTLSGIVYV 654
 Qy 655 DRIEFTPVDETEAEODLEAKKAVNALFTNTKGLRPGVTDYEVNQANLVECLSDLLY 714
 Db 655 DRIEFTPVDETEAEODLEAKKAVNALFTNTKGLRPGVTDYEVNQANLVECLSDLLY 714
 Qy 715 PNEKRLLFDAVREAKLSARNLLQDPDFOEINGENGWTAAGTIEVIEGDALFKGYRL 774
 Db 715 PNEKRLLFDAVREAKLSARNLLQDPDFOEINGENGWTAAGTIEVIEGDALFKGYRL 774
 Qy 775 PGAREIDTETPTLYLQKVEGVLKPYTRYLRGFGVSSQGLBIFTRHQTNRIVKNVPD 834
 Db 775 PGAREIDTETPTLYLQKVEGVLKPYTRYLRGFGVSSQGLBIFTRHQTNRIVKNVPD 834

Db 770 PGAREIDTETPTLYLQKVEGVLKPYTRYLRGFGVSSQGLBIFTRHQTNRIVKNVPD 829
 Qy 835 DLLPVPVNSDGSINRSEOKYVNSRLEVENRSGEAEHPSIPIDTGEIDYNNENAGIWWG 894
 Db 830 DLLPVPVNSDGSINRSEOKYVNSRLEVENRSGEAEHPSIPIDTGEIDYNNENAGIWWG 889
 Qy 895 FKITDPEGVATLGNLELVEEGPLSGDALERLQREEQWKKIOMTRRREEDRRYMAASKQAV 954
 Db 890 FKITDPEGVATLGNLELVEEGPLSGDALERLQREEQWKKIOMTRRREEDRRYMAASKQAV 949
 Qy 955 DRLYADYQDQQLNPVETITDLTAAQDLIQSIPIVYVNEPPEIPGMNYTKFTLTDLRLOA 1014
 Db 950 DRLYADYQDQQLNPVETITDLTAAQDLIQSIPIVYVNEPPEIPGMNYTKFTLTDLRLOA 1009
 Qy 1015 WSLYDQRIANPNDGFRNGLSNWNAATGVEVQOINHTSVLVIENWDEQVSQQFTVQPNORY 1074
 Db 1010 WSLYDQRIANPNDGFRNGLSNWNAATGVEVQOINHTSVLVIENWDEQVSQQFTVQPNORY 1069
 Qy 1075 VLRVTARKEGVNGVYVIRDDGNGQETLTTFSSASDYDTNGMNTQVSNYNTNGYNTNAYNQ 1134
 Db 1070 VLRVTARKEGVNGVYVIRDDGNGQETLTTFSSASDYDTNGMNTQVSNYNTNGYNTNAYNQ 1108
 Qy 1135 ASSTGYNNANNMYNTQASNTNGYNTNSVYNDQTGYITKTFTFYPTDQMWIEMSETEGTF 1194
 Db 1109 -----MYDQASNTNGYNTNSVYMIKPAISRKTVDISSVYNOMWIBISETEGTF 1157
 Qy 1195 YIESVELIVDVE 1206
 Db 1158 YIESVELIVDVE 1169

RESULT 4

AAR28900
 ID AAR28900 standard; Protein; 1157 AA.
 XX
 AC AAR28900;
 XX
 DT 01-APR-1993 (first entry)
 XX
 DE Toxin 50C.
 XX
 KW Endotoxin; acarides; pest; Two Spotted Spider; mite;
 KW phytophagus.
 XX
 OS Bacillus thuringiensis kumamotoensis PS50C.
 XX
 PN WO9219106-A.
 XX
 PD 12-NOV-1992.
 XX
 PF 30-APR-1992; 92WO-US03546.
 XX
 PR 30-APR-1991; 91US-0693210.
 PR 13-SEP-1991; 91US-0759248.
 PR 30-SEP-1991; 91US-0768141.
 XX
 PA (MYCO) MYCOGEN CORP.
 XX
 PI Bagley AL, Cannon RJC, Payne JM;
 XX
 DR WPI; 1992-398411/48.
 DR N-PSDB; AAQ30821.
 XX

PT New Bacillus thuringiensis isolates and toxins - used for
 PT controlling acarid pests of livestock, fowl, stored prods. and
 PT plants
 XX

PS Claim 16; Page 53 + 49-51; 62pp; English.

XX Gene sequences encoding a toxin which is active against acarides and
 CC is obtainable from B. thuringiensis isolates PS17a, PS17b, 33f2,
 CC PS52a1, PS69D1, PS86A1 and PS50C are given in AAQ30803-07 and
 CC AAQ30820-21 respectively. The toxin is a delta-endotoxin active against

CC acarid pests, including the Two Spotted Spider mite. The isolates can
 CC be used against non-phytophagous mites such as acarid pests of livestock,
 CC fowl and stored prods. The genes can be cloned and used to
 CC transform other hosts, which can be used to control mites, or in
 CC the case of transgenic plants, be resistant to mites.

XX
 SQ Sequence 1157 AA;

Query Match 62.4%; Score 3951.5; DB 13; Length 1157;
 Best Local Similarity 65.5%; Pred. No. 2e-256;
 Matches 804; Conservative 120; Mismatches 211; Indels 93; Gaps 19;

QY 1 MSPNNQNEYIIDATPSTSVSNDNRNPFANEPTNALQMDYKYLKMSAGNASPYGSP 60
 DB 1 MSPNNQNEYIIDATPSTSVSNDNRNPFANEPTDALQMDYKYLKMSAGNPELFGP 60
 QY 61 EYLVSGDAAKAAIDVCKLSGLGVPFVGPVIVSLYTOIIDILWPSGKSOWEIPMEOVE 120
 DB 61 EYFIS-SSTIGTIGIVRILGALGVPPASQIASFYSPFVIGQLWPSKSDVINGEIMERVE 119
 QY 121 ELINOKIAEYARNKALSELEGLGNNYQLYLTALBEEENPNPGRALDRVRNRFELDLSLP 180
 DB 120 ELVDOKIEKYVDKALAEKLGKGNALDYQOSLEWLENRDARTRSVVSQFALDLP 179
 QY 181 TQYNPSRVTVNPFVFFLYVAANLHLLLLKODASIPGEWGWSTTTINYYDQMKLTA 240
 DB 180 VSSIPSPAVSGHEVLLAVYAQAANVHLLLRDASIPGEWGWSTTIPGBISRFNRQVQLTA 239
 QY 241 EYSDHCWKVYETGLAKLGTSAKQWVDYNQFRRENTLAVLDVVALFPNDYTRTPMETKA 300
 DB 240 EYSDYCVKWKYIGLKLKGTTSKWLNTQFRRENTLAVLDVVALFPNDYTHYBIETTA 299
 QY 301 QLREVTYDPLGAVNVSSIGSWYDKAPSGV----IESSVIRPPHVRDYITGLTVYQSR 356
 DB 300 QLREVDYDPLAFNIVTSTGCPNWSHTSGILFYEVENNVRPPHLPDILSSVEINT-SR 358
 QY 357 ---SISARYIRHWAGHOISYHRVSRGSLAQMYGTQNLHSTSTFDFTNYDIYKLSKD 413
 DB 359 GGITLANDAYINWSGHLTKYRRTA-DSTVITYTANYGRITSEKNSFALEDRIPEINSTV 417
 QY 414 AVLLDIVPGYTYFFGMEPEVFPVNNQNNRKTLYKNPVSKDIIASTR--DSELELPP 471
 DB 418 ANLANYTQKAY-----GVPGSFHVMKRGSTSTAYLYSKHTALQCGCTQVYESSDEIPL 472
 QY 472 ETSQPNVYESYSHRLCHITSIPATGNTT---GLVPVSWTHRSADLNNITYSDKITQIPA 528
 DB 473 DRT-VPVABSYSHRLSHITSHSFSKNGSAYYGSFVFWTHTSADLNNITYSDKITQIPA 531
 QY 529 VKCWDNLPFV--PVVKGPGHGGDLLOYNRSTGSGVTGLFLARYGLALEKAGKYRVLRYA 586
 DB 532 VK--GDMLYLGGSVVQGFPGTGGDILK--RTNPSILGTFAVTVNGSLSQ--RYRVRIYA 585
 QY 587 --TDADIVLHVDA--QIQMPKTPWNGBDLSKTPKVAADAITLNL-ATDSSLAK--H 638
 DB 586 STTDPEFTLYLGTIEKNRPNKNTMDNGASLTETPKPASFITDFQFRETQDKILLSMGDF 645
 QY 639 NLGSDPNLSGLIVVDRIEPIVDVTEAEODLEAAKAVNALFTWTKDGLRPGVTIYE 698
 DB 646 SSGQE-----VYIDRIEPIVDVTEAEODLEAAKAVNALFTWTKDGLRPGVTIYE 697
 QY 699 VNQAANLVECLSDDLIPNEXKLLFDVAREAKRLSEARNLLODPDQFENGNGWTASTGI 758
 DB 698 VNQAANLVECLSDDLIPNEXKLLFDVAREAKRLSEARNLLODPDQFENGNGWASTGI 757
 QY 759 EIVSGDALFKGRLRLPGAREIDTETPTLYLQKVBEGLPKYTYRRLRGVSSQGLEI 818
 DB 758 EIVSGDAVFKGRLRLPGAREIDTETPTLYLQKVBEGLPKYTYRRLRGVSSQGLEI 817
 QY 819 FTIRHQTNRIVKNVDDLLDPVSPVNSDGSINRCSEQYVNSRLSEVENRSGEAHEFSPI 878
 DB 818 YTIIRHQTNRIVKNVDDLLDPVSPVNSDGSINRCSEQYVNSRLSEVENRSGDAHEFSPI 877
 QY 879 DTGBIDYNNENAGIWWGPKITDPEGYATLGNLVEEGLSGDALERLQREEQWKIQMTR 938

DB 878 DIGELDYNNENAGIWWGPKITDPEGYATLGNLVEEGLSGDALERLQREEQWKIQMTR 937
 QY 939 RREETDRRYMASKOAVDRLYADYQDQQLNPDVEITDLTAAQDLIQSIPIYVYNNEMFPEIPG 998
 DB 938 RREETDRRYMASKOAVDRLYADYQDQQLNPDVEITDLTAAQDLIQSIPIYVYNNEMFPEIPG 997
 QY 999 MNYTKFTELDRLOQAAWSLYDORNAIPNGDFRNLGSNNWNPATPGVEQOINHTSVLVIPINW 1058
 DB 998 MNYTKFTELDRLOQAAWNLVDORNAIPNGDFRNLGSNNWNPATPGVEQOINHTSVLVIPINW 1057
 QY 1059 DEQVSSQFTVQPNQRYVLRVTKARKEGVNGVYSIRDGNQGTETLTFSASDYDTNGMYNTQ 1118
 DB 1058 DEQVSSQFTVQPNQRYVLRVTKARKEGVNGVYSIRDGNQGTETLTFSASDYDTNGM---- 1113
 QY 1119 VSNVTNGVNTNAYNTQASSTNGVNNANNMYNTQASNTNGVNTNSVYNDOTGVIITKTVTPIP 1178
 DB 1114 -----YNDQTGYITKTVTPIP 1129
 QY 1179 YTDQMWIESETEGTFFYIESVELIVDVE 1206
 DB 1130 YTDQMWIESETEGTFFYIESVELIVDVE 1157

RESULT 5

AAR25997
 ID AAR25997 standard; Protein; 1157 AA.
 XX AAR25997;
 AC AAR25997;
 XX 27-JAN-1993 (first entry)
 DT Delta-endotoxin.
 DE B.t.P550C; colorado potato beetle; Leptinotarsa decemlineata;
 KW Pseudomonas; expression vector.
 XX Bacillus thuringiensis.
 OS EF498537-A.
 PN 12-AUG-1992.
 PD 16-JAN-1992; 92EP-0300366.
 PF 16-JAN-1991; 91US-0642112.
 PR (MYCO) MYCOGEN CORP.
 PA Foncerrada L, Payne JM, Sick AJ;
 PI WPI; 1992-270497/33.
 XX P-PSDB; AAR25997.
 DR New insecticidal Bacillus thuringiensis strain NRRL B-18746 - and
 PT toxin, DNA encoding it, vectors and transformed cells, effective
 PT against Coleoptera
 XX Claim 6; Page 11-14; 16pp; English.
 PS
 CC The sequence given is an approx. 130 kD protein known as Bacillus
 CC thuringiensis p550C (B.t.p550C). This novel delta-endotoxin has been
 CC shown to be active against the Colorado potato beetle (Leptinotarsa
 CC decemlineata). The gene encoding this toxin can be transformed into
 CC suitable hosts such as Pseudomonas, which can then be applied to the
 CC environment of coleopteran insects, where they will proliferate and be
 CC ingested by the insects. This DNA sequence can be inserted into an
 CC expression vector which contains a promoter/operator region, a ribosome
 CC binding site, polyadenylation signals, etc. This will allow
 CC transcription and translation of the cells in the appropriate host.
 XX Sequence 1157 AA;

Query Match 62.4%; Score 3950.5; DB 13; Length 1157;
Best Local Similarity 65.5%; Pred. No. 2.4e-256;
Matches 804; Conservative 120; Mismatches 211; Indels 93; Gaps 19;

QY 1 MSPNNQNEYIIDATPSTSVSDSNRYPPANETNALQNNMDYKYLKMSAGNASEYGPSP 60
DB 1 MSPNNQNEYIIDATPSTSVSDSNRYPPANETDALQNNMYKDYLKMSGGENPELFGNP 60

QY 61 EVLVSGODAAKAAIDIVGKLLSGLVPGVPVSVISYLTOLIDLWPSGKESQWEIFMEQVE 120
DB 61 ETFIS-SSTIQTGTGIVGRILGALGVPFASQIASFYFIVGQLWPSKSVDTWGEIMERVE 119

QY 121 ELINQKIAEYARNKALSEGLEGNMYQLYLTALBEEWENPNPGRALDRVRNRFILDSLP 180
DB 120 ELVDQKIEKYKDALAEKGLGNALDVYQOSLEDWLENDRDARTSVVSNQFIALDNP 179

QY 181 TQYMPSPRTNPFVFFLTVYMAANLHLLKDLASIFGEEWGSMTTINNYYDROMKLT 240
DB 180 VSSIPSPAVSGHEVLLAVYAQAANLHLLLDASIFGEEWGSTPGEISRYNRRQVQLTA 239

QY 241 EYSDHCYKWTETGLAKLGTSAKOWVDYNOFRREMTLAVLDVALFNYDRTYPMETKA 300
DB 240 EYSDYCKWYKIGLDKLGKGTGTSWLNHQPFRREMTLLVLDLVALFNYDTHMYPETTA 299

QY 301 QLTREVYTDPLGAVNVSSIGSWYDKAPSGV-IESSVIRPPHVFYITGLTVYQSR 356
DB 300 QLTREVYTDPLGAVNVSSIGSWYDKAPSGV-IESSVIRPPHVFYITGLTVYQSR 356

QY 357 ---SISARYIRHWAGHQISYHRSVRSNLOQMYGTGNLHSTSTFTDNYDIYKTLSDK 413
DB 359 GGITLNDAYINYSWGLTKYRRTA-DSTVYTYANYGRITSEKNSFALEDRIEINSTV 417

QY 414 AVLLDIYVPGVYTIFFGNGPEVEFFWQNLNTRKTLKYNVSKDIIASTR--DSELELPP 471
DB 418 ANLANYQKAY-----GVPGSWFHWKRGTSSTAYLSKTHKTHALQGTQVYESSDEIPL 472

QY 472 ETSQPNYESYSHRLCHITSPATGNTT---GLVPVPSWTHRSADLNNIYSDKITOIPA 528
DB 473 DRT-VPAVESYSHRLSHITSHSPKNGSAYYGSFPVFWTHTSADLNNIYSDKITOIPA 531

QY 529 VKCWDNLPFV--PVVKGPGHTGDLQVNRSTGVTFLFLARYGLALEKAGKYRRLRYA 586
DB 532 VK--GDMLYLGGSVVQPGFTGGDLK--RTNPSILGTFAVTVNGSLSQ--RYRVRIRYA 585

QY 587 --TDADIVLHND--QIOMPKTNPGEDLTSTFKYADAITLNL-ATDSSLAK---H 638
DB 586 STTDFEFTLIGDTIEKRNFKMTDNGASLTFTFKFASFTDFQFRETQDKILLSGDF 645

QY 639 NLGDEPNSTLSGIVVDRIEIPVDETYEABQDLAAKAVNALFTNTKGLRPGVTDYE 698
DB 646 SSGQE-----VIIDRIEIPVDETYEABQDLAAKAVNALFTNTKGLRPGVTDYE 697

QY 699 VNQAANLVECLSDLLYPNEKLLFDVAREAKRLSEARNLLQDPPQFQINGENGWASTGI 758
DB 698 VNQAANLVECLSDLLYPNEKLLFDVAREAKRLSEARNLLQDPPQFQINGENGWASTGI 757

QY 759 EVIEGDALFKGRYLRLPGAREIDTETPTLYLYQKVEGVLPKYTRYRLRGVSSQGLEI 818
DB 758 EIVEGDVAFKGRYLRLPGAREIDTETPTLYLYQKVEGVLPKYTRYRLRGVSSQGLEI 817

QY 819 FTIRHQTNRIVKVPDPLLDPVSPVNSDGSINRSCQKYNSRLEVENRSGEAHEFSIPI 878
DB 818 YTIHQTNRIVKVPDPLLDPVSPVNSDGSINRSCQKYNSRLEVENRSGDAHEFSIPI 877

QY 879 DTGEIDYNENAGIWWGFKITDPEGYATLGNLEVEEPLSGDALERLQREQQWKIQWTR 938
DB 878 DIGELDYNENAGIWWGFKITDPEGYATLGNLEVEEPLSGDALERLQREQQWKIQWTR 937

QY 939 RRETDTRYWASKOAVDRLYADYQDQQLNPVEITDLTAAQDLIQSIPYVYNNFPPIPG 998
DB 938 RRETDTRYWASKOAVDRLYADYQDQQLNPVEITDLTAAQDLIQSIPYVYNNFPPIPG 997

QY 999 MNTTKFTELTDLRLOQAWSLYDQRNAIPNGDFRNLGNLNNWATPGVEVQQLNHTSVLIPNW 1058

DB 998 MNTTKFTELTDLRLOQAWSLYDQRNAIPNGDFRNLGNLNNWATPGVEVQQLNHTSVLIPNW 1057
QY 1059 DEQVSQOFTVQPNQRYVLRVTARKEGVNGVSVIRDCGNQETELTTSASDYDNGMNTQ 1118
DB 1058 DEQVSQOFTVQPNQRYVLRVTARKEGVNGVSVIRDCGNQETELTTSASDYDNG----- 1112
QY 1119 VSNITNGYNTNAYNTQASSTNGYNNANNMYNTQASNTNGYNTNSVYNDQTCYITKVTTFIP 1178
DB 1113 -----VYNDQTCYITKVTTFIP 1129

QY 1179 YTDQMIEMSETEGTFFYIESVELIVDVE 1206
DB 1130 YTDQMIEMSETEGTFFYIESVELIVDVE 1157

RESULT 6
AAR33768
ID AAR33768 standard; Protein; 1157 AA.
XX
AC AAR33768;
XX
DT 15-JUL-1993 (first entry)
XX
DE Bt isolate Ps50C.
XX
KW Lepidopteran-active; toxin; Ti; Ri; plant; cell; Bt.
XX
OS Bacillus thuringiensis.
XX
PN WO9304587-A.
XX
PD 18-MAR-1993.
XX
PF 11-SEP-1992; 92WO-US07697.
XX
PR 12-SEP-1991; 91US-0758020.
PR 09-SEP-1992; 92US-0941650.
XX
PA (MYCO) MYCOGEN CORP.
XX
PI Bradfish GA, Uyeda KA;
XX
DR WPI; 1993-100566/12.
DR N-PSDB; AAR38653.
XX
PT Controlling lepidopteran pests - using compsn. of Bacillus
PT thuringiensis strains or plants or microorganisms transformed
PT with their toxin genes
XX
PS Claim 12; Page 22-25; 38pp; English.
XX

The sequences given in AAR33768-70 represent lepidopteran-active toxins.
The DNA encoding these sequences were used within a Ti or Ri plasmid,
to transform plant cells. Whole plants can then be regenerated from
the transformed cells. The toxin may also be produced by cloning
Bacillus thuringiensis (Bt). It may then be applied directly to
the plant locus.

Sequence 1157 AA;

Query Match 62.4%; Score 3950.5; DB 14; Length 1157;
Best Local Similarity 65.5%; Pred. No. 2.4e-256;
Matches 804; Conservative 120; Mismatches 211; Indels 93; Gaps 19;

QY 1 MSPNNQNEYIIDATPSTSVSDSNRYPPANETNALQNNMDYKYLKMSAGNASEYGPSP 60
DB 1 MSPNNQNEYIIDATPSTSVSDSNRYPPANETDALQNNMYKDYLKMSGGENPELFGNP 60

QY 61 EVLVSGODAAKAAIDIVGKLLSGLVPGVPVSVISYLTOLIDLWPSGKESQWEIFMEQVE 120
DB 61 ETFIS-SSTIQTGTGIVGRILGALGVPFASQIASFYFIVGQLWPSKSVDTWGEIMERVE 119


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Db 300 QLTRDVYTDPIAFNIVTSTGFCNPMWTHSGILFYEVENNVRPPLHFDILSSVEINT-SR 358
Qy 357 ---SISARVIRHWAGHOISVHRVSRGSLNQOMYGTQNLHSTSTFTPTNYDIYKTLSD 413
Db 359 GGITLNDAYINWSGHTLKYRRTA-DSTVITYANYGRITSKNSPALEDRDIFEINSTV 417
Qy 414 AVLLDIYVPGYTYIFFGMPEVEPPMVNQLNNTKILKYNPVSKDIIIASTR--DSELELPP 471
Db 418 ANLANYQKAY-----GVPGSWFHWKRVSTSTAYILYKTHLTALQCTQVYESSDEIPL 472
Qy 472 ETSQPNYESVSHRLCHITSTPATGNTT---GLYPVSWTHRSADIANNTIYSDKITQIPA 528
Db 473 DRT--VPAETYSHRLSHITSHSFKNKSAYYGSPFVFWTHTSADLNNIYSDKITQIPA 531
Qy 529 VKCWDNLPFV--PVKPGHGTGGDLQVNRSTGVTGLFLARYGALAKGKGYRVLRYA 586
Db 532 VK--GDMLYIGSVVQPGFGTGGDLK--RTNPILGTFAVTNGSLQ--RYRVRRYA 585
Qy 587 --TDADIVLHVND--QIOMPKNPGBDLTSKTKVADAITLNL-ATDSSLAK---H 638
Db 586 STTDPEFTLVLDITKRNFKNTWDNGASLTVEYFKFASPITDFQPRETDKILLSMGDF 645
Qy 639 NLGSDPNSTLSGIVYDRIBFIPVDETYEARQDLEAKKAVNALFTNTKQGLRPGVTDYE 698
Db 646 SSGQE-----VYIDRIEIPVDETYEARQDLEAKKAVNALFTNTKQGLRPGVTDYE 697
Qy 699 VNOQANLVECLSDDLYPNEKELLFDVAREAKRLSEARNLLQDPDFQINGENGWASTGI 758
Db 698 VNOQANLVECLSDDLYPNEKELLFDVAREAKRLSGARNLLQDPDFQINGENGWASTGI 757
Qy 759 EVIEGDALFKGRYLRLPGAREIDTETPTLYLKVEGVLPKYRYRLRFGVSSQGLEI 818
Db 758 EIVEGDVAFKGRYLRLPGAREIDTETPTLYLKVEGVLPKYRYRLRFGVSSQGLEI 817
Qy 819 FTIRHQNRIKVNVPDILLPVSPVNSDGSINRCSEQKYVNSRLSEVENRSGEAHEFSIPI 878
Db 818 YTIHQNRIKVNVPDILLPVSPVNSDGSINRCSEQKYVNSRLSEVENRSGEAHEFSIPI 877
Qy 879 DTGEIDYENAGIHWGPKITDPEGVATLGNLELVEEGLSGDALERLOREOQWKIOMTR 938
Db 878 DIGELDYENAGIHWGPKITDPEGVATLGNLELVEEGLSGDALERLOREOQWKIOMTR 937
Qy 939 RRETDTRYMASKQAVRLYADYQDQQLNPVVEITDLTAAQDLIQSIPIYVYNMFPPEIPG 998
Db 938 RRETDTRYMASKQAVRLYADYQDQQLNPVVEITDLTAAQDLIQSIPIYVYNMFPPEIPG 997
Qy 999 MNYTKFTLDRLOQAWSLYDORNAIPNGDFRNLGNLNNNATPGVEVQOINHTSVLVI PNW 1058
Db 998 MNYTKFTLDRLOQAWSLYDORNAIPNGDFRNLGNLNNNATPGVEVQOINHTSVLVI PNW 1057
Qy 1059 DEQVSQOFTVQPNORYLRLVTRARKEGUGNGYVSRDGGNQTETLTFSSADYDTNGMYTQ 1118
Db 1058 DEQVSQOFTVQPNORYLRLVTRARKEGUGNGYVSRDGGNQTETLTFSSADYDTNG----- 1112
Qy 1119 VSNNGYNTNAYNTQASSTGYNANMYNTQASNTNGYNTSVNDOTGYITKTVTFIP 1178
Db 1113 -----VNDOTGYITKTVTFIP 1129
Qy 1179 YTDQWMIEMSETGTFYIESVELIVDVE 1206
Db 1130 YTDQWMIEMSETGTFYIESVELIVDVE 1157

RESULT 9
AAR44208
ID AAR44208 standard; Protein; 1157 AA.
XX
AC AAR44208;
XX
DT 09-DEC-1995 (first entry)
XX
DE Bacillus thuringiensis crystal protein PS50C.
XX
```

```
KW Crystal protein; delta endotoxin; acaricide; pesticide;
KW biological control agent; transgenic plant; crop improvement.
OS Bacillus thuringiensis var. kumamotoensis (isolate PS50C).
PN US5262158-A.
PD 16-NOV-1993.
XX
XX 30-APR-1991; 91US-0693210.
XX
XX 30-APR-1992; 92US-0876280.
XX 30-APR-1991; 91US-0693210.
XX 13-SEP-1991; 91US-0759248.
XX 30-SEP-1991; 91US-0768141.
XX
XX (MYCO ) MYCOGEN CORP.
XX
XX Bagley AL, Cannon RJC, Payne JM;
XX WPI; 1993-377387/47.
XX N-PSDB; AAQ51704.
XX
XX Controlling acaride pests e.g. two spotted spider mite - utilising
XX PT Bacillus thuringiensis delta-toxins cloned into microbe hosts.
XX
XX Disclosure; Column 71-76; 42pp; English.
XX
XX DNA encoding the insecticidal toxin can be cloned into baculo
XX viruses and transferred to other host microbes, preferably E. coli
XX NM522 (pMYC 2320) NRRL B-18769, to control acaride pests, or to
XX plants which become resistant to the acaricide pests.
XX Specifically, the two-spotted spider mite (Tetranychus urticae) is
XX controlled.
XX
XX Sequence 1157 AA;
```

```
Query Match 62.2%; Score 3940.5; DB 14; Length 1157;
Best Local Similarity 65.4%; Pred. No. 1.le-255;
Matches 803; Conservative 119; Mismatches 213; Indels 93; Gaps 19;

Qy 1 MSPNNQNEYIIDATPTSVNSDNRYPFANEPNALONMDYKDYLRKMGAGNASEYPCGP 60
Db 1 MSPNNQNEYIIDATPTSVNSDNRYPFANEPNALONMDYKDYLRKMGAGNASEYPCGP 60
Qy 61 EVLVSGDAAKAAIDIVCKLLSGLVGVFVGVPIVSLYQLDILWPSEKSKSOWEIFMEQVE 120
Db 61 ETVFIS-SSTIQTGIGIVGRILGALGVFPFASQIASFYFIVGQLWPSKSVDIWGEIMERVE 119
Qy 121 ELINQKIAEYARNKALSEGLEGNVQLYLTALAEWEENPNRGRALDRVRNRFILDSLF 180
Db 120 ELVDQKLEKVKDKAKLAEKGLGNALQVQOSLEDWLENDRNDATRSVVSQFALDLNF 179
Qy 181 TQYMPFRVNTFVFPFLTVYMAAANLHLLKLDASIFGEEWGWSTTTNNYDRQMKLTA 240
Db 180 VSSIPSAVSHEVLLAVYAQAQVNLHLLLRDASIFGEEWGFTPGEISRFYRNQVQLTA 239
Qy 241 EYSHCVKWTETGLAKLGTSAKOWVDYQNPFRREMTLAVLDVVALFPNYDTRTPYMETKA 300
Db 240 EYSDYCVKWKYIGLDKLGTTSKSLNLYHQFRRMTLLVLDVLPFNYDTHMYPIETTA 299
Qy 301 QLTREVTVDPLGAVNVSSIGSWYDKAPSGV-----IESSVIRPPHVPDYITGLTVYTOSR 356
Db 300 QLTREVTVDPLGAVNVSSIGSWYDKAPSGV-----IESSVIRPPHVPDYITGLTVYTOSR 358
Qy 357 ---SISARVIRHWAGHOISVHRVSRGSLNQOMYGTQNLHSTSTFTPTNYDIYKTLSD 413
Db 359 GGITLNDAYINWSGHTLKYRRTA-DSTVITYANYGRITSEKNSFALEDRIPEINSTV 417
Qy 414 AVLLDIYVPGYTYIFFGMPEVEPPMVNQLNNTKILKYNPVSKDIIIASTR--DSELELPP 471
Db 418 ANLANYQKAY-----GVPGSWFHWKRVSTSTAYILYKTHLTALQCTQVYESSDEIPL 472
```

PD
 XX 24-MAY-2002.
 XX
 XX 24-OCT-2001; 2001WO-US45468.
 XX
 XX 24-OCT-2000; 2000US-242838P.
 PR
 PR 23-OCT-2001; 2001US-0032717.
 XX
 XX (DUPO) DU PONT DE NEMOURS & CO E I.
 PA
 XX
 XX Abad AR, Duck NB, Feng X, Flannagan RD, Kahn TW, Sims LE;
 PI
 DR WPI; 2002-519178/55.
 DR N-PSDB; ABK87238.
 XX
 XX New isolated pesticidal polypeptide useful for impacting insect pest
 PT e.g. Colorado potato beetle -
 PT
 XX
 XX Example 5; Page 117-118; 176pp; English.
 PS
 CC
 CC The present invention relates to a new pesticidal polypeptide. The
 CC invention is useful for impacting an insect pest by applying the
 CC molecules of the invention to the environment of the insect pest
 CC spraying, dusting, broadcasting, or seed coating, where the insect pest
 CC is selected from Colorado potato beetle, western corn rootworm or
 CC southern corn rootworm. The invention is also useful for increasing
 CC insect target range and for producing transgenic microorganisms and
 CC plants that express the pesticidal polypeptide. The invention is also
 CC useful for producing transformed plants and in transforming any organ-
 CC to produce the pesticidal polypeptide of the invention. The present
 CC amino acid sequence represents a *Bacillus thuringiensis* wild-type
 CC Cry1218 endotoxin protein.
 XX
 XX Sequence 669 AA;

Query Match	Score	DB	Length
Best Local Similarity	100.0%;	Pred. No. 3.5e-227;	
Matches 669; Conservative	0; Mismatches	0; Indels	0; Gaps

D6	181	QY	NSPSPRVNPFV	PFVFTVYV	YAMAA	NHLLK	DOAST	PGEE	WGS	TATTT	INNY	YD	QRM	KLTA	24
QY	241	EYSDHC	VKWTET	GLAKL	KGTS	SAQ	WDYNO	QF	RE	MTL	AVLD	VVAL	PNY	DT	VP
Db	241	EYSDHC	VKWTET	GLAKL	KGTS	SAQ	WDYNO	QF	RE	MTL	AVLD	VVAL	PNY	DT	VP
QY	301	QLTRE	VYTD	PLG	AVNV	SSIG	SWD	KAP	SGV	IESS	VR	PH	PDY	IT	GL
Db	301	QLTRE	VYTD	PLG	AVNV	SSIG	SWD	KAP	SGV	IESS	VR	PH	PDY	IT	GL
QY	361	ARYR	BWAG	HQI	SYHR	VS	RS	GS	NI	QOM	YGT	NQ	NH	ST	PD
Db	361	ARYR	BWAG	HQI	SYHR	VS	RS	GS	NI	QOM	YGT	NQ	NH	ST	PD
QY	421	YPGY	TF	FG	MP	VE	PE	PM	NQ	LN	TR	KL	KN	PV	SD
Db	421	YPGY	TF	FG	MP	VE	PE	PM	NQ	LN	TR	KL	KN	PV	SD
QY	481	SYSH	RL	CH	ITS	I	PAT	GN	TT	GL	AV	PF	VS	WTH	RS
Db	481	SYSH	RL	CH	ITS	I	PAT	GN	TT	GL	AV	PF	VS	WTH	RS

QY 541 VKPGHGTGDLLOYNRSTGSGVTLFLARYGLALEKAGKYRRLRYATDADIVLHVNDQI 600
 DB 541 VKPGHGTGDLLOYNRSTGSGVTLFLARYGLALEKAGKYRRLRYATDADIVLHVNDQI 600
 QY 601 QMPKTMNPGEDLTSKTFKVADAITTLNLTATDSSALAKHNLGDPNSTLSGIYVVDRIEPI 660
 DB 601 QMPKTMNPGEDLTSKTFKVADAITTLNLTATDSSALAKHNLGDPNSTLSGIYVVDRIEPI 660
 QY 661 PVDETYEAE 669
 DB 661 PVDETYEAE 669
 RESULT 11
 ID AAU99262 standard; Protein; 669 AA.
 XX
 AC AAU99262;
 DT 07-OCT-2002 (first entry)
 XX
 DE Bacillus thuringiensis Cry1218-1A truncated protein sequence.
 XX
 KW Pesticidal; spraying; dusting; broadcasting; seed coating; insect pest;
 KW Colorado potato beetle; western corn rootworm; southern corn rootworm;
 KW insect target range; endotoxin; Cry1218.
 XX
 OS Bacillus thuringiensis.
 XX
 PN WO200234774-A2.
 XX
 PD 02-MAY-2002.
 XX
 PF 24-OCT-2001; 2001WO-US45468.
 XX
 PR 24-OCT-2000; 2000US-242838P.
 XX
 PR 23-OCT-2001; 2001US-0032717.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 PI Abad AR, Duck NB, Peng X, Flannagan RD, Kahn TW, Sims LB;
 XX
 DR WPI; 2002-519178/55.
 DR N-PSDB; ASK87241.
 XX
 PT New isolated pesticidal polypeptide useful for impacting insect pest
 PT e.g. Colorado potato beetle -
 XX
 PS Claim 4; Page 125-127; 176pp; English.
 XX
 CC The present invention relates to a new pesticidal polypeptide. The
 CC invention is useful for impacting an insect pest by applying the
 CC the molecules of the invention to the environment of the insect pest by
 CC spraying, dusting, broadcasting, or seed coating, where the insect pest
 CC is selected from Colorado potato beetle, western corn rootworm or
 CC southern corn rootworm. The invention is also useful for increasing
 CC insect target range and for producing transgenic microorganisms and
 CC plants that express the pesticidal polypeptide. The invention is also
 CC useful for producing transformed plants and in transforming any organism
 CC to produce the pesticidal polypeptide of the invention. The present
 CC amino acid sequence represents a Bacillus thuringiensis wild-type
 CC Cry1218 endotoxin protein.
 XX
 SQ Sequence 669 AA;
 Query Match 55.4%; Score 3511; DB 23; Length 669;
 Best Local Similarity 100.0%; Pred. No. 3.5e-227;
 Matches 669; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSPNNQNEYIITDPTSTSVNSDNRYPANEPNTALQNMDYKDYLMKAGNASYFGSP 60
 DB 1 MSPNNQNEYIITDPTSTSVNSDNRYPANEPNTALQNMDYKDYLMKAGNASYFGSP 60

QY 61 EYLVSGQDAKAAIDIVGKLLSGLGVPFVGPVIVSLYTQIIDLWPSEKSGQWEIFMEQVE 120
 DB 61 EYLVSGQDAKAAIDIVGKLLSGLGVPFVGPVIVSLYTQIIDLWPSEKSGQWEIFMEQVE 120
 QY 121 ELINOKIAEYARNKALSEGLEGNNYQLYLTALEEENPNGSRALRDVRRNFEILDSLF 180
 DB 121 ELINOKIAEYARNKALSEGLEGNNYQLYLTALEEENPNGSRALRDVRRNFEILDSLF 180
 QY 181 TOYMPSFRVTNFEVPLTVYAMAANLHLLKDAISFGEWGWSTTTNNYDROMKLT 240
 DB 181 TOYMPSFRVTNFEVPLTVYAMAANLHLLKDAISFGEWGWSTTTNNYDROMKLT 240
 QY 241 EYSDHCVKWYETGLAKGTSKQWVDYNQFRREMTLAVLDVVALFPNYDTRTYPMETKA 300
 DB 241 EYSDHCVKWYETGLAKGTSKQWVDYNQFRREMTLAVLDVVALFPNYDTRTYPMETKA 300
 QY 301 QLTREVYTDPLGAVNVSSIGSWYDKAPSGVIESVIRPPHVFYITGLTVYTQSRSS 360
 DB 301 QLTREVYTDPLGAVNVSSIGSWYDKAPSGVIESVIRPPHVFYITGLTVYTQSRSS 360
 QY 361 ARYIRHWAGHOISYHRVSRGNSLQOMYGTNOLHSTSTFTDFTNYDIYKTLSDAVLLDIV 420
 DB 361 ARYIRHWAGHOISYHRVSRGNSLQOMYGTNOLHSTSTFTDFTNYDIYKTLSDAVLLDIV 420
 QY 421 YPGYTYIIFGMEPEVEFFMVNQLNTRKTLKYNPVSVDIIASTRDSELELPPTSDQPNYE 480
 DB 421 YPGYTYIIFGMEPEVEFFMVNQLNTRKTLKYNPVSVDIIASTRDSELELPPTSDQPNYE 480
 QY 481 SYSRLCHITSIPATGNTTGLVPVSWTHRSADLNNTIYSDKITQIPAVKCDNLPFVPV 540
 DB 481 SYSRLCHITSIPATGNTTGLVPVSWTHRSADLNNTIYSDKITQIPAVKCDNLPFVPV 540
 QY 541 VKGPGHGTGDLLOYNRSTGSGVTLFLARYGLALEKAGKYRRLRYATDADIVLHVNDQI 600
 DB 541 VKGPGHGTGDLLOYNRSTGSGVTLFLARYGLALEKAGKYRRLRYATDADIVLHVNDQI 600
 QY 601 QMPKTMNPGEDLTSKTFKVADAITTLNLTATDSSALAKHNLGDPNSTLSGIYVVDRIEPI 660
 DB 601 QMPKTMNPGEDLTSKTFKVADAITTLNLTATDSSALAKHNLGDPNSTLSGIYVVDRIEPI 660
 QY 661 PVDETYEAE 669
 DB 661 PVDETYEAE 669
 RESULT 12
 ID AAU99257 standard; Protein; 667 AA.
 XX
 AC AAU99257;
 XX
 DT 07-OCT-2002 (first entry)
 XX
 DE Bacillus thuringiensis Cry1218-1 truncated protein sequence.
 XX
 KW Pesticidal; spraying; dusting; broadcasting; seed coating; insect pest;
 KW Colorado potato beetle; western corn rootworm; southern corn rootworm;
 KW insect target range; endotoxin; Cry1218.
 XX
 OS Bacillus thuringiensis.
 XX
 PN WO200234774-A2.
 XX
 PD 02-MAY-2002.
 XX
 PF 24-OCT-2001; 2001WO-US45468.
 XX
 PR 24-OCT-2000; 2000US-242838P.
 XX
 PR 23-OCT-2001; 2001US-0032717.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX

PI Abad AR, Duck NB, Feng X, Flannagan RD, Kahn TW, Sims LE;
XX WPI; 2002-519178/55.
DR N-PSDB; ABK87236.
XX New isolated pesticidal polypeptide useful for impacting insect pest
PT e.g. Colorado potato beetle -
XX Claim 4; Page 108-109; 176pp; English.
XX The present invention relates to a new pesticidal polypeptide. The
CC invention is useful for impacting an insect pest by applying the
CC the molecules of the invention to the environment of the insect pest by
CC spraying, dusting, broadcasting, or seed coating, where the insect pest
CC is selected from Colorado potato beetle, western corn rootworm or
CC southern corn rootworm. The invention is also useful for increasing
CC insect target range and for producing transgenic microorganisms and
CC plants that express the pesticidal polypeptide. The invention is also
CC useful for producing transformed plants and in transforming any organism
CC to produce the pesticidal polypeptide of the invention. The present
CC amino acid sequence represents a *Bacillus thuringiensis* wild-type
CC Cry1218 endotoxin protein.
XX
SQ Sequence 667 AA;
Query Match 55.3%; Score 3502; DB 23; Length 667;
Best Local Similarity 100.0%; Pred. No. 1.4e-226;
Matches 667; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MSPNNQNEYIIDATPSTSVNSDNRYPFANEPTNALQNM DYKDYLMKMSAGNASYVPGSP 60
Db 1 MSPNNQNEYIIDATPSTSVNSDNRYPFANEPTNALQNM DYKDYLMKMSAGNASYVPGSP 60
Qy 61 EYLVSGQDAKAAIDIVGKLLSGLVFPVGPVIVSLYTQIDILWPSEKSOEWFMEQVE 120
Db 61 EYLVSGQDAKAAIDIVGKLLSGLVFPVGPVIVSLYTQIDILWPSEKSOEWFMEQVE 120
Qy 121 ELINOKIAEYARNKALSEGLEGNNGYQLYLTALBEEENPNSGRALDRVRNRFEL 180
Db 121 ELINOKIAEYARNKALSEGLEGNNGYQLYLTALBEEENPNSGRALDRVRNRFEL 180
Qy 181 TOYMSFRVTNEVPPLTYVYAAANLHLLLDKASIFGEWGSTTTINNYDRQMKLTA 240
Db 181 TOYMSFRVTNEVPPLTYVYAAANLHLLLDKASIFGEWGSTTTINNYDRQMKLTA 240
Qy 241 EYSDHCWKVETGLAKLKTSAQWVDYNQFREMTLAVLDVVALPNDYTRTYMETKA 300
Db 241 EYSDHCWKVETGLAKLKTSAQWVDYNQFREMTLAVLDVVALPNDYTRTYMETKA 300
Qy 301 QLTREYVTDPLGAVNVSSIGSWYDKAPSGVIESSVIRPPHVFDTYITGLVYTSRSISS 360
Db 301 QLTREYVTDPLGAVNVSSIGSWYDKAPSGVIESSVIRPPHVFDTYITGLVYTSRSISS 360
Qy 361 ARYIRHWAGHQISYHRVSRGSLQOMYGTGNLHSTSTFTDNYDIYKLSKDAVLLDIV 420
Db 361 ARYIRHWAGHQISYHRVSRGSLQOMYGTGNLHSTSTFTDNYDIYKLSKDAVLLDIV 420
Qy 421 YPGYTYIFPGMEVEFFPMYNLNTRKTLKYNPVSVDIIASTRDSLELPDTPSY 480
Db 421 YPGYTYIFPGMEVEFFPMYNLNTRKTLKYNPVSVDIIASTRDSLELPDTPSY 480
Qy 481 SYSHRLCHITSPATGNTTGLVPVSWTHRSADLNNTIYSDKITQIPAVKWNLPFPV 540
Db 481 SYSHRLCHITSPATGNTTGLVPVSWTHRSADLNNTIYSDKITQIPAVKWNLPFPV 540
Qy 541 VKGPHTGDLQYNRSTSGVTGLFLARYGLALEKAGKYRVLRYATDADIVLHVNDQI 600
Db 541 VKGPHTGDLQYNRSTSGVTGLFLARYGLALEKAGKYRVLRYATDADIVLHVNDQI 600
Qy 601 QMPKTMNPGEDLTSKTFKVADAITTLNLTADSSSLAKHNLGDPNSTLSGIVYVDRIEF 660
Db 601 QMPKTMNPGEDLTSKTFKVADAITTLNLTADSSSLAKHNLGDPNSTLSGIVYVDRIEF 660

Qy 661 PVDETYE 667
Db 661 PVDETYE 667
RESULT 13
AAU99260
ID AAU99260 standard; Protein; 673 AA.
XX AAU99260;
XX 07-OCT-2002 (first entry)
XX *Bacillus thuringiensis* NSRG.N1218-1 mutant protein sequence.
XX Pesticidal; spraying; dusting; broadcasting; seed coating; insect pest;
XX Colorado potato beetle; western corn rootworm; southern corn rootworm;
XX insect target range; endotoxin; Cry1218; mutant; mutein.
XX *Bacillus thuringiensis*.
XX Synthetic.
XX WO200234774-A2.
XX 02-MAY-2002.
XX 24-OCT-2001; 2001WO-US45468.
XX 24-OCT-2000; 2000US-242838P.
XX 23-OCT-2001; 2001US-0032717.
XX (DUPO) DU PONT DE NEMOURS & CO E I.
XX Abad AR, Duck NB, Feng X, Flannagan RD, Kahn TW, Sims LE;
XX WPI; 2002-519178/55.
XX N-PSDB; ABK87239.
XX New isolated pesticidal polypeptide useful for impacting insect pest
XX e.g. Colorado potato beetle -
XX Claim 23; Page 121-122; 176pp; English.
XX The present invention relates to a new pesticidal polypeptide. The
XX invention is useful for impacting an insect pest by applying the
XX the molecules of the invention to the environment of the insect pest by
XX spraying, dusting, broadcasting, or seed coating, where the insect pest
XX is selected from Colorado potato beetle, western corn rootworm or
XX southern corn rootworm. The invention is also useful for increasing
XX insect target range and for producing transgenic microorganisms and
XX plants that express the pesticidal polypeptide. The invention is also
XX useful for producing transformed plants and in transforming any organism
XX to produce the pesticidal polypeptide of the invention. The present
XX amino acid sequence represents a *Bacillus thuringiensis* mutant Cry1218
XX endotoxin protein.
XX Sequence 673 AA;
Query Match 55.3%; Score 3499; DB 23; Length 673;
Best Local Similarity 99.4%; Pred. No. 2.3e-226;
Matches 669; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
Qy 1 MSPNNQNEYIIDATPSTSVNSDNRYPFANEPTNALQNM DYKDYLMKMSAGNASYVPGSP 60
Db 1 MSPNNQNEYIIDATPSTSVNSDNRYPFANEPTNALQNM DYKDYLMKMSAGNASYVPGSP 60
Qy 61 EYLVSGQDAKAAIDIVGKLLSGLVFPVGPVIVSLYTQIDILWPSEKSOEWFMEQVE 120
Db 61 EYLVSGQDAKAAIDIVGKLLSGLVFPVGPVIVSLYTQIDILWPSEKSOEWFMEQVE 120
Qy 121 ELINOKIAEYARNKALSEGLEGNNGYQLYLTALBEEENPNSGRALDRVRNRFEL 176
Db 121 ELINOKIAEYARNKALSEGLEGNNGYQLYLTALBEEENPNSGRALDRVRNRFEL 180

QY 177 DLSFTQMPSPFRVTNEFVPLTVYMAANLHLLLDKASIFGEWGWSTTTINNYDROM 236
 |||||
 Db 181 DLSFTQMPSPFRVTNEFVPLTVYMAANLHLLLDKASIFGEWGWSTTTINNYDROM 240
 |||||
 QY 237 KLTAEYSDHCWKYETGLAKLKTSAKQWVDYQFREMFLAVLVDVVALPPNYDRTYPM 296
 |||||
 Db 241 KLTAEYSDHCWKYETGLAKLKTSAKQWVDYQFREMFLAVLVDVVALPPNYDRTYPM 300
 |||||
 QY 297 ETKAQLTREVTDPGLGAVNVSSIGSWYDKAPSGVIESSVIRPHVFDYITGLTVYTQSR 356
 |||||
 Db 301 ETKAQLTREVTDPGLGAVNVSSIGSWYDKAPSGVIESSVIRPHVFDYITGLTVYTQSR 360
 |||||
 QY 357 SISSARYIRHWAGHQISYHRVSRGSLQOMWGTNQLNLTSTFDTNYDIYKTLSDAVL 416
 |||||
 Db 361 SISSARYIRHWAGHQISYHRVSRGSLQOMWGTNQLNLTSTFDTNYDIYKTLSDAVL 420
 |||||
 QY 417 LDIVPGYTYIFFGMPVEFVFMVNLNTRKTLKYNPVSKDIIASTRDSLELPPTSQ 476
 |||||
 Db 421 LDIVPGYTYIFFGMPVEFVFMVNLNTRKTLKYNPVSKDIIASTRDSLELPPTSQ 480
 |||||
 QY 477 PNYESYSHRLCHITSPATGNTTGLVPSWTHRSADLNTIYSDKLTQIPAVKCDNLP 536
 |||||
 Db 481 PNYESYSHRLCHITSPATGNTTGLVPSWTHRSADLNTIYSDKLTQIPAVKCDNLP 540
 |||||
 QY 537 FVPVKGPGHGTGDLQYNRSTGSGVGLFLARYGLALEKAGKYRRLRYATDADIVLHVN 596
 |||||
 Db 541 FVPVKGPGHGTGDLQYNRSTGSGVGLFLARYGLALEKAGKYRRLRYATDADIVLHVN 600
 |||||
 QY 597 DAQIQMPKTMNPGEDLTSTKTFKVADAITTLNLTADSSALKHNLGDPNSTLSGIVVYDR 656
 |||||
 Db 601 DAQIQMPKTMNPGEDLTSTKTFKVADAITTLNLTADSSALKHNLGDPNSTLSGIVVYDR 660
 |||||
 QY 657 IEFIPVDETYEAE 669
 |||||
 Db 661 IEFIPVDETYEAE 673
 |||||

RESULT 14

AAU99265
 ID AAU99265 standard; Protein; 673 AA.

XX
 AC AAU99265;

XX
 DT 07-OCT-2002 (first entry)

XX
 DE Bacillus thuringiensis LKMS.N1218-1 mutant protein sequence.

XX
 KW Pesticidal; spraying; dusting; broadcasting; seed coating; insect pest;
 KW Colorado potato beetle; western corn rootworm; southern corn rootworm;
 KW insect target range; endotoxin; Cry1218; mutant; mutein.

XX
 OS Bacillus thuringiensis.
 OS Synthetic.

XX
 PN WO200234774-A2.

XX
 PD 02-MAY-2002.

XX
 PF 24-OCT-2001; 2001WO-US45468.

XX
 PR 24-OCT-2000; 2000US-242838P.

XX
 PR 23-OCT-2001; 2001US-0032717.

XX
 PA (DUPO) DU PONT DE NEMOURS & CO E. I.

XX
 PI Abad AR, Duck NB, Feng X, Flannagan RD, Kahn TW, Sims LE;

XX
 DR WPI; 2002-519178/55.

XX
 DR N-PSDB; ABR87244.

XX
 PT New isolated pesticidal polypeptide useful for impacting insect pest
 e.g. Colorado potato beetle -

XX

PS Claim 23; Page 138-139; 176pp; English.

XX
 CC The present invention relates to a new pesticidal polypeptide. The
 CC invention is useful for impacting an insect pest by applying the
 CC the molecules of the invention to the environment of the insect pest by
 CC spraying, dusting, broadcasting, or seed coating, where the insect pest
 CC is selected from Colorado potato beetle, western corn rootworm or
 CC southern corn rootworm. The invention is also useful for increasing
 CC insect target range and for producing transgenic microorganisms and
 CC plants that express the pesticidal polypeptide. The invention is also
 CC useful for producing transformed plants and in transforming any organism
 CC to produce the pesticidal polypeptide of the invention. The present
 CC amino acid sequence represents a *Bacillus thuringiensis* mutant Cry1218
 CC endotoxin protein.

XX
 SQ Sequence 673 AA;

Query Match 55.3%; Score 3499; DB 23; Length 673;
 Best Local Similarity 99.4%; Pred. No. 2.3e-226;
 Matches 669; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 MSPNNQNEYIIDATPSTSVSNDNRYPPANEPTNALQNMNDYKDYKMSAGNASEYPGSP 60

Db 1 MSPNNQNEYIIDATPSTSVSNDNRYPPANEPTNALQNMNDYKDYKMSAGNASEYPGSP 60

QY 61 EVLVSGQDAAKAIDIVGKLLSGLGVFPVPTVSLYTOLIDILMPGSKSOWEIFMEQVE 120

Db 61 EVLVSGQDAAKAIDIVGKLLSGLGVFPVPTVSLYTOLIDILMPGSKSOWEIFMEQVE 120

QY 121 ELINQKIAEYARNKALSELEGLGNNTQVLTALKEEENP---NGSRALRDVNRNFEIL 176

Db 121 ELINQKIAEYARNKALSELEGLGNNTQVLTALKEEENP---NGSRALRDVNRNFEIL 180

QY 177 DLSFTQMPSPFRVTNEFVPLTVYMAANLHLLLDKASIFGEWGWSTTTINNYDROM 236

Db 181 DLSFTQMPSPFRVTNEFVPLTVYMAANLHLLLDKASIFGEWGWSTTTINNYDROM 240

QY 237 KLTAEYSDHCWKYETGLAKLKTSAKQWVDYQFREMFLAVLVDVVALPPNYDRTYPM 296

Db 241 KLTAEYSDHCWKYETGLAKLKTSAKQWVDYQFREMFLAVLVDVVALPPNYDRTYPM 300

QY 297 ETKAQLTREVTDPGLGAVNVSSIGSWYDKAPSGVIESSVIRPHVFDYITGLTVYTQSR 356

Db 301 ETKAQLTREVTDPGLGAVNVSSIGSWYDKAPSGVIESSVIRPHVFDYITGLTVYTQSR 360

QY 357 SISSARYIRHWAGHQISYHRVSRGSLQOMWGTNQLNLTSTFDTNYDIYKTLSDAVL 416

Db 361 SISSARYIRHWAGHQISYHRVSRGSLQOMWGTNQLNLTSTFDTNYDIYKTLSDAVL 420

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Db 421 LDIVPGYTYIFFGMPVEFVFMVNLNTRKTLKYNPVSKDIIASTRDSLELPPTSQ 480

QY 477 PNYESYSHRLCHITSPATGNTTGLVPSWTHRSADLNTIYSDKLTQIPAVKCDNLP 536

Db 481 PNYESYSHRLCHITSPATGNTTGLVPSWTHRSADLNTIYSDKLTQIPAVKCDNLP 540

QY 537 FVPVKGPGHGTGDLQYNRSTGSGVGLFLARYGLALEKAGKYRRLRYATDADIVLHVN 596

Db 541 FVPVKGPGHGTGDLQYNRSTGSGVGLFLARYGLALEKAGKYRRLRYATDADIVLHVN 600

QY 597 DAQIQMPKTMNPGEDLTSTKTFKVADAITTLNLTADSSALKHNLGDPNSTLSGIVVYDR 656

Db 601 DAQIQMPKTMNPGEDLTSTKTFKVADAITTLNLTADSSALKHNLGDPNSTLSGIVVYDR 660

QY 657 IEFIPVDETYEAE 669

Db 661 IEFIPVDETYEAE 673

RESULT 15
 AAU99271

ID AAU99271 standard; Protein; 673 AA.
AC AAU99271;
XX
DT 07-OCT-2002 (first entry)
XX
DE Bacillus thuringiensis LRNS.N1218-1 mutant protein sequence.
XX
XX Pesticidal; spraying; dusting; broadcating; seed coating; insect pest;
KW Colorado potato beetle; western corn rootworm; insect pest;
KW insect target range; endotoxin; Cry1218; mutant; mutein.
XX
OS Bacillus thuringiensis.
OS Synthetic.
XX
PN WO200234774-A2.
XX
PD 02-MAY-2002.
XX
PF 24-OCT-2001; 2001WO-US45468.
XX
PR 24-OCT-2000; 2000US-242838P.
PR 23-OCT-2001; 2001US-0032717.
XX
XX (DUPO) DU PONT DE NEMOURS & CO E I.
XX
XX Abad AR, Duck NB, Feng X, Flannagan RD, Kahn TW, Sims LE;
PI WPI; 2002-519178/55.
XX N-PSDB; ABK87256.
DR
XX
XX New isolated pesticidal polypeptide useful for impacting insect pest
PT e.g. Colorado potato beetle
PT
XX
XX Claim 23; Page 162-164; 176pp; English.
XX
XX The present invention relates to a new pesticidal polypeptide. The
CC invention is useful for impacting an insect pest by applying the
CC the molecules of the invention to the environment of the insect pest by
CC spraying, dusting, broadcating, or seed coating, where the insect pest
CC is selected from Colorado potato beetle, western corn rootworm or
CC southern corn rootworm. The invention is also useful for increasing
CC insect target range and for producing transgenic microorganisms and
CC plants that express the pesticidal polypeptide. The invention is also
CC useful for producing transformed plants and in transforming any organism
CC to produce the pesticidal polypeptide of the invention. the present
CC amino acid sequence represents a Bacillus thuringiensis mutant Cry1218
CC endotoxin protein.
XX
SQ Sequence 673 AA;

Query Match 55.3%; Score 3499; DB 23; Length 673;
Best Local Similarity 99.4%; Pred. No. 2.3e-226;
Matches 669; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 MSPNNQNEVEIIDATPSTSVNSDNRYPFANEPTNALQNDYKDYLMKAGNASEYPPGSP 60
DB 1 MSPNNQNEVEIIDATPSTSVNSDNRYPFANEPTNALQNDYKDYLMKAGNASEYPPGSP 60
QY 61 EVLVSGQDAKAAIDIVGKLLSGLVGPPVGVPIVSLYTLQIDILWPSGKSWEIFMEQVE 120
DB 61 EVLVSGQDAKAAIDIVGKLLSGLVGPPVGVPIVSLYTLQIDILWPSGKSWEIFMEQVE 120
QY 121 ELINOKIARYARNKALSEGLEGNQYLYLTALKEEENP-----NGSRALRDVRNRFELL 176
DB 121 ELINOKIARYARNKALSEGLEGNQYLYLTALKEEENPRLMSNGSRALRDVRNRFELL 180
QY 177 DSLFTQYMPSPRVTFNFEVFLTYAAMAHLHLLKLDASIFGEWGWSTTTINNYDROM 236
DB 181 DSLFTQYMPSPRVTFNFEVFLTYAAMAHLHLLKLDASIFGEWGWSTTTINNYDROM 240
QY 237 KLTAESYDHCVKWYETGLAKGTSAKQWVDYNOFREMFTLAVLDVVALFPNYDTRTYPM 296
DB 237 KLTAESYDHCVKWYETGLAKGTSAKQWVDYNOFREMFTLAVLDVVALFPNYDTRTYPM 296

DB 241 KLTAESYDHCVKWYETGLAKGTSAKQWVDYNOFREMFTLAVLDVVALFPNYDTRTYPM 300
QY 297 ETKAQLTREVTTDPLGAVNVSSIGSWYDKAPSGFVIESVIRPPHVPDYITGLTVYTQSR 356
DB 301 ETKAQLTREVTTDPLGAVNVSSIGSWYDKAPSGFVIESVIRPPHVPDYITGLTVYTQSR 360
QY 357 SISSARYIRHWAGHQISYHRVSRGSLQOQMYGTGNQNLHSTSTFTDFTNYDIYKTLSDAVL 416
DB 361 SISSARYIRHWAGHQISYHRVSRGSLQOQMYGTGNQNLHSTSTFTDFTNYDIYKTLSDAVL 420
QY 417 LDIVYPGTYIIFPGMEPEVFPFVWNLNTRKTLKPNVSKDIIASTRSELELPETSQ 476
DB 421 LDIVYPGTYIIFPGMEPEVFPFVWNLNTRKTLKPNVSKDIIASTRSELELPETSQ 480
QY 477 PNYESYSHRLCHITSIPTAGNTTGLVPVFSWTHRSADLNNTIYSDKITQIPAVKCDNLP 536
DB 481 PNYESYSHRLCHITSIPTAGNTTGLVPVFSWTHRSADLNNTIYSDKITQIPAVKCDNLP 540
QY 537 FVPVVKPGHTGGDLLOYNRSTGVTGLFARYGLALEKAGKYRVLRYATDADIVLHVN 596
DB 541 FVPVVKPGHTGGDLLOYNRSTGVTGLFARYGLALEKAGKYRVLRYATDADIVLHVN 600
QY 597 DAQIOMPKTMPPGEDLTSTKPKVADAITTLNLTATDSSSLAKHNLGDEPNSTLSGIVYVDR 656
DB 601 DAQIOMPKTMPPGEDLTSTKPKVADAITTLNLTATDSSSLAKHNLGDEPNSTLSGIVYVDR 660
QY 657 IEFIPVDETYEAE 669
DB 661 IEFIPVDETYEAE 673

Search completed: January 7, 2003, 05:13:49
Job time : 75 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 05:12:43 ; Search time 26 Seconds
(without alignments)
1364.771 Million cell updates/sec

Title: US-10-032-717-2

Perfect score: 6332

Sequence: 1 MSPNNQNEYIIDPTSTV.....MSETEGTFYIESVELIYDVE 1206

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4959.5	78.3	1169	1	US-08-315-468-4
2	3950.5	62.4	1157	1	US-07-876-280-30
3	3950.5	62.4	1157	1	US-07-812-180A-2
4	3950.5	62.4	1157	1	US-08-315-468-2
5	3950.5	62.4	1157	4	US-07-941-650A-2
6	3021	47.7	1149	1	US-07-915-203-2
7	3021	47.7	1149	1	US-08-272-887-2
8	3021	47.7	1149	2	US-08-789-449-2
9	2595.5	41.0	1157	2	US-08-532-547-5
10	2595.5	41.0	1157	2	US-08-379-656B-5
11	2595.5	41.0	1157	3	US-08-455-838-5
12	2595.5	41.0	1157	4	US-09-013-809-5
13	2595.5	41.0	1157	4	US-09-471-177-5
14	2590	40.9	1156	4	US-09-002-285-72
15	2558.5	40.4	1169	1	US-08-542-921-2
16	2558.5	40.4	1169	2	US-08-880-685-2
17	2558.5	40.4	1169	2	US-08-880-684-2
18	2449	38.7	1150	4	US-09-002-285-74
19	2419.5	38.2	1134	4	US-09-002-285-76
20	2397	37.9	1138	1	US-07-973-320-2
21	2391.5	37.8	1229	1	US-08-100-709-4
22	2391.5	37.8	1229	1	US-08-176-865-4
23	2391.5	37.8	1229	1	US-08-474-038-4
24	2391.5	37.8	1229	2	US-08-779-046-4
25	2391.5	37.8	1229	2	US-08-881-340-4
26	2380	37.6	1138	1	US-07-973-320-4
27	2353.5	37.2	1227	1	US-08-448-170-8

Sequence 9, Appli
Sequence 23, Appli
Sequence 2, Appli
Sequence 7, Appli
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Sequence 7, Appli
Sequence 7, Appli
Sequence 8, Appli
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Sequence 2, Appli
Patent No. 5188960
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-08-315-468-4
; Sequence 4, Application US/08315468
; Patent No. 5554534
; GENERAL INFORMATION:
; APPLICANT: Michaels, Tracy Ellis
; APPLICANT: Focerrada, Luis
; TITLE OF INVENTION: Process for Controlling Scarab Pests
; TITLE OF INVENTION: with Bacillus thuringiensis Isolates
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/315,468
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/014,941
; FILING DATE: 01 FEB 1993
; APPLICATION NUMBER: 07/828,430
; FILING DATE: 30-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/808,316
; FILING DATE: 16-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA73.C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1169 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES

ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bacillus thuringiensis
STRAIN: kumamotoensis
INDIVIDUAL ISOLATE: 50C
IMMEDIATE SOURCE:
LIBRARY: LambdaGEM-11 library of L. Poncerra
CLONE: 50C (b)
US-08-315-468-4

Query Match 78.3%; Score 4959.5; DB 1; Length 1169;
Best Local Similarity 79.8%; Pred. No. 0;
Matches 967; Conservative 68; Mismatches 128; Indels 49; Gaps 8;

QY 1 MSPNNQNEVEIIDATPSTVSNDNSNRYPPANEPTNALQNDYKDYDKMAGNASVPGSP 60
DB 1 MSPNNQNEVEIIDATPSTVSNDNSNRYPPANEPTNALQNDYKDYDKMAGNASVPGSP 60
QY 61 EYLVSGQDAKAAIDIVGKLLSGVFPVGPVIVSLYQLIDILWPSEKSKQWEIFMEQVE 120
DB 61 EYLVSEQDAKAAIDIVGKLLSGVFPVGPVIVSLYQLIDILWPSEKSKQWEIFMEQVE 120
QY 121 ELINOKIABYARNKALSELEGLGNNYQLYLTALHEEHPNGSRALRDVNRFEILDSLF 180
DB 121 ELINOKIABYARNKALSELEGLGNNYQLYLTALHEEHPNGSRALRDVNRFEILDSLF 180
QY 181 TOYMPSEFRVTNEFVPELTVYMAANLHLLLDKASIFGEWGWSTTTINNYDROMKLT 240
DB 181 TOYMPSEFRVTNEFVPELTVYMAANLHLLLDKASIFGEWGLSTTTINNYDROMKLT 240
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DB 301 QUTREVYTDPLGANNVSSIGSWYDKAPSGVIESSVIRPHVFDYITGLTYTQSRISGS 360
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DB 361 ARYIRHWAGHOISYHRVSRGSLNQMGYTNONLHSTDFNTYDLYKTLKSDAVLLDIV 420
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DB 421 YPGYTYIFFGMPPEVFMVNLNRTKLKYNPVSXIIASTRDSSELEPPETSDQPNYE 480
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DB 481 SYSHRLCHITSPATGNTGLVPVFSWTHRSADLNNTIYSDKTIQTPAVKWCNDLFPVPV 540
QY 541 VKPGCHTGGDLQYNRSTGSGVTLFLARYGLALEKAGYVRVRYATDADIVLHV---N 596
DB 541 VKPGCHTGGDLQYNRSTGSGVTLFLARYGLALEKAGYVRVRYATDADIVLHV---N 596
QY 597 DAQIQMPT-MNPG-ELTSKTFKVDALITLNLATDSSLAKHNLGDPNLSIGIVYV 654
DB 597 DAQIQMPT-MNPG-ELTSKTFKVDALITLNLATDSSLAKHNLGDPNLSIGIVYV 654
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DB 655 DRIEIPVDTEAEQDLBAKAVNALFTNKGRLPGVTDYEVNQANLVECLSDLLY 714
QY 715 PNEKRLFPDFAVEAKLSEARNLQDPDQOEINGENGWSTASTGIEVEGDALPKGYRL 774
DB 715 PNEKRLFPDFAVEAKLSEARNLQDPDQOEINGENGWSTASTGIEVEGDALPKGYRL 774
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DB 775 PGAREIDTETPTLYLQKVEEGLKPYTRYLRGFGVSSQGLEIFIRHQTNRIVKNVPD 834
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DB 895 FKITDPEGYATLGNLELVEEGPLSGDALERLQREEQWKIOMTRREETDRYMASKOAV 949
QY 955 DRLYADYQDQQLNPVDITDLTAAQDLIQSIPIYVYNMPPPEIPGMNYTKFTLTDLRLOA 1014
DB 955 DRLYADYQDQQLNPVDITDLTAAQDLIQSIPIYVYNMPPPEIPGMNYTKFTLTDLRLOA 1009
QY 1015 WSLYDORNAIENGDFRNLGNLNNATPGVEVQOINHTSVLVIENWDEQVSOQFTVQBNORY 1074
DB 1015 WSLYDORNAIENGDFRNLGNLNNATPGVEVQOINHTSVLVIENWDEQVSOQFTVQBNORY 1069
QY 1075 VLRTARKEGVNGVSVIRDDGNGQETETLTFSSASDYDTNGMYNTQVSNNGYNTNAYNTQ 1134
DB 1075 VLRTARKEGVNGVSVIRDDGNGQETETLTFSSASDYDTNGMYNTQVSNNGYNTNAYNTQ 1108
QY 1135 ASSTNGYNNANNMYNTQASNTNGYNTNSVNDQGTGTYTKTVPYPTDQMWIEMSETEGTF 1194
DB 1135 ASSTNGYNNANNMYNTQASNTNGYNTNSVNDQGTGTYTKTVPYPTDQMWIEMSETEGTF 1157
QY 1195 YIESVELIVDVE 1206
DB 1195 YIESVELIVDVE 1169
RESULT 2
US-07-876-280-30
; Sequence 30, Application US/07876280
; Patent No. 5262158
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel M.
; APPLICANT: Cannon, Raymond J.C.
; APPLICANT: Bagley, Angela L.
; TITLE OF INVENTION: No. 5262158el Bacillus thuringiensis Isolates for
; TITLE OF INVENTION: Controlling Acarides
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/876,280
; FILING DATE: 19920430
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: M/S 104
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1157 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; STRAIN: kumamotoensis
; INDIVIDUAL ISOLATE: PS50C

IMMEDIATE SOURCE:
CLONE: E. coli NM522(pMYC2320) NRRL B-18769
US-07-876-280-30

Query Match 62.4%; Score 3950.5; DB 1; Length 1157;
Best Local Similarity 65.5%; Pred. No. 5.9e-284;
Matches 804; Conservative 120; Mismatches 211; Indels 93; Gaps 19;

QY 1 MSPNNQNEYIIDATPSTSVNSDNRPPANEPTNALQNDMDYDYLKMSAGNASYPCSP 60
DB 1 MSPNNQNEYIIDATPSTSVNSDNRPPANEPTDALQNNYKDYLYKMSGGENFELGNP 60
QY 61 EVLVSGDAKAAIDIVGKLSGLGVFPVGVIVSLYTLQIDILWPSGEKSQWEIPEQVE 120
DB 61 ETEPIS-SSTIQTGIGIVGRILGALGVFPASQIASFYFIVGQWLPFSKVDIWIEMERVE 119
QY 121 ELINOKIAYARNKALSELGELGNQYQLYLTALZEWENPNGLRDVRNRPFILOSFP 180
DB 120 ELVDQKIEKYVKOKALAEKGLGNALDVYQOQSLDLENRNDARTSRVSVNQFALDLNF 179
QY 181 TQMPSPRVNTNFVFPFLTVYVMAANLHLIKDASIFGEHMGWSTTTNNYDROMKLT 240
DB 180 VSSIPSPAVSGHEVLLAVYAQVNLHLLLRDASIFGEHMGWSTTTNNYDROMKLT 239
QY 241 EYSDHCYKWTETGLAKLGTSAKQWQVNDYQPREMTLAVLDVVALFPNYDTRTYPMETKA 300
DB 240 EYSDCYKWKYKIGLDKLGTSKSLWNLTHQPREMTLLVLDLVALFPNYDTHMPTIETTA 299
QY 301 QLRVYVTDPLGAVNVSSIGSWDKARSPGV-----ISSVIRPHVFDYITGLTYTQSR 356
DB 300 QLRVYVTDPLGAVNVSSIGSWDKARSPGV-----ISSVIRPHVFDYITGLTYTQSR 356
QY 357 -SISARVIRHWAGHOISYHRSRSGNLQOMGTQNLHSTSTFDPTNYDIVKTLSD 413
DB 357 -SISARVIRHWAGHOISYHRSRSGNLQOMGTQNLHSTSTFDPTNYDIVKTLSD 413
QY 359 GGITLNDAINVSGHTLKYRRTA-DSTVYTYANYGRITSEKSPALEDRDIFEINSTV 417
DB 359 GGITLNDAINVSGHTLKYRRTA-DSTVYTYANYGRITSEKSPALEDRDIFEINSTV 417
QY 414 AVLDDIVPGYTIYIFGMEVEFFVMVQNLNTRKLYNPVSKDIIASTR--DSELELPP 471
DB 414 AVLDDIVPGYTIYIFGMEVEFFVMVQNLNTRKLYNPVSKDIIASTR--DSELELPP 471
QY 472 ETSQDPNYESYSHRLCHITSPATGNVT---GLVPVSWTHRSADLNTIYSDKITQIPA 528
DB 472 ETSQDPNYESYSHRLCHITSPATGNVT---GLVPVSWTHRSADLNTIYSDKITQIPA 528
QY 473 DRT-VPVAESYSHRLSHITSHSPKNGSAYGSPFVFWTHTSADLNTIYSDKITQIPA 531
DB 473 DRT-VPVAESYSHRLSHITSHSPKNGSAYGSPFVFWTHTSADLNTIYSDKITQIPA 531
QY 529 VKCWDNLPEV--PVVKGPHGTGDLLOYNRSTGVTGLFLARYGLALEKAGKYRVLRYA 586
DB 529 VKCWDNLPEV--PVVKGPHGTGDLLOYNRSTGVTGLFLARYGLALEKAGKYRVLRYA 586
QY 532 VK--GDMILGGSVVQPGFTGGDLK--RTNPSILGTFAVTVNGSLSQ--RYRVRIRYA 585
DB 532 VK--GDMILGGSVVQPGFTGGDLK--RTNPSILGTFAVTVNGSLSQ--RYRVRIRYA 585
QY 587 --TDADIVLHVND--QIQPKTNWPGEDLTSKTFKVADAITLNL-ATDSSLAK--H 638
DB 587 --TDADIVLHVND--QIQPKTNWPGEDLTSKTFKVADAITLNL-ATDSSLAK--H 638
QY 586 STTDFEFTLYLGDITKRNPNKMDNGASLYTETFKPASFTDPQRETQDKILLSMGDF 645
DB 586 STTDFEFTLYLGDITKRNPNKMDNGASLYTETFKPASFTDPQRETQDKILLSMGDF 645
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DB 639 NLGSDPNSTLSGIVYVDRIEPIVDTEYAEODLEAKKAVNALFTNTKQGLRPGVTDYE 698
QY 646 SSGOE-----VYIDRIEPIVDTEYAEODLEAKKAVNALFTNTKQGLRPGVTDYE 697
DB 646 SSGOE-----VYIDRIEPIVDTEYAEODLEAKKAVNALFTNTKQGLRPGVTDYE 697
QY 699 VNOANLVECLSDLLYNEKELLFVAREKXLSSEARNLQDDPQFQINGENGWASTGI 758
DB 699 VNOANLVECLSDLLYNEKELLFVAREKXLSSEARNLQDDPQFQINGENGWASTGI 757
QY 759 EVIEGDALFKGRYLRLPGAREIDTETTYLYQKVEGVLPYTRYLRGFGVSSQGLEI 818
DB 759 EVIEGDALFKGRYLRLPGAREIDTETTYLYQKVEGVLPYTRYLRGFGVSSQGLEI 817
QY 819 FTIRHQRNRIKVNVPDILLPVSPVNSDGSINRCSQKYVNSRLRLEVENRSGEAHEFSLPI 878
DB 819 FTIRHQRNRIKVNVPDILLPVSPVNSDGSINRCSQKYVNSRLRLEVENRSGEAHEFSLPI 877
QY 879 DTGEBIDNENAGIIVGFKITDPEGVATLGNLEVEEGLSGDALERLQRESQWKKIOWTR 938
DB 879 DTGEBIDNENAGIIVGFKITDPEGVATLGNLEVEEGLSGDALERLQRESQWKKIOWTR 937
QY 939 RREEDRRYMASQAVDRLYADYQDQQLNPDVEITDLTAAQDLIQSIPIVYVNMFPPEIPG 998
DB 939 RREEDRRYMASQAVDRLYADYQDQQLNPDVEITDLTAAQDLIQSIPIVYVNMFPPEIPG 998

DB 938 RREEDRRYMASQAVDRLYADYQDQQLNPDVEITDLTAAQDLIQSIPIVYVNMFPPEIPG 997
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DB 998 MNYTKFTLDRQQAWSLYDORNAIPNGDFRNLGSNNWNPATPGVEVQOINHSTSVLVI PNW 1057
QY 1059 DEQVSQOFTVQPNQRVYLRVYRTARKEGVNGYVSGIRGNGNOTETLTFSASDYDTNGMYNTQ 1118
DB 1058 DEQVSQOFTVQPNQRVYLRVYRTARKEGVNGYVSGIRGNGNOTETLTFSASDYDTNGMYNTQ 1112
QY 1119 VSNVNGYNTNNAYNQASSTNGYNANNMYNTQASNTNGYNTNSVYNDQTYITKTVTFIP 1178
DB 1113 -VYNDQTYITKTVTFIP 1129
QY 1179 YTDMMIEMSETEGTFYIESVELIVDVE 1206
DB 1130 YTDMMIEMSETEGTFYIESVELIVDVE 1157
RESULT 3
US-07-812-180A-2
; Sequence 2, Application US/07812180A
; Patent No. 5366892
; GENERAL INFORMATION:
; APPLICANT: Foncerrada, Luis R
; APPLICANT: Payne, Jewel M
; APPLICANT: Sick, August J
; TITLE OF INVENTION: No. 5366892el Coleopteran-Active Bacillus
; TITLE OF INVENTION: thuringiensis Isolate and a No. 5366892el Gene Encoding a
; TITLE OF INVENTION: Coleopteran-Active Toxin
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Roman Saliwanchik
; STREET: 2421 N.W. 41st Street, Ste A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/812,180A
; FILING DATE: 19920102
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, Roman
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1157 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; STRAIN: Kumamotoensis
; INDIVIDUAL ISOLATE: PS50C
; IMMEDIATE SOURCE:
; LIBRARY: Lambdagem (TM) - 11 LIBRARY OF LUIS
; LIBRARY: FONCERRADA
; CLONE: 50C
; US-07-812-180A-2
Query Match 62.4%; Score 3950.5; DB 1; Length 1157;

Best Local Similarity 65.5%; Pred. No. 5.9e-284;
Matches 804; Conservative 120; Mismatches 211; Indels 93; Gaps 19;

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QY 1 MSNNQNEYIIDATPSTSVNSNRPPEANEPTNALQNDYDYLKMSAGNASEYGPSP 60
Db 1 MSNNQNEYIIDATPSTSVNSNRPPEANEPTDALQNNYKDYDKMSGGENPELFGNP 60
QY 61 EVLVSGDAAKAAIDIVGKLLSGLVGFVGVIVSLYQLDILWPSGKSEWEIFMEQVE 120
Db 61 ETIS--SSTQTGIGIVRGILGALGVFAQIASFYFIVQLWPSKSVDLWIMERVE 119
QY 121 ELINQKIARYARKALSELGELGNNYOLYLTALREWENPNGSALRDVNRPIILDSLF 180
Db 120 ELVDQKIEKYVKAKALAEKGLGNALDVIYQOSLELDWLENRDARTSRVSNQFALDLNF 179
QY 181 TOYMSPRVNTFVFPFLTVVYMAANLHLLKLDASIFGEWGWSTTTNNYDROMKLT 240
Db 180 VSSIPFAVSGHEVLLLAVALAQAQVNLHLLLRDASIFGEWGFPGELISRPYNQVOLT 239
QY 241 EYSDHCYKVTETGLAKLGTSAKOWVDYNQPRREMTLAVLDVVALFPNYDTRTYPMETKA 300
Db 240 EYSDYCVKWKIGLKLGTSTKSWLNHQPRREMTLLVLDLVALFPNYDTHMYPITTA 299
QY 301 QLTREVYTDPLGAVNVSIGSWDKAPSGV-----IBSSVIRPHVFDYIYGLTVYTOSR 356
Db 300 QLTREDVYTDPIAFNIVTSTGFCNPWSTHSGILFYEVENNVRPPHLLFDILSSVEINT-SR 358
QY 357 ---SISARVIRHWAGHQSIVHRVSRGSNLQOMYGTQNLHSTSTFDPYNDIYKTLSD 413
Db 359 GGITLNDAYINWSGHTLYKRRTA-DSTVTYTYANYGRITSEKNSPALEDRIFEINSTV 417
QY 414 AVLLDIVVPGYTYIFFGMEPEVEFFMVLQNLNTRKTLKPNVSKDIIAISTR--DSELELPP 471
Db 418 ANLANYQKAY-----GVPGSWFHWVRGTSSTYALYSKTHLTALQCTQVYESDRIPL 472
QY 472 ETSQPNYESYSHRLCHITSIPATGNTT---GLVPVFSWTHRSADLNNITYSDKITQIPA 528
Db 473 DRT--VPAESYSHRLSHITSFSKNGSAYYSGFPFVWTHTSADLNNITYSDKITQIPA 531
QY 529 VKCWDNLFPV--PVVKGPGHTGGDLLQYNRSTGSGVGLFLARYGLALEKAGKYRURYA 586
Db 532 VK--GDMLYLGGSVVQPGFTGGDILK--RTNPSILGTFAVTVNGSLSQ--RYRVRIRYA 585
QY 587 --TDADIVLHVND--OIQPKTNPGEDITSKTFKVADAITLNL-ATDSSLALK--H 638
Db 586 STTDFEFTLVGLDTIEKNRKNKNDNGASLYTFYFKFASFTDQFRETQDKILLSWGDP 645
QY 639 NLGEDPNSTLSGIYVVDRIEPIVDETYEAEQDLEAAKAVNALFTNTKGLRPGVTDYE 698
Db 646 SSGQE-----VYIDRIEPIVDETYEAEQDLEAAKAVNALFTNTKGLRPGVTDYE 697
QY 699 VNQAANLVECLSDDLYPNEKELLFDVAREAKRLSEARNLLQDPDFQINGENGHTASTGI 758
Db 698 VNQAANLVECLSDDLYPNEKELLFDVAREAKRLSGARNLLQDPDFQINGENGWAASTGI 757
QY 759 EVLEGDALFKGRYLRLRGAREIDTETPTLYQKVEEGLKPYTRYLRGPFVSGSQGLEI 818
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Db 878 DIGELDYNENAGIIVWPKITDPEGATLGNLELVEEGLSGDALERLQREQQWKIOWTR 937
QY 939 RREEDRRYKASKAVDRLYADYQDQQLNPDEITDLTAAQDLQSIPIVYNEMFPEIPG 998
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Db 1058 DEQVSOQFTVQPNQVRVLRVTARKEGVGNGYVIRDGGQOSETLTFASDYDNG----- 1112
QY 1119 VSTNGYNTNNAYNTOASSTNGYNNANMYNTQASNTNGYNTNTNSVYNDQGTGYIKTYTFIP 1178
Db 1113 -----VYNDQGTGYIKTYTFIP 1129
QY 1179 YTDQMIEMSETEGTFTYIESVELIVDVE 1206
Db 1130 YTDQMIEMSETEGTFTYIESVELIVDVE 1157
RESULT 4
US-08-315-468-2
; Sequence 2, Application US/08315468
; Patent No. 5554534
; GENERAL INFORMATION:
; APPLICANT: Michaels, Tracy Ellis
; APPLICANT: Foncerrada, Luis
; APPLICANT: Narva, Kenneth E.
; TITLE OF INVENTION: Process for Controlling Scarab Pests
; TITLE OF INVENTION: with Bacillus thuringiensis Isolates
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/315,468
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/014,941
; FILING DATE: 01 FEB 1993
; APPLICATION NUMBER: 07/828,430
; FILING DATE: 30-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/808,316
; FILING DATE: 16-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MAY73.C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1157 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; STRAIN: kumamotoensis
; INDIVIDUAL ISOLATE: PS50C
; IMMEDIATE SOURCE:
; LIBRARY: Landdagem (TM) - 11 LIBRARY OF LUIS FONCERRADA
; CLONE: 50C(a)
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US-08-315-468-2

Query Match 62.4%; Score 3950.5; DB 1; Length 1157;
Best Local Similarity 65.5%; Pred. No. 5.9e-284;
Matches 804; Conservative 120; Mismatches 211; Indels 93; Gaps 19;

QY 1 MSPNNQNEVEIIDATSTSVNSDSNRYPFANEPNALONMDYKDYLOASAGNASEVPGSP 60
DB 1 MSPNNQNEVEIIDATSTSVNSDSNRYPFANEPNALONMDYKDYLOASAGNASEVPGSP 60

QY 61 EVLVSGQDAKAADIDVGLKSLGLGVPFVPIVSLYTLQDILILPSPCKSQWEIFMEOVE 120
DB 61 ETPIIS-SSTIQTGIGVIRILGALGVPFASQIASFYSFIVGLWPSPKSDVIGSEIMERVE 119

QY 121 ELINQIAEYARNKALSELGLGNVYQLYLTALKEEENPENGSRALDRVNRPEILDLSLF 180
DB 120 ELVDQKIEKIVKDKALAEKGLGNALDVYQOSLEDMLENRDARTSVSVNQFALDLP 179

QY 181 TQYMPFRVTVNFVFTVYVYMAANLHLLKODASIFGBGWSMTTNNYIDRQMKLTA 240
DB 180 VSSIPSPFANSCHVLLAVTAQAANLHLLLRDASIFGBGWSMTTNNYIDRQMKLTA 239

QY 241 EYSDHCWKYETGLAKCTSAKQVVDVNPFRMTLAVLDVVALPNYDTRTYPMETKA 300
DB 240 EYSDYCVKWKYKIGLDKGLTTSKSWLNYHOFREMTLLLDLVALPNYDTHMYPIETTA 299

QY 301 QLTREVYTDPLGAVVSSIGSWYDKAPSGV-IESSVIRPPHVDYITGLTVYQSR 356
DB 300 QLTREVYTDPLGAVVSSIGSWYDKAPSGV-IESSVIRPPHVDYITGLTVYQSR 356

QY 357 ---SISARYIRHWAGHOISYHRVSRGSLQOMYGTGNLHSTSTFPTNYIYKTLISKD 413
DB 356 GGITLNDVAVYWSGHTLYKRTA-DSTVITYTANYGRITSEKNSPALEDKRDPEINSTV 417

QY 414 AVLDIVYPCYTYFFGMPVEFPMVQNLNTRKLNPNVSKDIIASTR--DSELELPP 471
DB 413 ANLANYQKAY-----GVPGSWFHMVRKGTSSITAYLYSKTHALQCGTQVYESSDRIPL 472

QY 472 ETSQDPNYSYSHRLCHITSPATGNTT---GLVPVSWTHRSADLNTIYSDKITQIPA 528
DB 471 DRT-VFVAESYSHRLCHITSHSFKNGSAYYGSPFVFWTHTSADLNTIYSDKITQIPA 531

QY 529 VKCWDNLFPV--PVVKGFGHTGDLQYNRSTSGVGLFLARYGLALEKAGKYRVLRYA 586
DB 528 VK--GDMVLYGSSVVGPGFTGGDILK--RTNPSILGTFVAVNGSLSQ--RYRVRIRYA 585

QY 587 --TDADIVLHVND--QIQMPKTNWPEDELTSTFKVADAITTLNL-ATDSSLAK--H 638
DB 586 STTDFEFTLYLGDITIEKNRPNKNDNGASLTETFKPASFITDFQFRETQDKILLSMGDF 645

QY 639 NLGSDPNSTLSGIVVYDRIEPIVDETYEASQDLEAAKAVNALFTNTKGLRPGVTDYE 698
DB 638 SSGQ8-----VYIRIEPIVDETYEASQDLEAAKAVNALFTNTKGLRPGVTDYE 697

QY 699 VNQAANLVECLSDDLYPNEKELLFPAVREAKRLSEARNLLQDPDFQIEINGENGWASTGI 758
DB 698 VNQAANLVECLSDDLYPNEKELLFPAVREAKRLSEARNLLQDPDFQIEINGENGWASTGI 757

QY 759 EVIEGDALFKGRYLRLPGAREIDTETTYLYQKVEGVLKPYTRYLRGLRFGVSSQGLEI 818
DB 758 EVIEGDALFKGRYLRLPGAREIDTETTYLYQKVEGVLKPYTRYLRGLRFGVSSQGLEI 817

QY 819 FTIRHQTNRIVKNVDPDLDPVSPNDSGSLNRCSEQKYNVSRLEVENRSGEAHEFSPI 878
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DB 878 DIGELDYNENAGIWWGFKITDPEGVATLGNLELVEEGPLSGDALERLQREBQWQKIOMTR 937

QY 939 RREETDRRYMASKQAVDRLYADYQDQQLNPVDEITDLTAAQDLIQSIPIVYVNMPEPIPG 998
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DB 998 MNYTKFTELTLRLOQAWNLVDQRNAIPNGDFRNLGNLNMNATPEVEVQOQNHSTSVLPINW 1057

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DB 1058 DEQVSQOFTVQPNQRYVLRVARTARKEGVGVYVIRGGNQOTETLTFSASDYDTNGMYNTQ 1112

QY 1119 VSNNTGYNNTNNAVNTQASSTNGYNANNMYNTQASNTNGYNTNSVYNDQTYIKTVTFIP 1178
DB 1113 -----VYNDQTYIKTVTFIP 1129

QY 1179 YTDQMIEMSETEGTFYIESVELIVDVE 1206
DB 1130 YTDQMIEMSETEGTFYIESVELIVDVE 1157

RESULT 5
US-07-941-650A-2
; Sequence 2, Application US/07941650A
; Patent No. 6294184
; GENERAL INFORMATION:
; APPLICANT: Uyeda, Kendrick A.
; APPLICANT: Bradfisch, Gregory A.
; TITLE OF INVENTION: Process for Controlling Lepidopteran Pests
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/941,650A
; FILING DATE: 19920908
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/758,020
; FILING DATE: 12-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/658,935
; FILING DATE: 21-FEB-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/642,112
; FILING DATE: 16-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1157 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; STRAIN: kumamotoensis
; INDIVIDUAL ISOLATE: PS50C
; IMMEDIATE SOURCE:
; CLONE: E. coli NM522(pMYC1638), NRRL B-18751

US-07-941-650A-2

Query Match 62.4%; Score 3950.5; DB 4; Length 1157;
Best Local Similarity 65.5%; Pred. No. 5.9e-284;
Matches 804; Conservative 120; Mismatches 211; Indels 93; Gaps 19;

QY 1 MSPNNQNEYEIIDATPSTSVSNDNRYPFANEPTNALQNDYKYLKMSAGNASYPGSP 60
DB 1 MSPNNQNEYEIIDATPSTSVSNDNRYPFANEPTDALQNMNYKYLKMSGGENPELFGNP 60

QY 61 EVLVSGQDAAKAAIDIVCKLISGLGVPFVGIVSYLTQILDLWPSGKSKWEIPMEQVE 120
DB 61 ETVFIS-SSTIQGTGIGVRIIGLIGLGVFASQIATSFYSFIVGQLWPSKSDVINGEIMERVE 119

QY 121 ELINOKIAEYARNKALSLEGLGNNYQLYLTALBEWENPNRSGRALDRVRNFEILDSLF 180
DB 120 ELVDQKTEKYVKDKALAEKLGKGNALDVQQSLEDWLENRDNRTRSVSVNQFIALDLNF 179

QY 181 TQYMPFSRVTFNFPFLFVYAMAANLHLLLLKDAIFGEEWGSTTTINNYDROMKLLTA 240
DB 180 VSSIPSPAVSGHEVLLALLVAYAAVNLHLLLRDASIFGEEWGFTRPGEISRFVNRQVQLTA 239

QY 241 EYSDHCWKYETGLAKLKGTSKQWQDYNQFRREMTLAVLDVVALFPNYDTRTPMETKA 300
DB 240 EYSDYCYKWKYIGLDKKGTTSKWLNHQFRREMTLLVLDLVALFPNYDTHMYPETTA 299

QY 301 QLTREVYTDPLGAVNVSSIGSWYDKAPSGV-IESSVIRPHVFDYITGLTVYTOSR 356
DB 300 QLTREVYTDPLGAVNVSSIGSWYDKAPSGV-IESSVIRPHVFDYITGLTVYTOSR 356

QY 357-SSISSARYIRHWAGHOISYHRSVRSNQQMGYGTNQLNSTSTFTDNYDIYKTLKSD 413
DB 359 GGITLNDAYINYSHTLKYRRTA-DSTVITYTANYGRITSEKNSFALEDREDIPEINSTV 417

QY 414 AVLLDIVYPGYTYLFGFMEPEFPMVQNLNTRKTLKXNPVSKDIIASTR-DSELELPP 471
DB 418 ANLANYQKAY-----GVGFSWFHMKRGTSSTAYLYSKTHTALQGTQVYESSDEIPL 472

QY 472 ETSQPNVYESHRLCHITSIPATGNTT--GLPVFSWTHRSADLNTIYSDKTIQIPA 528
DB 473 DRT-VPVAESYSHRLSHITSHSPKNGSAYYSGPFVFWTHTSADLNTIYSDKTIQIPA 531

QY 529 VKQWNLFPV--PVKPGHGTGDLQVNRSTGVTGLFLARYGLALEKAGKYRVLRYA 586
DB 532 VK--GDMLYLGGSVVQGGFGTGGDLK--RTNPSILGTFFAVTVNGSLQ--RYRVRIRYA 585

QY 587--TDADIVLHUNDA--QIQPKTNPGEDLTSKTFKVADATITNL-ATDSSLAK---H 638
DB 586 STTDFETLYLGDTEKRNFKNTMDNGASLTFTYFKFASFTIDFQFRETQDKILLSMGDF 645

QY 639 NLGEDPNSTLSGIVVDRIBFIPVDETYEABODLEAAKAVNALPTNTKGLRPGVTDYE 698
DB 646 SSGQE-----VYIURIBFIPVDETYEABODLEAAKAVNALPTNTKGLRPGVTDYE 697

QY 699 VQAANLVECLSDLYPNEKRLFDVAREAKRLSEARNLLQDDPQFQINGENGWTAETGI 758
DB 698 VQAANLVECLSDLYPNEKRLFDVAREAKRLSEARNLLQDDPQFQINGENGWTAETGI 757

QY 759 EVLEGDALFKGRYLRLPGAREIDTETPTLYLYQKVEGVLKPYTRYRLRPGVSSQGLEI 818
DB 758 EIVEGDVAFKGRYLRLPGAREIDTETPTLYLYQKVEGVLKPYTRYRLRPGVSSQGLEI 817

QY 819 FTIRHOTNRIVKXNPVDDLDPVSPVNSDGSINRCSEOKYVNSRLEVRNRSCEAHEFSIPI 878
DB 818 YTIHQTNRIKXNPVDDLDPVSPVNSDGSINRCSEOKYVNSRLEVRNRSCEAHEFSIPI 877

QY 879 DTGEIDYNENAGIIVGPKITDPEGYATLGNLELVEEGLSGDALERLQREEQWKKIOMTR 938
DB 878 DIGELDYNENAGIIVGPKITDPEGYATLGNLELVEEGLSGDALERLQREEQWKKIOMTR 937

QY 939 RRETDTRYNASKQAVDRLYADYQDQQLNPDVEITDTLTAADLIQSIPIVYNEMFPPIPG 998
DB 938 RRETDTRYNASKQAVDRLYADYQDQQLNPDVEITDTLTAADLIQSIPIVYNEMFPPIPG 997

QY 999 MNYTKFTELTDLQOANSLYDORNALPNGDFRNLGNLNNATPGVEVQOINHTSVLVIPIW 1058
DB 998 MNYTKFTELTDLQOANSLYDORNALPNGDFRNLGNLNNATPGVEVQOINHTSVLVIPIW 1057

QY 1059 DEQVSQOFTVQPNQRYVLRVTARKEGVNGVYSIRDGNGQOTETILTFASDYDTNGMYNQ 1118
DB 1058 DEQVSQOFTVQPNQRYVLRVTARKEGVNGVYSIRDGNGQOTETILTFASDYDTNGMYNQ 1112

QY 1119 VSTNGYNTNAYNTQASSTNGYNNANMYNTQASNTNGYNTNSVYNDQTYITKVTTFIP 1178
DB 1113 -----VYNDQTYITKVTTFIP 1129

QY 1179 YTDQWMIEMSETEGTFYIESVELIVDVE 1206
DB 1130 YTDQWMIEMSETEGTFYIESVELIVDVE 1157

RESULT 6

US-07-915-203-2
; Sequence 2, Application US/07915203
; Patent No. 5359048
; GENERAL INFORMATION:
; APPLICANT: Ohba, Michio
; APPLICANT: Iwabana, Hidenori
; APPLICANT: Sato, Reichi
; APPLICANT: Suzuki, No. 5359048ukazu
; APPLICANT: Ogiwara, Katsutoshi
; APPLICANT: Sakanaka, Kazunobu
; APPLICANT: Hori, Hidetaki
; APPLICANT: Asano, Shouji
; APPLICANT: Kawasaki, Tadaaki
; TITLE OF INVENTION: No. 5359048el Microorganism and Insecticide
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; APPLICATION NUMBER: US/07/915,203
; FILING DATE: 19920723
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: M/K 301
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1149 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-915-203-2

Query Match 47.7%; Score 3021; DB 1; Length 1149;
Best Local Similarity 50.2%; Pred. No. 4.3e-215;
Matches 623; Conservative 177; Mismatches 295; Indels 146; Gaps 23;

QY 1 MSPNNQNEYEIIDATPSTSVSNDNRYPFANEPTNALQNDYKYLKMSAGNASYPGSP 60
DB 1 MSPNNQNEYEIIDATPSTSVSNDNRYPFANEPTNALQNDYKYLKMSAGNASYPGSP 60

QY 61 EVLVSGQDAKAAIDIVGKLLSGVFPVGVPIVSLYLTQLIDILWPSGKSEOWEIFMEOVE 120
Db 61 GTFISAQDAVGTDIVSTIIISGLGIPVLGEVFSILGSLGLWPSNNENWQIFNRVE 120
QY 121 ELINQKIAEYARNKALSELEGLGNVQLYLTALKEEENPNSGRALRDVNRFEILDSLF 180
Db 121 ELTDQKILDSVRSRAIALANSIAVEYYQNALEDWKRNPSTRSAALVKERFGNAEAIL 180
QY 181 TQMPSPFRVNFVPELTVYAMAAHLHLLKXASIFGEWGHSTTTINNYDROMKLT 240
Db 181 RTNMGFSQNTYPTLPTTPTAQASLHLLVRDQVLYGKEWGPQNDIDLIFYKEQVSYTA 240
QY 241 EYSDHCVKMYETCLAKLKGTSKQWVDYNQPREMTLAVLDVVALFENYDRTYPMETKA 300
Db 241 RYSDHCVQWYNAGLKLKGTSKQWVDYNEFRREMNWVLDVVALFENYDARLYPLETNA 300
QY 301 QLTREYVTPDLGAV---NVSSISGSWD---KAPSGVIESSVIRPPHVPDYITGLTYVT 353
Db 301 ELTREITFDVPGSVYVTCQSSTLISWYDMIPAALPFSFTLE-NLLRKPDFTLLQEIWMYT 359
QY 354 QSRSSISARYIRHWAGHQISYHRVSRGSLNQMYGTNQLHS-----TSTPFTYDIY 407
Db 360 SFRQNGTIIYNYMGQRLT-----LSYTGSSFNKYSGLVLAGAEDIIPVGQNDIY 410
QY 408 KTLSDKAVLLDIVPG-YTVIFPGMEPEVFPVWVNLNTRKTLKYNPVSVDIIASTRDS 466
Db 411 RVV-----WTYIGRYNLSLGVNPVTFP---SNNTQKTVS-RPKQFAGIKTIDSG 458
QY 467 LELPPTSDQPNYESYSHRLCHITS--IPATGNTT-GLVFPVSWTHRSADLNNTIYSDKI 523
Db 459 EELTYE-----NYQSYSHRVSYITSPEIKSTGTGLGVVPIFGWTHSSASRNNFIYATKI 513
QY 524 TQIPAVKC-----WDNLFPV---PVVKGPGHTGDDLQVNRSTGSGVTGLFLARYGL 571
Db 514 SQIPINKASRTSGAVWVNFQGLYNGGVPVKLSG-SGSQVNLRVATDAGKA----- 564
QY 572 ALEKACKYRVLRYATDADIVLHVN-----DAQIOMPKTMPGDELTSKTFKVD 621
Db 565 ----SQRIRIRIYASDRACKFTISSRSPENPATYSIAIYTMSTNASLTSTFAYAE 620
QY 622 AITTLNLTADSS-----LALKHNLGSDPNSTLSGIVVVDRIEPIVDTEYAEQDLEAAK 676
Db 621 S-GPINLIGSGSRTFDSITKEAG-----AANLYIDRIEPIVNTLFEAEEDLDVAK 672
QY 677 KAVNALPTWTKDLRGVTDYVNOANLVCLSDLLYPNEKLLFPANVREAKRLSEARN 736
Db 673 KAVNGLTFTEKDALQTSVTDVQVQAANLIECLSDLELYPNEKRLMDAVKEAKRLVQARN 732
QY 737 LLQDDPQFQINGENGWGTAGTGVIEGDALFKGRYELPGAREIDTETPTLYYQKVEEG 796
Db 733 LLQDTGFRINGENGWGTAGTGVIEGVDVLPKORSLSLTARSIEDTETPTLYYQKIDES 792
QY 797 VLKPYTRYRLRGVSGSQGLEIFTRHQTNRIVKQVDPDILLPVSPVNSDGSINRCSEOK 856
Db 793 LLKPYTRYKLKGISSQDLEIKLIRHANOIVKQVDPDILLPVSPVNSCGVDRCSEQQ 852
QY 857 YNRSLEVENR-----SGBAHFSIPIDTGEIDYNEAGIWWGFKITDPEGATLGNLE 910
Db 853 YVDANLALNENGNGNMSDSHAFPHIDTGEIDLNENTGTIWIIVFKIPTTNGNATLGNLE 912
QY 911 LVZEGPLSGDALRELQBEQOQKIQWTRREEDTDRRYNASKQVADRLYADYQOQLNPDV 970
Db 913 FVEEGPLSGTLEWAQOQOQOQWQVARKRAASEKTYAAKQAIIDLFLADYQOQLNSGV 972
QY 971 EITDLTAADLIOSIPVYNEMPEPIPGMYTKFTLTDLRQOAWSLYDORNALPNDGR 1030
Db 973 EMDLQAQLVQOSIPVYNALPEIPGMYYTSTFETNRLQOAWNLYDQNALPNDGR 1032
QY 1031 NGLSNWATPGVQVQINHTSVLVPNWDEQVQSQOFTVQPNQRYLVRTARKEGVNGYV 1090
Db 1033 NGLSNWATSDVAVQQLSDTSVLVVPWNQSVQSQOFTVQPNRYLVRTARKEGVGDYV 1092
QY 1091 SIRDGNGQETTLTFSASDYDTNGMYNTQVNTNGNTYNTNNAINTQASSTNGYNNANNMTQ 1150

Db 1093 IIRDGANQETLTFNICDDDT-GVLST----- 1118
QY 1151 ASNTNGYNTSNVNDOTGHTITVTPIFYPTDQWMIEMSETE 1191
Db 1119 -----DQTSYITKTVEFTPTSTEQWIDMSETE 1145

RESULT 7

US-08-272-887-2
; Sequence 2, Application US/08272887
; Patent No. 5747450
; GENERAL INFORMATION:
; APPLICANT: Obba, Michio
; APPLICANT: Iwahana, Hidenori
; APPLICANT: Sato, Relichi
; APPLICANT: Suzuki, No. 5747450kazu
; APPLICANT: Ogiwara, Katsutoshi
; APPLICANT: Sakanaka, Kazunobu
; APPLICANT: Hori, Hidetaki
; APPLICANT: Asano, Shouji
; APPLICANT: Kawasugi, Tadaaki
; TITLE OF INVENTION: No. 5747450el Microorganism and Insecticide
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/272,887
; FILING DATE: 08-JUL-1994
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/915,203
; FILING DATE: 23-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: M/K 301
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1149 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-272-887-2

Query Match 47.7%; Score 3021; DB 1; Length 1149;
Best Local Similarity 50.2%; Pred No. 4.3e-215;
Matches 623; Conservative 177; Mismatches 295; Indels 146; Gaps 23;

QY 1 MSPNNQNEYIIDATPSTSVNSDSNRYPPANFTNALQNMKYDYLKMGASNASEYPGSP 60
Db 1 MSPNNQNEYIIDALSPSTSVNSDSNRYPLANDQNTNLQNMKYDYLKMTSTNAELSRNP 60
QY 61 EVLVSGQDAKAAIDIVGKLLSGVFPVGVPIVSLYLTQLIDILWPSGKSEOWEIFMEOVE 120
Db 61 GTFISAQDAVGTDIVSTIIISGLGIPVLGEVFSILGSLGLWPSNNENWQIFNRVE 120
QY 121 ELINQKIAEYARNKALSELEGLGNVQLYLTALKEEENPNSGRALRDVNRFEILDSLF 180
Db 121 ELTDQKILDSVRSRAIALANSIAVEYYQNALEDWKRNPSTRSAALVKERFGNAEAIL 180

QY 181 TOYMPSEFRVTNEVEPPLTVYAMAANLHLLLDKASIFGEGWGSTTTTINNYDQMKLTA 240
DB 181 RTNMGFSFQTNVETPLPTTAAQASLHLVWMDVQVIGKMGFPQNDIDLFEYKEQVSYTA 240
QY 241 EYSDHCWYETGLAKLKTSAQWVDYNOFRREMTLAVLDVVALPPNYDTRTYPMETKA 300
DB 241 RYSDHCWYVWAGNKLKRGTAQWVDYNRFRREMNWVLDLVALPPNYDARIYPLETNA 300
QY 301 QLTREYVTDPLGAV---NVSSIGSWD---KAPSEGVIESSVIRPHVFDYITGLTVVT 353
DB 301 ELTREIFDTPVGSYVYGQSTLISWYDMIPALPSEFSTLE-NLLRKPDEFLLQEIIRMT 359
QY 354 QRSISARYIRHWAGHOISYHVRSGSNLQWYGNQNLHS-----TSTFDFTNYDIY 407
DB 360 SFQNGTIEYNYWGGORUT-----LSYIGSFSFKVGLAGAEIIPVGVNDIY 410
QY 408 KTLSDKAVLLDIVPG-YTYIFPGMEVEBFMVNQLNTRKTLKYNPVSQDIIASTRDSE 466
DB 411 RVV-----WTYIGRYTNSLLGVNPTFYF---SNNTQKTVS-KPKQFAGGKTIIDSG 458
QY 467 LELPETSQPNYESYSHRLCHITS--IPATGNTT-GLVPVFSWTHRSADLNNIYSDKI 523
DB 459 EELTYE-----NYQSYSHRVSIVTSFEIKSTGCTVLGVVPIFGWTHSSASRNNFIYATKI 513
QY 524 TOIPAVKC-----WDNLFPV---PVVKGPHGTGDLLOYNRSTGSGVGLFLARYGL 571
DB 514 SOIPINKASRTSGGAVNWPQELGYNGPWNKLSG-SGSQVINLRVAIDAKGA----- 564
QY 572 ALEKAGKYRVLRYATDADIVLHVN-----DAQIOMPKTMPNGBDLTSKTFKVAD 621
DB 565 ---SORVIRIRYASDRAGKTISSRSPENPATYSASITAYNTWSTNASLTVSTPAYAE 620
QY 622 AITTLNLTADSS-----LAKENLGEDPNSTLSGIYVDRIEFIPVDETYEABQLEAK 676
DB 621 S-SPINLIGSGSRFTDISITKEAG-----AANLYIDRIEFIPVNTLFEABEDLDVAK 672
QY 677 KAVNALFTNTKDLRPGVTDYEVNOAANLVECLSDLYENEXRLLFDVAREAKRLSEARN 736
DB 673 KAVNGLFTNEKDALQTSVDYQVNOANLIECLSDLYENEXRMLMDVAREAKRLVQARN 732
QY 737 LQADPDFOINGEWGTAETGIEVGDALFKGRVYRLFGAREIDTETPTTYLYQKVEEG 796
DB 733 LQADTFGNRNGENGWGTSGTIEVGEVDLFDKDRSLRLTSAREIDTETPTTYLYQKIDBS 792
QY 797 VLKPTRYRLRGVSSQGLEIFTRHONRIVKNVDPDLLDPVSPVNSDGSINRCSEOK 856
DB 793 LLKPYTRYKLGFIGSSQDLKLEIKLIRHRANQIVKNVDPNLLPDVRPVNSCGGVDRCSQO 852
QY 857 YVNSRLEVENR-----SGEAHEFSIPIDTGRIDYNNENAGIIVGPKITDPEGVATLGNLE 910
DB 853 YVDANLALNNGENGMSSDSHAFSHIDTGEIDNENTGIWIFKIPPTNGATLGNLE 912
QY 911 LVEEGLSGDALERLQREBQWKIOWTRREEDTDRRYMASKQAVDRLVADYQDQQLNPNV 970
DB 913 FVEEGLSGTLEWAQQSQQWQDKWARKAASEKTYAAKQAIQDLFPADYQDQQLNSGV 972
QY 971 EITDLTAQADLIQSPYVYNEMPEIPGMNYTKFTLTDRLQOANSLYDQRNAIENGDP 1030
DB 973 EMSDLLAAQNLVQSPYVYNNDALPEIPGMNYTSFTLTDRLQOANSLYDQNAIENGDP 1032
QY 1031 NGLSNWNTTPGVEVQOINHVSVLVLPNWDQVQSQPTVQPNORYLVRVTRKEGVNGVY 1090
DB 1033 NGLSNWNTSDVNVQOLSDTSVLVLPNWNQSQPTVQPNORYLVRVTRKEGVNGVY 1092
QY 1091 SIRDCGNQTEITLTFGASDYDNGMYNTQVSNNTNGYNNAYNTQASSTNGYNNANMYNQ 1150
DB 1093 IIRDCANQTEITLTFNICDDDT-GVLST----- 1118
QY 1151 ASNTNGYNTSNVNDQGTGIVTITVTFTPIVTDQWIMSETE 1191
DB 1119 -----DQTSYITKTVEFTPTSEQWIDMSETE 1145

RESULT 8
US-08-789-449-2
; Sequence 2, Application US/08789449
; Patent No. 5824878
; GENERAL INFORMATION:
; APPLICANT: Ohba, Michio
; APPLICANT: Iwahana, Hidenori
; APPLICANT: Sato, Reichi
; APPLICANT: Suzuki, No. 5824878kukazu
; APPLICANT: Ogiwara, Katsutoshi
; APPLICANT: Sakanaka, Kazunobu
; APPLICANT: Hori, Hidetaki
; APPLICANT: Asano, Shouji
; APPLICANT: Kawasugi, Tadaaki
; TITLE OF INVENTION: No. 5824878el Microorganism and Insecticide
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/789,449
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,887
; FILING DATE: 08-JUL-1994
; APPLICATION NUMBER: US 07/915,203
; FILING DATE: 23-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: M/K 301
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1149 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-789-449-2

Query Match 47.7%; Score 3021; DB 2; Length 1149;
Best Local Similarity 50.2%; Pred No. 4.3e-215;
Matches 623; Conservative 177; Mismatches 295; Indels 146; Gaps 23;

QY 1 MSPNNQNEYIIDAIPSTSVSDNSNRYPFANEPTNALQNMDDYKDYKMSAGNASEYPCGP 60
DB 1 MSPNNQNEYIIDAIPSTSVSDNSIRYPLANDQNTLQNNMYKDYKMTSTNAELSRNP 60
QY 61 EVLVSGDAAKAAADIYKLLSGLVGPVGVIVSLYQLIDILWPSGKSWEIFMEQVE 120
DB 61 GTFISAQDAVGTGIDIVSTIIISGLGIPVLGEVFSILGILLWPSNNENYMQIFMNRVE 120
QY 121 ELINQKIAEYARNKALGEGLGNMYQLYLTALBEWENPNNGSRALRDVRNRFELDSL 180
DB 121 ELIDQKILDSVRSRAIDLANSRIAIFYQVQALDWRKNPHSTSAALVKERFGNAEIL 180
QY 181 TOYMPSEFRVTNEVEPPLTVYAMAANLHLLLDKASIFGEGWGSTTTTINNYDQMKLTA 240
DB 181 RTNMGFSFQTNVETPLPTTAAQASLHLVWMDVQVIGKMGFPQNDIDLFEYKEQVSYTA 240

QY 241 EYSDHCWKVETGLAKLGTSAKQWVDYNOFRBMTLAVLDVVALFPNYDTRTPMETKA 300
Db 241 RYSDHCQWYNAGLNLKRGYGAQWVDYNOFRBMTLAVLDVVALFPNYDTRTPMETKA 300
QY 301 QLTREVTDPGLGAV---NVSGISGWYD---KAPSGVGVSSVIRPPHVPDYITGLVYIT 353
Db 301 ELTREIFTPGVSVYVQSTLSWYDMIPAALPSFTLE-NLLKDPDPFTLQEIEMYT 359
QY 354 QSRSSISARYIRHWAGHOISYHRVSRGSLNQMYGTGNTQNLHS-----TSTPDPFTNYDIY 407
Db 360 SPQNGTIEYNNYWGQRLT-----LSYIYGSFKNYSVGLAGAEIDIIPVGQNDIY 410
QY 408 KTLKSDAVLLDIYVPG-YTIFPGMPVEYFPMVQNLNTRKILKYNPVSKDIITASTRDSZ 466
Db 411 RVV-----WTYIGRYTNSLLGVNPTVYF---SNNOKTYS-KPKQFAGGKITIDSG 458
QY 467 LELPPTSDQPNYESYSHRLCHITS--IPATGNTT-GLVPFSTWTHESADLNNTIYSDKI 523
Db 459 EELTYE-----NQSYSHRYSYITSEIKSTGGTVLGVVPIFGWTHSSASRNNFIYATKI 513
QY 524 TQIPAVKC-----WDNLFPV---PVVKGPGHGTGDLLOYNRSTGSGVTGLFLARYGL 571
Db 514 SQIPINKASRTSGAVNFOELNGYGVKDLG-SGSQVNLNVAIDAKA-----564
QY 572 ALEKAGYRVLRYATDADIVLHVN-----DAQIQMKTNPGEIDLTSKTFKVAD 621
Db 565 ---SQYRIRIRYASDRAGKFTISSRPNPATYTSASIAVTNTMTNAGLTYSTPAYAE 620
QY 622 AITLNLATDSS-----LALKHNLGEPDNSTLSGIYVDRIEFTPVDEYAEQDLBAK 676
Db 621 S-SPINIGISGSRTPDISITKEAG-----AANLYIDRIEFIPVNTLFEAEEDLDVAK 672
QY 677 KAVNALFTNTKQRLPGVTDYEVNQAANLVECLSDDLVPNEKRLLDFAVREAKRLSBARN 736
Db 673 KAVNGLFTNEKDALQTSVTDYQVNAANLIECLSDDELVPNEKRLMDFAVREAKRLVARN 732
QY 737 LQDPDFQENGNGWTAETGIEVIGDALPKGYRLPGAREIDTETPTLYLYQKVEEG 796
Db 733 LQDTGPNRNGNGWGTGTGIEVVEGDLVFKDRSLRLTSAREIDTETPTLYLYQKIDES 792
QY 797 VLKPYTRYLRGLGVSSQGLEIFIRHQTRIVKGVDPDDLDPVYSPNSDGSINRCSEOK 856
Db 793 LKPYTRYRLKLGFTGSSQDLLEIKLIRHRANQIVKXVPDNLDPVYSPNSCGVDRCSQEQ 852
QY 857 YVNSRLVEVNR-----SGRAHEPSIPTDGTGEIDYVNEAGIUVGFKITDPEGYATLGNLE 910
Db 853 YVDANLANENNGNNGNSSDSHAFSHFIDTGEIDLNENTGIWIFKIPTTNGNATLGNLE 912
QY 911 LVBEGLSGDALRLQREEQWQKIQTMRREBETDRRYMASQAQVDRLYADYQDQQLNPDV 970
Db 913 FVEEGPLSGETLEWAQQEQWQDMKRAAASEKTYAAQAIDRLFADYQDQQLNPGV 972
QY 971 EITDLTAQDLIQSIPIVYNNEMPEIPGMNTYKFTETLDRLOQAWSLYDORNAIPNGDPR 1030
Db 973 EMSDLAQAQNLVQSIPIVYNDALPEIPGMNTYKFTETLDRLOQAWNLVYDQNALPNGDPR 1032
QY 1031 NGLSNWATPEVYVQOINHTSVLVI PNWDEQVSOQTPQPNQRYLRTARKEGVGVY 1090
Db 1033 NGLSNWATSDVNYQQLSDTSVLVIPNWSQVSOQTPQPNRYLRTARKEGVGVY 1092
QY 1091 SIRDGNQOTELTFSASDYDNGMYNTQVSNNGYNTNNAVNTQASSTNGYNNANNMYNTQ 1150
Db 1093 IIRDCANQOTELTNI CDDDT-GVLST-----1118
QY 1151 ASNTNGYNTSVYNDQTYITKTTPYTPYDQMIEMSETE 1191
Db 1119 -----DQTSYITKTEFTSTEQWIDMSETE 1145

RESULT 9

US-08-532-547-5

; Sequence 5, Application US/08532547

; Patent No. 5861543

GENERAL INFORMATION:
APPLICANT: LAMBERT, BART
APPLICANT: JANSSENS, STEFAN
APPLICANT: VAN AUDENHOVE, KATHRIEN
APPLICANT: PEPEROEN, MARNIX
APPLICANT: VAN RIE, JEROEN
APPLICANT: VAN AARSSEN, ROEL
TITLE OF INVENTION: NEW BACILLUS THURINGIENSIS STRAINS AND THEIR
TITLE OF INVENTION: INSECTICIDAL PROTEINS.
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/532,547
FILING DATE: 06-DEC-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: SVENSSON, LEONARD R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 2121-109P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1157 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-532-547-5

Query Match 41.0%; Score 2595.5; DB 2; Length 1157;
Best Local Similarity 44.1%; Pred. No. 1.5e-183;
Matches 554; Conservative 197; Mismatches 348; Indels 157; Gaps 22;

QY 1 MSPNQNEHYEIIIDATSTSVNSDNRYPFANBFTNALQNDYKYLKMSAGNASEYEGSP 60
Db 1 MNRNQNEHYEIIIDAPHCPCFDDVRYPLASDPAALQNNYKDYLMQTDYDTSYINP 60
QY 61 EVLVSGDAAKAALDIVKLLSLGLGVFPVGVPIVSLYLTQILDILWPSEKQWIFMEQVE 120
Db 61 SLISGRDAVQTALTUVGRILGALGVFPFGQIVSFYQFLNTLWPNVDTAWEAFMQVE 120
QY 121 ELINQKIAEYARNKALSELEGLNGNTQLYLTALKEEENPNSGRALDRVNRFEILDLSLF 180
Db 121 ELVYNOQITEFARNQALRQLGLGDSFNVOYQSLQNLADNRDNTLSVVRQAQFIALDLDF 180
QY 181 TQYMPFRVNTFVPFLTVVYAMAANLHLLLLKQASIPGEWGWSTTTNNYIDROMKLT 240
Db 181 VNAIPLFVNGQVPLLSVYVAQVNLHLLLLKQASIPGEWGWSTTTNNYIDROMKLT 240
QY 241 EYSDHCWKVETGLAKLGTSAKQWVDYNOFRBMTLAVLDVVALFPNYDTRTPMETKA 300
Db 241 KYTNYCETWNTGLDRGNTSRLRYHQFRREMTLVLDVVALFPYDRLYPTGSPN 300
QY 301 QLTREVTDPGLGAV---NVSGISGWYD---KAPSGVGVSSVIRPPHVPDYITGLVYIT 353
Db 301 QLTREVTDPGLGAV---NVSGISGWYD---KAPSGVGVSSVIRPPHVPDYITGLVYIT 356
QY 354 QSRSSISARYIRHWAGHOISYHRVSRGSLNQMYGTGNTQNLHS-----TSTPDPFTNYD 405
Db 357 SNRPVSSNFMVWSGHTLRRSYLNSDAVQEDSYGLITTTTTRATINPGVDGNTRIESTAVD 416

QY 406 IYKLSKDAVLLDIVPGYTYIFFGMEPEVEFFMNNLNTRKTLKYNPVSKDIIASTRDS 465
Db 417 FRSLIG-----IYGVNRASFPVGLFNGT--TSPANGCGRDLY-----DT 455
QY 466 ELEPPETSDOPNYESYHRLCHTISIPATN-----TTGLVPVFSWTHRSADLNNTIY 519
Db 456 NDELFPEDEST---GSSTHRLSHVTFQTNQAGSIANAGSVPTVYVTRDRDVLNNTIT 511
QY 520 SDKITQIPAVKCDNLPPVPVKGPHGTGGLLOYNRSTGSGVTLFLARYGALAEKAGKY 579
Db 512 PNRITQPLVKAAPVSGTIVLKGFGTGGILR-RTTNGTGTIL---RVTVNSPLTQOY 567
QY 580 RVRLRYATDADIVLH-----VNDIAQIMPKTMNPGEDLTSK-----TF 617
Db 568 RLVRFASTGNFIRVLRGVSGIDVRLGSTMNRQELTYESFFTRFTTTGPFNPPPTF 627
QY 618 KVADAILTNLATOSSALKENLGEDPNSTLSGIVYVDRIFIPVDETYEABQDLAAKK 677
Db 628 TQAEIILTVNAEGVST-----GGEYIDRIEIVPVNPAREAEEDLEAAKK 672
QY 678 AVNALFTNTKDLRPGVTDYEVNQAANLVECLSDOLYPNEKRLLLFDVAREAKRLSEARNL 737
Db 673 AVASLFRTRDGLQVNYDYDVOQAANLVSCLSDEQYGHDKKMLLEAVRAAKRLSRERNL 732
QY 738 LQDPDFQIEING--ENGWMTASTGIEVIEGDALFKGRYLRLPGAREIDTETPTLYLYQKVEE 795
Db 733 LQDPDFNTINSTENGWKASNGVTSIEGGPFKGEALQASAR---ENYFTIYQKDA 788
QY 796 GVLKPYTRYRLRGVSGSQGLEIFTRIRHOTNRIVKNVPPDLLPVPSPVSDGS---INRC 852
Db 789 SVLKPYTRYRLDGFVKSSQDLEIDLHKKVHLVKNVDPNL---VSDTYSVSGSCGINRC 845
QY 853 SEOKYVNSRLVEN-----RSGEAHEESIDTGEIDYENAGIHWGFKITDPEGATL 906
Db 846 DEQHQVMDQLDAEHPMDCCAAQTHEFSSYINTGDLNASVDQGGVVLKVRTTDDGYATL 905
QY 907 GNLEVEEGLSGDALRLOREEQOWKIOMTRREEDTRRYMASKQAVDRLYADYQDOOL 966
Db 906 GNLEVEEGLSGSLREQRDNKAKNAELGKRAEDRVVLAQAQINHLFVYDQDOOL 965
QY 967 NPDVEITDLTAQDLIQSIPVYNEMPEIPGMNYTKFTLTDLRQQAWSLYDORNAIPN 1026
Db 966 NPEIGLAEINAEASLVESISGVSDTLQIPGINVEIYITELSDRLOQAASLYTSRNAVN 1025
QY 1027 GDFRNGLSNNATPGVEVQQLNHTSVLVI PNWDEQVSQOFTVQNRVLRVARTARKEGVG 1086
Db 1026 GDFNSGLSDSWNTTMDASVQODGNMHLVLHSHWDAQVSQQLRVNPNCKYVLRVARTARKEGVG 1085
QY 1087 NGVYSIRDDGNOTELTAFSADYDTNGMYNTQVNTNGYNTNNAINTQASSTNGYNANM 1146
Db 1086 DGYVTRIDGAHQHQTAFNACDYVNGTY-----1114
QY 1147 YNTQASNTNGYNTSVNVNDQGYTKTKVTFIPYDQMIEMSETEGYIESVELI 1202
Db 1115 -----VNDNS-----YITEEVVFYFETKHMVVESESEGSFYIDSIEFI 1153

RESULT 10

US-08-379-656B-5
; Sequence 5, Application US/08379656B
; Patent No. 5885571
; GENERAL INFORMATION:
; APPLICANT: Lambert Bart
; APPLICANT: Jansens, Stefan
; APPLICANT: Van Audenhove, Katrien
; APPLICANT: Peteroen, Marnix
; TITLE OF INVENTION: NEW BACILLUS THURINGIENSIS STRAINS AND
; TITLE OF INVENTION: THEIR INSECTICIDAL PROTEINS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 8110 Gatehouse Road, Suite 500 East

; CITY: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,656B
; FILING DATE: 23-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/01820
; FILING DATE: 12-JULY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93400949.9
; FILING DATE: 27-AUG-1992
; APPLICATION NUMBER: EP 92402358.8
; FILING DATE: 27-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 2121-104P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-379-656B-5

Query Match 41.0%; Score 2595.5; DB 2; Length 1157;
Best Local Similarity 44.1%; Pred. No. 1.5e-183;
Matches 554; Conservative 197; Mismatches 348; Indels 157; Gaps 22;

QY 1 MSPNNQNEYIIDIATSTSVSNDNRPYFANEPTNALQNNQNDYKDYLKMSAGNASYEGSP 60
Db 1 MNRNNQNEYIIDIAPHCGCPSDDVRYPLASDPAALQNNYKDYQNTDEDYDTSINP 60
QY 61 EVLVSGODAAKAIDIVGKLLSGLVFPVGPVYSVLTQLIDILWPSEKSKQWIFMEQVE 120
Db 61 SLSISGRDAVQTALTIVVGRILGALGVFPFSQIVSFYQFLNTLWPNVNDTAEAFMEQVE 120
QY 121 ELINOKIAEYARNKALSELEGNNYQLYLTALEEEENPNGSRALDVRNRFELDLSLF 180
Db 121 ELVNNQITEFARQALARQLGLGDSFNVYQSRSLQNLADRNDTRNLSSVRAQIALDLDF 180
QY 181 TQYMPFRVNTNFEVPLTVYMAANLHLKDKASIFGEGWGSTTTINNYYDROMKLT 240
Db 181 VNAIPLFVNGQVPLSVVAQAVNLHLLKDKASIFGEGWGSTTQGEISTYIDROELTA 240
QY 241 EYSDHCVKVYETGLAKGTSKQWVDYQFREMVLVDVVALFPNYDTRTPMETKA 300
Db 241 KYTNYCETWYNTGLDRLGRTNTESMLRYHQFREMVLVDVVALFPYDVRVLYPTGSP 300
QY 301 QLTREVVYDPL---GAVNYSSIGSW---YDKAPSGVIESSVIRPHVDPDYITGLTVYT 353
Db 301 QLTREVVYDPIVFNPPANVGLCRRWCTNPNY---TFSELENAFIRPPLFLDLNLSLT 356
QY 354 QSRISISSARYIRHWAGHQISYHRVSRGSLQOQYMG-----TNQNLHSTSTFFDFTNYD 405
Db 357 SNRPVSSNFMNDYWSGHTLRSLVINDSAVQEDSYGLITTRATINPGVCGTNRISTAVD 416
QY 406 IYKLSKDAVLLDIVPGYTYIFFGMEPEVEFFMNNLNTRKTLKYNPVSKDIIASTRDS 465
Db 417 FRSLIG-----IYGVNRASFPVGLFNGT--TSPANGCGRDLY-----DT 455

Q. C-08769

Db 512 PNRITQLPLVKASAPVSGTTLVKGPGFTGGILR-RTINGTGLT---RVTVNSPLTQOY 567
QY 580 RVLRYATDADIVLH-----VNDQAIQMPKTMNCEDLTSK-----TF 617
Db 568 RLRVRFSTGNSFIRVLRGGVSGIDVRLGSTMNGOELTYSFFTRFTTTGPFNPPFTF 627
QY 618 KVADAITTLNLTADSSALKHNLGDPNSTLSGIVVVDRIEPIFVDETYEAEQDLAAK 677
Db 628 TOAQEILTVNAEGYST-----GGEYIIDRIEIVPNPAREAEEDLEAAK 672
QY 678 AVNALFTNTKGLRPGVTDYEVNQAANLVECLSDLLYNEKRLIFDVAERAKRLSEARNL 737
Db 673 AVASLFTRTDGLQVNTDYQVDAQANLVSCLSDEQYGHDKMLLEAVRAAKRLSRNL 732
QY 738 LQDPDFQOING--ENGWTAAGIEVIEDALFKGRLPLGAREIDTETPTLYKQVEE 795
Db 733 LQDPDFNTINSTENGWKAANGVTSISEGPPFKRALQASAR-----ENYPTIYQKVA 788
QY 796 GVLKPYTRYRLRGFGVSGSQGLEIFTIRHOTNRIKVNQVPDDLPLDVPSPVNSDGS---INRC 852
Db 789 SVLKPYTRYRLDGFVKSSQDLEIDLIHHKHVHLKVNVEDNL---VSDTYSGSCGINRC 845
QY 853 SEQKYNSRLVEN-----RSGAEHFSIPIDTGEIDYNENAGIWWGFKITDPEGYATL 906
Db 846 DEQHOVMDQDAEHHPMDCCCEAAQTHEFSSVINTGDLNASVDQGLIWWVLKVRTTDDGYATL 905
QY 907 GNLLEVEGPLSGDALERLQREEQWIKOMTTRREEDTDRRYMAKQVADRLYADYQDQOL 966
Db 906 GNLLEVEGPLSGSLEREORDNAKNAELGRKRAEIDRVVLAAKOAINHLFVDYQDQOL 965
QY 967 NPQVEITDLTAQDLOIOSIPVYVNMPEPIPCMYKTFELTDLRLOQAWSLYDORNAIPN 1026
Db 966 NPEIGLAINEASNLVSGVSDTLQIPEGINYEITELSDRLOQASYLYTERNAVON 1025
QY 1027 GDFRNLGNMNAATPGVEVQOQINHTSVLVPNWDQVQSQFTVQPNQRYVLRVARTARKEGVG 1086
Db 1026 GDFNSGLDSWNTTMDASVQDQGNMHFLVLSHWDQVQSQLRVNPENCKYVLRVARTARKEGVG 1085
QY 1087 NGVYSIRDDGNQOTELTFSASDYDTNGMYNTQVNTNGYNTNAYNTQASSTNGYNNNM 1146
Db 1086 DGYVITRDGAHQHQLTFNACDYDNGFY----- 1114
QY 1147 YNTQASNTNGYNTSVYNDQGYITKTFTVPIYTDQMIEMSETEGYFIBSEVELI 1202
Db 1115 -----VNDNS-----YITEVWFYFETGHWVEVSESEGFYIDSIEFI 1153

RESULT 12

US-09-019-809-5
Sequence 5, Application US/09019809
Patent No. 6143550

GENERAL INFORMATION:

APPLICANT: LAMBERT, BART
APPLICANT: JANSSENS, STEFAN
APPLICANT: VAN AUDENHOVE, KATRIEN
APPLICANT: PEPEROEN, MARNIX
APPLICANT: VAN RIE, JEROEN
APPLICANT: VAN AARSEN, ROEL

TITLE OF INVENTION: NEW BACILLUS THURINGIENSIS STRAINS AND THEIR
TITLE OF INVENTION: INSECTICIDAL PROTEINS.

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
STREET: P.O. Box 747

CITY: Falls Church

STATE: Virginia

COUNTRY: USA

ZIP: 22040-0747

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/019,809

FILING DATE: 02-FEB-1998

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: SVENSSON, LEONARD R.

REGISTRATION NUMBER: 30,330

REFERENCE/DOCKET NUMBER: 2121-135P

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 205-8000

TELEFAX: (703) 205-8050

TELEX: 248345

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 1157 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-019-809-5

Query Match 41.0%; Score 2595.5; DB 4; Length 1157;

Best Local Similarity 44.1%; Pred. No. 1.5e-183;

Matches 554; Conservative 197; Mismatches 348; Indels 157; Gaps 22;

QY 1 MSPNNONEVEIIDATPSTSVNSDNRYPPANEPTNALONMDYKDYKMSAGNASEYPCSP 60

Db 1 MNRNNOXEYIIDAPHGCGPSDDVDVPLASDDNNAALNNYKDYLOMTDEDVYDSINP 60

QY 61 EVLVSGDAAKAIDIVGKLLSGLVGPFVGVPIVSLVLTQILIDILWPSEKQWEIEMEQVE 120

Db 61 SLGISGEDAVQALTGVGRILGALGVFPFSQIVSFQFLNTLWPNVDTAIWEAFMEQVE 120

QY 121 ELINQIAEYARNKALSELEGLNNYQLYLTALKEEENPNNGSRALRDVNRREILDSLF 180

Db 121 ELVNNQIQTEPARNQALRQLGDSFNVYQSRQLONWLADRNDTRNLVSVRAQFIALDLDF 180

QY 181 TOYMPSFRVTFVPELTVYAMAANLHLLKDASTEGEWGHSTTTNNYIDROMKLLTA 240

Db 181 VNAIFLPVANGQVPLSVYAQAANLHLLKDASTEGEWGHSTTTNNYIDROMKLLTA 240

QY 241 EYSDHCWKVZETGLAKLKGTSKQWVDYNOFREMTLVLVDVVALFNYDRTVPMETKA 300

Db 241 KYTNYCETWNTGLDRLGINTESMLRYHFREMTLVLVDVVALFNYDRTVPMETKA 300

QY 301 QLTREVYTDPL---GAVNVSSISGW---YDKAPSGVIESSVIRPPHVDYITGLTVYT 353

Db 301 QLTREVYTDPIVENPPANVGLCRRWGTNPYN---TFSELENAFIRPHLPDLRLSLTI-S 356

QY 354 QSRSSISARYIRHWAGHOISYHRVSRGSLNQMYG-----TNQNLHSTSTDFDFTNYD 405

Db 357 SNRFPVSSNFMFYMWSGHTLRRSYLNDLSAQEDSYGLITTTTRATINPGVDGNTRIESTAVD 416

QY 406 IYKTLKSDAVLLDIVPGYTYIIFGMPVEVEFMVNQNLNTRKTLKYNPVSQDIIASTRDS 465

Db 417 FRSAALIG-----IYGNRASFPVPGGLFNGT--TSPANGGCCRDLY-----DT 455

QY 466 ELPLPETSQPNYESYSHRLCHITSIPATGN-----TTGLVPVFSWTHRSADLNNITIY 519

Db 456 NDELPPDEST---GSSTHRLSHVTFPSFOTNQAGSIANAGSVPTVYVTRRDVDLNNIT 511

QY 520 SDKITQIPAKVCWDLNLPFPVVKVGRGHTGDLLOYRSTGVSUGTLFLARYGLALEKAGKY 579

Db 512 PNRITQLPLVKASAPVSGTTLVKGPGFTGGILR-RTINGTGLT---RVTVNSPLTQOY 567

QY 580 RVLRYATDADIVLH-----VNDQAIQMPKTMNCEDLTSK-----TF 617

Db 568 RLVRFSTGNSFIRVLRGGVSGIDVRLGSTMNGOELTYSFFTRFTTTGPFNPPFTF 627

QY 618 KVADAITTLNLTADSSALKHNLGDPNSTLSGIVVVDRIEPIFVDETYEAEQDLAAK 677

Db 628 TOAQEILTVNAEGVST-----GGEYIIDRIEIVPNPAREAEEDLEAAK 672

Qy 678 AVNALFTNTKGLRPGVTDYEVNQANLVESLSDLLXPNKRLLFPDAVREAKRLSEARNL 737
Db 673 AVASLFTTRDGLQVNTDYQVDAQANLVSLSDQYGHDKKMLLEAVRAAKRLSRNL 732
Qy 738 LQDDPFOEING--ENGWTASTGIEVIEGDALFKGRLPLPGAREIDTITYTYLYOKVEE 795
Db 733 LQDDPFTNTTEENGWAKASGVITISEGPPFKGRALQALASAR-----ENPTYTYQKVD 788
Qy 796 GVLKPYTRYRLRGVSSQGLEIFIRHTNRIVKVNPPDDLLPVPSPNSDGS---INRC 852
Db 789 SVLKPYTRYRLDGFVKSSQDLEIDLHKKHVLKVNVPDNL---VSDTYSDGSCGINRC 845
Qy 853 SEQYVNSRLVEN-----RSGNAHEFSIPIDTGEIDYENAGIHWGFKITDPEGATL 906
Db 846 DEQVMDQLDAEHPHMDCCBAATHPESSVINTGDLNASVDQGIWVVLKVRTTIDGYATL 905
Qy 907 GNLEIVREGPLSGDALRELQREEQWKLQMTREETDRRYWASKQAVDRLYADYQDQOL 966
Db 906 GNLEIVEGVLPGSLERQEDNKAQNAELGRKRAEIDRVYLAQAQINHLFVYQDQOL 965
Qy 967 NPDEVEITDLTAAODLIQSIPIVYVYVEMPEIPGMNYTKETELTDRLQQAWSLYDORNAIPN 1026
Db 966 NPEIGLAINEASNLVESISGVSYDTLQIPGINVEIYTELSDRLQQAWSLYTSENAYQN 1025
Qy 1027 GDFRGLSNWNPATPGVEVQOQNHITSVLVIPNWDQVSOQFTVQPNQRYLVRTARKEGV 1086
Db 1026 GDFNSGLDSWNTTMDASVQDQGNHFLVLSHWDQAQVSOQLKVPNCKYVLRVTRARKVGG 1085
Qy 1087 NGYVIRDGNGQETLTPSASDYDTNGMYNTQVSNYNTGNTYNTNAYNTQASSTNGYNANM 1146
Db 1086 DGYVTRDGAHQETLTPNACDYVNGTY----- 1114
Qy 1147 YNTQASNTNGYNTNSVYNDQGYTKTYTPIPYTDOMIEMSEGTFTVIESVELI 1202
Db 1115 -----VNDNS-----YITERVVFYPTKHMVVESESGSYIDSIEPI 1153

RESULT 13

US-09-471-177-5
; Sequence 5, Application US/09471177
; Patent No. 648226
; GENERAL INFORMATION:
; APPLICANT: LAMBERT, BART
; APPLICANT: JANSSENS, STEFAN
; APPLICANT: VAN AUDENHOVE, KATRIEN
; APPLICANT: PEPEROEN, MARINX
; APPLICANT: VAN RIE, JEROEN
; APPLICANT: VAN AARSENE, ROEL
; TITLE OF INVENTION: NEW BACILLUS THURINGIENSIS STRAINS AND THEIR
; TITLE OF INVENTION: INSECTICIDAL PROTEINS.
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/471.177
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/019.809
; FILING DATE: 02-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: SVENSSON, LEONARD R.
; REGISTRATION NUMBER: 30,330

; REFERENCE/DOCKET NUMBER: 2121-135P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-471-177-5

Query Match 41.0%; Score 2595.5; DB 4; Length 1157;
Best Local Similarity 44.1%; Pred. No. 1.5e-183;
Matches 554; Conservative 197; Mismatches 348; Indels 157; Gaps 22;
Qy 1 MSPNQNEYIIDIATPSTSVNSNRYPFANEPTNALQNMNDYKDYLOKASAGNASEYFGSP 60
Db 1 MNRNQNEYIIDIAPHCGCPDSDVRYPLASDPNAALQNMNYKDYLOMTDEDYTDYINP 60
Qy 61 EVLVSGQDAKAAIDIVGKLLSGLVGPFVGPVIVSLYLTOLIDILWPSGKESOWEIFMEQVE 120
Db 61 SLISGSDAVQTATVTVGRILGALGVFPSCQIVSYQFLNLTLPVNDTALWEAFMQVE 120
Qy 121 ELINQKIARYARKALSEGLGNNYQLYLTALKEEENPNGSRALDRVRNRFELDSL 180
Db 121 ELVYQQTITEFARNOALQGLGDSFNVYQSLQNLADRNLTENLSVVAQFIALDLDF 180
Qy 181 TQYMPFRVNTFVFFITVYAMAANLHLLKQASIFGEGWGWSTTTINNYDRQMKLTA 240
Db 181 VNAIFPAVNGQQVPLLSVYQAQVNLHLLKQASIFGEGWGFQGEISTYDRQLELTA 240
Qy 241 EYSDHCVKWYETGLAKLGTSAKQWVDYNGFRREMTLAVLDVVALFPNYDTRTYPMETKA 300
Db 241 KYTYCYCTWNTGLDRGTNTESWLRHYHQFRREMTLWLDVVALFPYDVRLYPTGSNP 300
Qy 301 QLREVTYTDPL--GAVNVSSIGSW---YDKAPSGFVIBSSVIRPPHVPFYITGLTVYT 353
Db 301 QLREVTYTDIVFPNPPANVGLCRWGTNPYN---TFSELENAFIRPPHLDRLNSLII-S 356
Qy 354 QSRSSISARYIRHWAGHOISYHRVSRGNSNLQQMYG-----TNQNLHSTSTFDFTNYD 405
Db 357 SNRPVSNFMDYWSGHTLRRSYLNDSAVEDSYGLITTTTTRATINPGVDGTNRISTAVD 416
Qy 406 IYKTLKDAVLLDIVPGYIVIFGMEPEVEFFVWVQNLNTRKTLKYNPVSKDIIASTRDS 465
Db 417 FRSLIG-----IYGVNRASFPVPGGLFNGT--TSPANGGCRDLX----DT 455
Qy 466 ELELPPESTQPNYESYSHRLCHITSIIPATGN-----TTGLVPVFSWTHRSADLNNTIY 519
Db 456 NDELPPDEST----GSSTHRLSHVTFPSFQTNQAGSIANAGSVFTYVWTRDVLNNTIT 511
Qy 520 SDKITQIPAVKWNLPFPVVKPGHTGGDLLQYNRSTSGVGLFLARYGLALEKAGKY 579
Db 512 PNRITQLPLVKASAPVSGTTLKPGFTGGGILR-RITNGTFGTL---RVTVNSPLTQQY 567
Qy 580 RVRLRYATDADIVLH-----VNDQAIQMPKTMNPDGDLTSK-----TF 617
Db 568 RLVRFPASTGNFPIRVLRGGVSGIDVRLGSTMNRQBELTYESFFTRFTTTTGPFPNPPFT 627
Qy 618 KVADAITTLNLTSSLLAKHNLGCEDPNSTLSGIVVYVDRIEFPVDETYEARQOLEAAKX 677
Db 628 TQAOEILTVNAGVST-----GGEYIIDRIEIVPNPAREAEDELEAAKX 672
Qy 678 AVNALFTNTKGLRPGVTDYEVNQANLVESLSDLLXPNKRLLFPDAVREAKRLSEARNL 737
Db 673 AVASLFTTRDGLQVNTDYQVDAQANLVSLSDQYGHDKKMLLEAVRAAKRLSRNL 732
Qy 738 LQDDPFOEING--ENGWTASTGIEVIEGDALFKGRLPLPGAREIDTITYTYLYOKVEE 795
Db 733 LQDDPFTNTTEENGWAKASGVITISEGPPFKGRALQALASAR-----ENPTYTYQKVD 788

Qy	796	GVLKPYTRYRLRGFVSSQGLEFTTTHQTNRIVKXVPDDLDPVSPVNSDGS-----INRC	852
Dd	789	SVLKPYTRYRLDGFVKSSODLEIDLHHKHVHLVKMVPNL---VSDTYSDGSCSGINRC	845
Qy	853	SEOKYVNSRLEVEN-----RSCEAEHFSIPIDTGEIDYNENAGIHWGFKITDPEGYATL	906
Dd	846	DEQHQQVNDQDAEHPHMDCCEAAQTTFESSYINTGLNASVDQGJVVWLKVRTTDGYATL	905
Qy	907	GNLVBEGPLSGDALERLQRBEQOWKI QWTRRRRETDRRYMASKQAQVDRLYADYQDOOL	966
Dd	906	GNLVEVGPLSGESLEREQDNAKNALGRKRAEIDRVYLAKQA INHLFVDYQDOOL	965
Qy	967	NPDVEITDLFAAODLIQSIPYYVNEMPPEI PGMYNTKYTELTRLQQAWSLYDORNAIPN	1026
Dd	966	NPEIGLAINEASNLVESISGVSDTLQLTPGINYEIYTELSDRLQQA SYLTSRNAVON	1025
Qy	1027	GDERNGLSNNAIPGVEVOQII NHTSVLVLPINWDEQVSOQFTVPQNR VYLRVTARKEGVG	1086
Dd	1026	GDNFNGSLDSWNTTWDIASVQODGNMHFLVLSHDAAQVSQOULRNPNCKYVLRVTARKVGGG	1085
Qy	1087	NGYVISRDGGNQTEITLFFSASYDYTNMGMTNTQVSTNGTYNTNNAYNTQASSTNGYANNMM	1146
Dd	1086	DGYVITRDGAHQETLTFNACDDVNGTY-----	1114
Qy	1147	YNTQASNTNGYNTNSVYNDGTGYITKTFTPIPYTDQMIMSETGTFYIESVELI	1202
Dd	1115	-----VNDS-----YITEVVFYPPTKMWVEVSEGSGFYDISIRPI	1153

RESULT 14

US-09-002-285-72
Sequence 72, Application US/09002285
Patent No. 6369213
GENERAL INFORMATION:
APPLICANT: Schnepf, H. Ernest
APPLICANT: Wicker, Carol
APPLICANT: Narva, Kenneth E.
APPLICANT: Walz, Michelle
APPLICANT: Stockhoff, Brian
APPLICANT: Muller-Cohn, Judy
TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/002,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/886,615
FILING DATE: 1-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/674,002
FILING DATE: 1-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-701C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:

Db 961 MDCBAAQTHFSSVINTGDLNAAVDOGIWVVLKVRITDGTATGNLSELVEGFLSGESL 920
Qy 923 ERLQEEQOWKIOMTRREEDRRYMASQKQAVDRLYADYQOQNLNPDVIEITDLTAADLI 982
Db 921 EREQDNKNAWELGRKABIDRVYLAQAQNLHFLVDYQOQNLNPEIGLAEINASLV 980
Qy 983 QSIPTVNEPPEIPGMNYPKTELTDLRQAQMSLYDORNAIPNGDFRNGLSNMNATPGV 1042
Db 981 ESIQSVSDTLQIPGINIYETLSLDRQAQSYLYTSRNVQNGDFRNGSLDSWNTTMDA 1040
Qy 1043 EVQOINHTSVLIPNWDQVSOQFVQPNORVLTARKEGNGVGYVSIIRDGNQOTEL 1102
Db 1041 SVQOQNMHFLVSHWDAQVSOQLRVNPNCKYLRVARTARKVGGGSGYVYIIRDAHQHETL 1100
Qy 1103 TFSASDYDNGMYNTQVSNITNGYNTNAYNTQASSTNGYNANNMYNTQASNTNGYNTNSV 1162
Db 1101 TFNACDYVNGTY-----VNDNS- 1118
Qy 1163 YNDQGYITKTPTIPYTDQMIENSETGTFYIESVELI 1202
Db 1119 -----YITEBWFYPTKHMWVEVSESGSYIDSIEFI 1152

RESULT 15
US-08-542-921-2
; Sequence 2, Application US/08542921
; Patent No. 5736514
; GENERAL INFORMATION:
; APPLICANT: IIZUKA, TOSHIHIKO
; APPLICANT: TAGAWA, MICHITO
; APPLICANT: ARAI, SATOSHI
; APPLICANT: NIIZEKI, MASATSUGU
; APPLICANT: MIYAKE, TOSHIO
; TITLE OF INVENTION: NOVEL BACILLUS STRAIN AND HARMFUL
; TITLE OF INVENTION: ORGANISM CONTROLLING AGENTS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/542,921
; FILING DATE: 13-OCT-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 276082/94
; FILING DATE: 14-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN P
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 49-209-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1169 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-542-921-2

Query Match 40.4%; Score 2558.5; DB 1; Length 1169;
Best Local Similarity 43.8%; Pred. No. 8.1e-181;

Matches 555; Conservative 188; Mismatches 356; Indels 169; Gaps 25;
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Db 1 MNRNNQNEYEVIDAPHGCCPADVVKIPLDLDDPNAGLQNNYKEYLQTYGGDYTDPLNP 60
Qy 61 EVLVSGDAAKAAADIYVGLKSLGSLGVFPVGPVLSYLTQIDILWPSGEKSQWEIEMEVE 120
Db 61 NLSVSGKDVIVQGINIVGRLLSPFGFPSSQWTVVYLLNSLWPDDESSVMDAFMERVE 120
Qy 121 ELINOKIAEYARNKALSELGEGNNYOLYLTAEWEENNGSALDRVRNRPDLDSLF 180
Db 121 ELIDOKISEAVKRGALDDLTGLQYNYLYEALDEWLNRPNGARSL-VSQRFNLDLSLF 179
Qy 181 TOYMPSE-----RVNFEVPLTVYMAANLHLLKDAISFGEBWGSTTTNNYVDRQM 236
Db 180 TOFMPFSGSGSQVATILLPVYQAANLHLLKDAIDYGARWGLNQTOIDQFHSQQ 239
Qy 237 KLTAEYSDHCYKMETGLAKLKGTSAKQWVDYNOFREMTLAVLDVVALFPNYDRTYPM 296
Db 240 SLTQTYTNHCVTA YNDGLAELRGTTAESWPKYQVRRMTLTAMDVALFPYVNLRYQPD 299
Qy 297 ETKAQLTREVYT-----DPLGANNVSSIGSWYDAP-----SFGVIESSTVRPHVPIYI 346
Db 300 GTNPQLTREVYTDPIAFDPLEQPTTQLCRSWYINPAFRNHLNFSVLENSLIRPPLFERL 359
Qy 347 TGLTVYTQSRSSISSARIYRWAGHQISYHVRSGNSNLQWY-----GTNQLHSTSTF 399
Db 360 SNLQILVNYOTNGS-----WRGSRVRYHYLHSSIIKEKSYGLLSDPVGANINQ----- 409
Qy 400 DFTNYDIYKTLSDKADVLDDIYPGYT-----YIFPGMEVEFFFMVNO 441
Db 410 ---NNDIYQIISQVSNFASPVGSSYWDNTNLYSSGOVSGISGYTQGIIPAV---CLQQ 463
Qy 442 LNTRTKLKNPVSQDIIASTRDSELELPPTSQPNVESYSHRLCHITSI----- 492
Db 464 RNSTDPLSLNP-EGDII-----RNYSHRLSHITQYRFOATQSGS 502
Qy 493 PATGNTTGLVPVFSWTHRSADLNNTIYSDKITQIPAVKCDNLPFPVWPKPGHGGDL 552
Db 503 PST--VSANLPTCVWTHRDVDLNTITANQITQPLVKAELSSGATVVRGFGTGGDVI 560
Qy 553 QYNRSTSGVGTFLARYGLALEKAGKYRVRLYATDADIVLHVND-----QIQPKTMN 607
Db 561 R-RTNTGFGGAIRVSVTGPLTQ---RYRIRFYASTIDDFVTRGGTTINFRFRTMN 616
Qy 608 PGEILTSKTFKVAADAITLNLATSSALKKNLGEDPNSTLSGIVYVDRIEPIPVDEYIE 667
Db 617 RGESRYESYRTVEFTTFFNFTSQDIIRTSIQGLSGN---GEVYLDRIEIIIPVNPARE 672
Qy 668 AEQLEAAKAVNA-LPTNTKDLRPGVTDYEVNQAANLVECLSDDLVPNEKRLLFDAVR 726
Db 673 AEEDLEAAKAAARQNLFTTRDRGLQVNVTDYQVQAAANLVCLSDQEGYGHDKMQLLEAVR 732
Qy 727 EAKLSEARNLLQDPDFOEING--ENGWTAETAGIEVIEGDFALFKGRYLRLPGAREIDTET 784
Db 733 AAKLSEARNLLQDPDFNTINSTENGWKAANGVTISEGGGFFKGRALQLASAR---EN 788
Qy 785 YPTLYQKVEGVLPKYTRYRLRGVSSQGLEIFTIRHQTNRIVKXNVDPDLLDPVSPN 844
Db 789 YPTVIYQKVDASVLKPYTRYRLDGFVKSSQDLEIDLHYHKVHLVKNVDPNL---VSDTY 845
Qy 845 SDGS---INRCSEQYNSRLIVEN-----RSGEAHEFSIPIDTGEIDYNEAGIWWG 894
Db 846 SDGSCGMNRCCEQQMVNAQLETSHHPMDCCAAQTHEFSSYINTGDLNASVDGIGWV 905
Qy 895 FKIDPEGYATLGNLVEEGPLSGDALERQREEQWKIQMTRRREEDRRYMASQKQAV 954
Db 906 LKVRTTDGYATLGNLVEGVPLSGESLERQDRDNKNAWELGRKABIDRVYLAQKAI 965
Qy 955 DRLVADYQDQQLNPDEITDLTAADLIQSIPTVYVNEPPEIPGMNYPKTELTDLRQQA 1014
Db 966 NHLFVDYQDQQLNPEIGLAEINASLVESISGVYSDTLQIPGINIYETLSLDRQAQ 1025


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QY 1015 WSLYDQNAIPNGDFRNGLSNWNATPGVEVQOINHTSVLIPNWDQVSOQFTVQPNORY 1074
Db 1026 SYLTSRNVQNGDFNSGLDSWNITTDASVQDDGMMHFLVLSHWDQVSOQLRVNPNCKY 1085
QY 1075 VLRVTARKEGVNGYVSIIRDGNQOTETLTFASDYDTNGMYNTQVSNNGYNTNNAYNTQ 1134
Db 1086 VLRVTARKEGVNGYVSIIRDGNQOTETLTFASDYDTNGMYNTQVSNNGYNTNNAYNTQ 1134
QY 1135 ASSTNGYNANMMYNTQASNTNGYNTNSVYNDQTCYITKTVTFIPYTDMMIEMSETEGTF 1194
Db 1127 -----VNDNS-----YITEEVVFPETKMMVVEVSESEGSF 1157
QY 1195 YIESVELI 1202
Db 1158 YIDSIEFI 1165

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Search completed: January 7, 2003, 05:18:17
 Job time : 32 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 7, 2003, 00:49:27 ; Search time 89 Seconds
(without alignments)

12477.265 Million cell updates/sec

Title: US-10-032-717-1

Perfect score: 3621

Sequence: 1 atgagtcacaaataacaaaa.....tgattgtagacgtagagtaa 3621

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA.*
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2: /cgm2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgm2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgm2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgm2_6/ptodata/1/ina/PTUS_COMB.seq.*
6: /cgm2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2565.2	70.8	3507	1	US-08-315-468-3
2	1812.2	50.0	3471	1	US-07-876-280-29
3	1812.2	50.0	3471	1	US-07-812-180A-1
4	1812.2	50.0	3471	1	US-08-315-468-1
5	1812.2	50.0	3471	4	US-07-941-650A-1
6	1180	32.6	3797	1	US-07-915-203-1
7	1180	32.6	3797	1	US-08-272-887-1
8	1180	32.6	3797	1	US-08-789-449-1
9	893.4	24.4	4344	2	US-08-532-547-4
10	893.4	24.4	4344	2	US-08-379-656B-4
11	893.4	24.4	4344	3	US-08-455-838-4
12	893.4	24.4	4344	3	US-09-019-809-4
13	893.4	24.4	4344	4	US-08-471-177-4
14	882.8	24.4	3471	4	US-09-002-285-73
15	848.6	23.4	3759	1	US-08-542-921-1
16	848.6	23.4	3759	2	US-08-880-685-1
17	848.6	23.4	3759	2	US-08-880-684-1
18	822.2	22.7	3453	4	US-09-002-285-75
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20	733.6	20.3	3414	1	US-07-973-320-3
21	731.4	20.2	3414	1	US-07-973-320-1
22	678	18.7	3934	1	US-08-100-709-3
23	678	18.7	3934	1	US-08-176-865-3
24	678	18.7	3934	1	US-08-474-038-3
25	678	18.7	3934	2	US-08-779-046-3
26	678	18.7	3934	2	US-08-881-340-3
27	673.6	18.6	4074	1	US-08-377-690-1

28 559.2 18.2 3684 1 US-08-448-170-7 Sequence 7, Appli
29 559.2 18.2 3684 3 US-08-961-803-5 Sequence 5, Appli
30 618.6 17.1 3567 6 5188960-5 Patent No. 5188960
31 615.4 17.0 3567 2 US-08-980-071-58 Sequence 5, Appli
32 615.4 17.0 3567 2 US-08-980-071-58 Sequence 58, Appli
33 615.4 17.0 3567 2 US-08-757-536-5 Sequence 5, Appli
34 615.4 17.0 3567 3 US-09-314-093-5 Sequence 5, Appli
35 615.4 17.0 3567 3 US-09-314-093-58 Sequence 58, Appli
36 615.4 17.0 3567 3 US-09-250-848-5 Sequence 5, Appli
37 615.4 17.0 3567 4 US-09-251-885-5 Sequence 5, Appli
38 615.4 17.0 3567 4 US-09-337-635-5 Sequence 5, Appli
39 615.4 17.0 3567 4 US-09-337-635-58 Sequence 58, Appli
40 615.4 17.0 3567 4 US-09-337-280-5 Sequence 5, Appli
41 615.4 17.0 3567 1 US-08-602-737-1 Sequence 1, Appli
42 613.8 17.0 3567 2 US-08-980-071-1 Sequence 1, Appli
43 613.8 17.0 3567 2 US-08-980-071-9 Sequence 9, Appli
44 613.8 17.0 3567 2 US-08-980-071-11 Sequence 11, Appli
45 613.8 17.0 3567 2 US-08-980-071-11

ALIGNMENTS

RESULT 1
US-08-315-468-3
; Sequence 3, Application US/08315468
; Patent No. 5554534
; GENERAL INFORMATION:
; APPLICANT: Michaels, Tracy Ellis
; APPLICANT: Ponceirada, Luis
; TITLE OF INVENTION: Process for Controlling Scarab Pests
; TITLE OF INVENTION: with Bacillus thuringiensis Isolates
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/315,468
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/014,941
; FILING DATE: 01 FEB 1993
; APPLICATION NUMBER: 07/828,430
; FILING DATE: 30-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/808,316
; FILING DATE: 16-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA73.C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3507 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO

ANTI-SENSE: NO
ORIGINAL SOURCE: Bacillus thuringiensis
STRAIN: kunamotoensis
INDIVIDUAL ISOLATE: 50C
IMMEDIATE SOURCE: LambdaGEM-11 (tm) library of L. Poncerrada
LIBRARY: 50C(b)
CLONE: 50C(b)
US-08-315-468-3

Query Match 70.8%; Score 2565.2; DB 1; Length 3507;
Best Local Similarity 85.1%; Pred. No. 0;
Matches 2906; Conservative 0; Mismatches 493; Indels 15; Gaps 3;

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Db 1 ATGAGTCCAAATATCAAAATGAATGAATGAATATAGATCGACACCTCTTCTCTGTA 60

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Qy 241 CTATCAGGTTTAGGGTCCCATTTGTTGGCCGATAGTAGTCTTTTACTCAACTTTAT 300
Db 241 CTAAACAGGTTTAGGGTCCCATTTGTTGGCCGATAGTAGTCTTTTACTCAACTTTAT 300

Qy 301 GATATTTCTGTGGCTTCAGGGGAAAGAGTCAATGGGAAATTTTATGGAAACAAGTAGAA 360
Db 301 GATATTTCTGTGGCTTCAGGGGAAAGAGTCAATGGGAAATTTTATGGAAACAAGTAGAA 360

Qy 361 GAAGTCAATTAATCAAAATATGACAGATATGCAAGGAAATTAAGCGCTTCGGAATTAGAA 420
Db 361 GAAGTCAATTAATCAAAATATGACAGATATGCAAGGAAATTAAGCGCTTCGGAATTAGAA 420

Qy 421 GGATAGGTAATTAATCAATATATATCTAATCTGCGCTTGAAGAAATGGGAAAGAAATCCA 480
Db 421 GGCTAGGGAATTAATCAATATATATCTAATCTGCGCTTGAAGAAATGGGAAAGAAATCCA 480

Qy 481 AATGGTTCAGAGCTTACAGATGTCGGAATCGAATTCGAAATCTCGGATAGTTATTT 540
Db 481 AATGGTTCAGAGCTTACAGATGTCGGAATCGAATTCGAAATCTCGGATAGTTATTT 540

Qy 541 ACGCAATATATGCGCATCTTTTAGAGTGACAAATTTTGAAGTACCATTCCTTACTGTATAT 600
Db 541 ACGCAATATATGCGCATCTTTTAGAGTGACAAATTTTGAAGTACCATTCCTTACTGTATAT 600

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Db 601 ACAATGGCAGCCAACTTCAATTTACTGTTATTAAGGACGCGTCAATTTTGGAGAGAA 660

Qy 661 TGGGGATGTCACAACTACTATTAATTAATCTATATGATCGTCAATGAACTTACTGCA 720
Db 661 TGGGGATGTCACAACTACTATTAATTAATCTATATGATCGTCAATGAACTTACTGCA 720

Qy 721 GAATATTTCTGATCACTGTGTAAAGTGTATGAACTGTTTAGCAAAATTAAGAGGCAAG 780
Db 721 GAATATTTCTGATCACTGTGTAAAGTGTATGAACTGTTTAGCAAAATTAAGAGGCTCG 780

Qy 781 AGCGCTAAACAATGGGTGATGATTAACCAATTCGGTAGAGAAATGACACTGGCGTTTGA 840
Db 781 AGCGCTAAACAATGGGTGATGATTAACCAATTCGGTAGAGAAATGACACTGGCGTTGTA 840

Qy 841 GATGTTGTCGATTTTCCCAAAATTAATGACACAGCGAGTACCCCAATGGAAACGAAAGCA 900
Db 841 GAGCTGTTGTCGATTTTCCCAAAATTAATGATGACAGCGAGTACCCCAATGGAAACGAGCT 900
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Qy 901 CAACTAAACAGGGAAGTATATACAGATCACTGGGCGCGTAAACGCTGCTTCAATTTGGT 960
Db 901 CAGCTTTACAGGGAAGTATATACAGATCCACTTGGCGCGTAGATGCTGCTTAATTTGGC 960

Qy 961 TCCTGATATGACAAAGACCTTCTTTGGAGTATAGATCACTCCGTTATTCGACACCC 1020
Db 961 TCCTGATATGACAAAGACCTTCTTTCTCAGAAATAGAAAAGCGGCTATTCGTCACCT 1020

Qy 1021 CATGTATTTGATTTATTAACGGGACTCACAGTGTATACAAATCAAGAGCATTTCTTCC 1080
Db 1021 CATGTATTTGATTTATTAACGGGACTCACAGTGTATACAAATCAAGAGCATTTCTTCT 1080

Qy 1081 GCTCGCTATATAGACATTTGGGCTGCTCAATAAAGCTTACCATCGTGTAGTAGGGT 1140
Db 1081 GATCGTTATATGAGATTTGGGCTGCTCAATAAAGCTTATAGCATATCGTACGAGT 1140

Qy 1141 AGTAATCTTCAACAAATGATGGAACATAAATAAATCTACAGCACTAGTACTCTTTGAT 1200
Db 1141 AGTACCTTTTACACAGATGATGGAACCAATCAAAATTTTACAAAGTACTAGCAATTTGAT 1200

Qy 1201 TTTTACGAATTTATGATTTTACAGACTCTATCAAAAGGATGCGAGTACTCTTGTATTTGTT 1260
Db 1201 TTTTACGAATTTATGATTTTACAGACTCTTATCAAAATGGTGCAGTACTCTCTTGATATAGTT 1260

Qy 1261 TACCTCTGTTTATACGTATATATTTTGGAAATGCCAGAAAGTCCAGTCTTTCATGTTAAAC 1320
Db 1261 TACCTCTGTTTATACGTATATATTTTGGAAATGCCAGAAAGTCTTTCATGTTAAAT 1320

Qy 1321 CAATTGAATTAATACCAAGAAAGCTTTAAAGTATAATCTTCCAAAGATATTTATAGCG 1380
Db 1321 CAATTGAATTAATACCAAGAAAGCTTTAAAGTATAATCTTCCAAAGATATTTATAGAT 1380

Qy 1381 AGTACAGAGATTCGGAATTTAGNAATTTACTTCCAGAACTTTCAGATCAACCAATTTAG 1440
Db 1381 CGGACAGAGATTCGGAATTTAGNAATTTACTTCCAGAACTTTCAGATCAACCAATTTAG 1440

Qy 1441 TCATATAGCATATAGATTTATGTCATATCAAAAGTATTTCCGCGGACGGTAACTTACCGGA 1500
Db 1441 TCATATAGCATATAGATTTATGTCATATCAATTTTACTTCCA---GTTCACTAGCAG 1497

Qy 1501 TTAGTACCTGTTATTTTCTTGGACACATCGAAGTGCAGATTTAAACAATATATATTTCA 1560
Db 1498 TATGTACCTGTTATTTTCTTGGACACATCGAAGTGCAGATCTTAAACAATACAGTTAAAGT 1557

Qy 1561 GATAAATCACTCAAAATTCGGCGGTTAAATGTTGGGATAATTTACCGTTTGTTCAGTG 1620
Db 1558 GCGGAAATCACCCAAATACCGGGGCAAGTCTAGCAACCATAGGCGAATACTTTATATA 1617

Qy 1621 GTAAAAAGGACACAGGACATACAGGAGGGGATTTATTACAGTATATAGNAAGTACTGGTTCT 1680
Db 1618 ATAAAAAGGAGGGGTTTATACAGGGGAGACTTAGTGGCTTTAACGGACCGCATCGGAGT 1677

Qy 1681 GTAGGAACCTTATTTCTAGCTCGATATGCCCTAGCATTTAGAAAAAGCAGGGAATATCGT 1740
Db 1678 TGTGAGTTTCAGATGATCTTTCCAGAGTCTCAACGATTCGGTATTCGGATTCGTTAGCT 1737

Qy 1741 GTAGAGTCTGATATGCTACTGATGATATGTTATGTCATGTAACGATTCGTCAGATT 1800
Db 1738 TCTAATGAAATCTAGTTTATATTTATGCGGACTAAACCAAGCGGAACTTTTAAATTC 1797

Qy 1801 CAGATGCCAAAAACAATGAACCCAGGTGAGGATCTCAGCATCTAAAACTTTTAAAGTTGCA 1860
Db 1798 AACCAAGCATATTTCTAATAAATAAATGAATGATTTAACAATATATGATTTCAATATATA 1857

Qy 1861 GATGCTTACACATTAATTTAGCAACAGATAGTTCGCTAGCATTTGAAACAATAATTTA 1920
Db 1858 GAATATC---CAAGAGTCAATTCAGTAAATGCTTCTTCAAAACATACAGAGGTTATCTATA 1914

Qy 1921 GGTGAGACCTTAATTTCAACATTTATCTGTTATAGTTTACGTTGACCGAATCGAATTCATC 1980
Db 1915 GGTATATCAAAACGAATACAAATTTATTTATTTTAA-----GACCGAATCGAATTCATC 1965
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QY 1981 CCAGTAGATGAGACATATGAGCGGAAACAAGATTTAGAACGACGAGAAAGCAGTGAAT 2040
DB 1966 CCAGTAGATGAGACATATGAGCGGAAACAAGATTTAGAACGACGAGAAAGCAGTGAAT 2025
QY 2041 GCCTTTGTTTACCAATACAAAGATGCTTACGACGAGGCTTACGAGATTTAGAGTGAAT 2100
DB 2026 GCCTTTGTTTACCAATACAAAGATGCTTACGACGAGGCTTACGAGATTTAGAGTGAAT 2085
QY 2101 CAAGCGGCAAACTTAGTGAATGCTTATCGGATGATTTGCTATCCAAATCAAAACGATTTG 2160
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QY 2161 TTATTTGATGAGTGAAG 2220
DB 2146 TTATTTGATGAGTGAAG 2205
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DB 2386 TACACAGGATATAGATTTGAGAGGCTTTGTCGGAAGCAGTCAAGGATTTGAAATTTTAC 2445
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DB 2446 ATTCTGCTATCAACCAACCGATTTGTAAGAAATGCTTACGAGGCTTACGAGGCTTAC 2505
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DB 2566 CGTTTGAAGTATAGAAAACGCTTCTGCTGAGGCTTACGAGGCTTACGAGGCTTAC 2625
QY 2641 GGTGAATTCGATTAACAATGAAATGCTTACGAGGCTTACGAGGCTTACGAGGCTTAC 2700
DB 2626 GGAGAGCTGATTAACAATGAAATGCTTACGAGGCTTACGAGGCTTACGAGGCTTAC 2685
QY 2701 GAGGATATGCAACCTCGGAAACCTAGATTTGCTGAGAGGCTTACGAGGCTTAC 2760
DB 2686 GAGGATATGCAACCTCGGAAACCTAGATTTGCTGAGAGGCTTACGAGGCTTAC 2745
QY 2761 GCATTAGAACGCTTCAAG 2820
DB 2746 GCATTAGAACGCTTCAAG 2805
QY 2821 GAAGAAACAGATAGAGGCTTATGCTATCGAATGCTTACGAGGCTTACGAGGCTTAC 2880
DB 2806 GAAGAAACAGATAGAGGCTTATGCTATCGAATGCTTACGAGGCTTACGAGGCTTAC 2865
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DB 2866 TATCAGGATCAGCAACCTGATGCTATGAGATTTACAGATTTTACTGCGGCTTAC 2925
QY 2941 CTGATACAGTCAATCTTACGATTAACGAAATGCTTCCAGAGATTTACGAGGATGAC 3000
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DB 3106 GGTGTGAATGTATCAACAAATCAATCATATCATCTGCTTGTGATTTCCAAACTGGAAATGAA 3165
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DB 3166 CAAAGTTTCGCAACAGTTTACAGTTTCAACCGAATCAAGATATGCTTACGAGTACTGCA 3225
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QY 3361 AATCAAAATGATATACCAAAATTAATCGTATATATACCAAGCATCGAGTACA 3414
DB 3346 AATCAAAAGGATATACCAAAATGATGTCATGATCAAAACCGGCTATATCA 3399

RESULT 2

US-07-876-280-29
; Sequence 29, Application US/07876280
; Patent No. 5262158
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel M.
; APPLICANT: Cannon, Raymond J. C.
; APPLICANT: Bagley, Angela L.
; TITLE OF INVENTION: No. 5262158el Bacillus thuringiensis Isolates for
; TITLE OF INVENTION: Controlling Acarides
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/876,280
; FILING DATE: 19920430
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: M/S 104
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3471 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; STRAIN: kumamotoensis
; INDIVIDUAL ISOLATE: PS50C
; IMMEDIATE SOURCE:
; CLONE: E. coli NM522 (pMYC2320) NRRL B-18769

QY 2074 CCAGCGGTAAACGGAATATGAAAGTGAATCAAGCGGCAAACTTAGTGGAAATGCTATCGGAT 2133
DB 2071 CCAGGTGTAAACGGAATATGAAAGTGAATCAAGCGGCAAACTTAGTGGAAATGCTATCGGAT 2130
QY 2134 GATTGTATCAAAATGAAAGGATGTTATTTGATGACAGTGAAGAGGCGAAAAGCGCTC 2193
DB 2131 GATTGTATCAAAATGAAAGGATGTTATTTGATGACAGTGAAGAGGCGAAAAGCGCTC 2190
QY 2194 AGTGAAGCAGTAAATTTGCTTCAAGATCCAGATTTCCAGAGAGATAAATGGAGAGAAATGGC 2253
DB 2191 AGTGGGCGACGTAACTTACTACAGATCCAGATTTCCAGAGAGATAAATGGAGAGAAATGGC 2250
QY 2254 TGGAGCGCACTACCGGAATGAGGTTATAGAGGGGATGCTTTATCAAGGGCGTTAT 2313
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QY 2374 AAAGTAGAGGAAGGTGTATTAACCACTACACAGATATAGATTGAGAGGGTTTGTGCGA 2433
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DB 2491 GTACCGGATGATTTGCTGCCAGATGATCTCTGTTAACTCGGATGAGTATCAATCGA 2550
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DB 2551 TGCAGCGCAACAAAGTATGTAATAGCGTTTAGAAGTAGAAGAACCGTTCTGTTGAGAGCG 2610
QY 2614 CATGAGTCTCTATTCCTATGATACAGGTGAATTCGATTAATGAAGAAATGCAAGGAATA 2673
DB 2611 CATGAGTCTCTATTCCTATGATACAGGTGAATTCGATTAATGAAGAAATGCAAGGAATA 2670
QY 2674 TGGTTCGATTTAAGATTACGACCCAGAGGGATATGCAACACTCGGAACCTGAGATTG 2733
DB 2671 TGGTTCGATTTAAGATTACGACCCAGAGGGATATGCAACACTCGGAACCTTGGAAATTA 2730
QY 2734 GTCGAGAGGAGCCTTTATCAGGAGAGCGATTAGAACGCTTGCAAGAGAGAGAACACAG 2793
DB 2731 GTCGAGAGGAGCCTTTATCAGGAGAGCGATTAGAACGCTTGCAAGAGAGAGAACACAG 2790
QY 2794 TGGAGAGATTCAATGACAAGAGACGTGAAGAAAACAGATAGAGGATATGCGCATCGAAA 2853
DB 2791 TGGAGAGATTCAATGACAAGAGACGTGAAGAAAACAGATAGAGGATATGCGCATCGAAA 2850
QY 2854 CAAGCGGTAGATCGTTTATATGCGGATATCAGATCAGCACTGAATCTGTATGATAG 2913
DB 2851 CAAGCGGTAGATCGTTTATATGCGGATATCAGATCAGCACTGAATCTGTATGATAG 2910
QY 2914 ATTACAGATCTTACTGCGGCCAAGATCTGATACAGTCCATCTCTACGTATATAACGAA 2973
DB 2911 ATTACAGATCTTACTGCGGCCAAGATCTGATACAGTCCATCTCTACGTATATAACGAA 2970
QY 2974 ATGTTCCAGAAATACAGGGATGAATCTATACGAAGTTTACAGAAATTAACAGATCGACTC 3033
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QY 3034 CAACAGCGGTGGATTGTTATGATCAGGAAATGCCATACCAATGTTGATTTTGGAAAT 3093
DB 3031 CAACAGCGGTGGATTGTTATGATCAGGAAATGCCATACCAATGTTGATTTTGGAAAT 3090
QY 3094 GGGTTAAGTAATTTGGAATGCAACGCTGGGTAGAGTACAGCAAAATCAATCATCATCT 3153
DB 3091 GGGTTAAGTAATTTGGAATGCAACGCTGGGTAGAGTACAGCAAAATCAATCATCATCT 3150
QY 3154 GTCCTTTGTGATTTCCAACTGGGATGAGCAAGTTTTCGCAACAGATTTCAGTTTCAACCGAAT 3213

DB 3151 GTCCTTTGTGATTTCCAACTGGGATGAGCAAGTTTTCACACAGTTTACAGTTCAACCGAAT 3210
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DB 3211 CAAGAGATATGTTTACAGATTACTGCGAGAAAAGAGGGGTAGGAAATGATATGTAAGT 3270
QY 3274 ATCCGTGATGTTGGAATCAACACAGAAACGCTTACTTTTAGTCCAGCGAATATGATACA 3333
DB 3271 ATCCGTGATGTTGGAATCAACACAGAAACGCTTACTTTTAGTCCAGCGAATATGATACA 3330
QY 3334 AATGGAATGTTAATACGCAAGTGTCCAATACAAATGATATTAACACAAATTAATGCGTAT 3393
DB 3331 AATGTTGTGTTAATACGCAAAACCGGCTATATCAAAAAACAGTGACATTCATCCCGTAT 3390
QY 3394 AATACACAGCATCGAGTACAAAGCGGATATAACGCAAAATTAATATGATATA 3442
DB 3391 ACAGATCAATGTGGATTGGAATTAAGTGAAACAGAGAGGTACGTTCTATA 3439

RESULT 3

US-07-812-180A-1
; Sequence 1, Application US/07812180A
; Patent No. 5366892
; GENERAL INFORMATION:
; APPLICANT: Fonzerrada, Luis R
; APPLICANT: Payne, Jewel M
; APPLICANT: Sick, August J
; TITLE OF INVENTION: No. 5366892el Coleopteran-Active Bacillus
; TITLE OF INVENTION: thuringiensis Isolate and a No. 5366892el Gene Encoding a
; TITLE OF INVENTION: Coleopteran-Active Toxin
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Roman Saliwanchik
; STREET: 2421 N.W. 41st Street, Ste A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/812,180A
; FILING DATE: 19920102
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, Roman
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3471 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; STRAIN: kumamotoensis
; INDIVIDUAL ISOLATE: PS50C
; IMMEDIATE SOURCE:
; LIBRARY: LAMBDAEM (TM) - 11 LIBRARY OF LUIS
; LIBRARY: FONCERRADA
; CLONE: 50C

US-07-812-180A-1

Query Match 50.0%; Score 1812.2; DB 1; Length 3471;

Best Local Similarity 72.2%; Pred. No. 0;
 Matches 2504; Conservative 0; Mismatches 908; Indels 57; Gaps 9;

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Db	61	TCCAGTGAATCTAACAGATACCCCTTTGCGAATGAGCCAAACAGATGCGTTACAAAATATG	120
Qy	121	GATTATAAGATTTATTTAAAAATGTCGTGGGAAATGCTAGTGAATACCCCTGGTTCACCT	180
Db	121	AATATAAAGATTTATCTGAAAAATGTCGTGGGAGAGAAATCCTGAATATTATTGGAAAAATCCG	180
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Db	181	GAGAGCTTTATTA--GTTCACTCCAGATTCAACTGGAAATGGCATTTGGTGTGCAATTA	237
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Db	238	CTAGGAGCTTTAGGGTCCCATTTGCTAGTCAGATAGCTAGTTCTCTATAGTTTCATTGTT	297
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Db	358	GAACTCGTTGATCAAAAAATAGAAAATATGTAAGATTAAGGCTCTTCTGTAATTAATAA	417
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Db	418	GGGCTAGGAATGCTTTGGATGTATATCAGCAGTCACTTGAAGATTGGCTGGAATAATCGC	477
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Db	898	CAACTTAACGGGATGTATACAGATCCGATAGCATTTTAACATAGTACAGACTACTGGA	957
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DB 2131 GATTATATCCAAATGAAAAACGATTGTTATTTGATCAGTGAAGGCGGCAAAACGCGCTC 2190
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DB 2791 TGAAGATTCAAATGACAGAGACGCTGAGAGAACAGATAGAGGATATGCGCATCGAA 2850
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DB 2851 CAAGCGGTAGATCGTTTATGATGCGGATTTATCAGGATCAGCAACTGATCTGATGTAGAG 2910
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QY 3154 GTCTTGTGATTCCAACTGGGATGAGCAGTTTTCGCAACAGTTTACAGTTCAACCGAAT 3213
DB 3151 GTCTTGTGATTCCAACTGGGATGAGCAGTTTTCGCAACAGTTTACAGTTCAACCGAAT 3210

QY 3214 CAAAGATATGTTTACGAGTTTCTCGAGAAAAGAGGGGTAGGAATATGATATGTAAGT 3273
DB 3211 CAAAGATATGTTTACGAGTTTCTCGAGAAAAGAGGGGTAGGAATATGATATGTAAGT 3270
QY 3274 ATCCGTGATGTTGGAATCAAAACAGAAACGCTTACTTTTAGTGCAGGCGATTTATGATACA 3333
DB 3271 ATCCGTGATGTTGGAATCAAAACAGAAACGCTTACTTTTAGTGCAGGCGATTTATGATACA 3330
QY 3334 AATGGAATGTAATAATACGCAAGTGTCCAAATACAAATGGAATATAACACAAATATGCGTAT 3393
DB 3331 AATGGAATGTAATAATACGCAAGTGTCCAAATACAAATGGAATATAACACAAATATGCGTAT 3390
QY 3394 AATACACAGCAATCGAGTACAAACGCGATATAACGCAAAATATATGATATA 3442
DB 3391 ACAGATCAATGTTGGAATGGAATAGTGAACAGAGGTACGTTCTATA 3439

RESULT 4

US-08-315-468-1
Sequence 1, Application US/08315468
Patent No. 5554534
GENERAL INFORMATION:
APPLICANT: Michaels, Tracy Ellis
APPLICANT: Poncerrada, Luis
APPLICANT: Narva, Kenneth E.
TITLE OF INVENTION: Process for Controlling Scarab Pests
with *Bacillus thuringiensis* Isolates
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/315,468
FILING DATE:
CLASSIFICATION: .424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/014,941
FILING DATE: 01 FEB 1993
APPLICATION NUMBER: 07/828,430
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/808,316
FILING DATE: 16-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA73.C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3471 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: *Bacillus thuringiensis*
STRAIN: kumamotoensis
INDIVIDUAL ISOLATE: PS50C
IMMEDIATE SOURCE:

LIBRARY: LAMBDAGEN (TM) - 11 LIBRARY OF LUIS
LIBRARY: FONCERRADA
CLONE: 50C(a)
US_08-315-468-1

Query Match 50.0%; Score 1812.2; DB 1; Length 3471;
Best Local Similarity 72.2%; Pred. No. 0;
Matches 2504; Conservative 0; Mismatches 908; Indels 57; Gaps 9;

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DB 1 ATGAGTCCAAATATCAAAATGAATATGAATATATAGATGGACACCTTCTACTCTCTGA 60
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DB 61 TCCAAATGATCTCAACAGATACCTTTTCGGAATGAGCAACAAATGCGCTACAAATATG 120
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QY 1774 GTATTTGATGTAAAGCTGCTCAGATTCAGATGCCAAACAAATGAACCCAGGTGAGAT 1833
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QY 1834 CTGACATCTAAACATTTTAAAGTTGCGAGATGCTATCAACATTTAAATTTAGCAACAGAT 1893
DB 1831 AATGGGCACTTTTAAACGTATGAACATTTTAAATTCGCAAGTTTCAATTTACTGATTTCCAA 1890
QY 1894 AGTTGCTGATGATTAACATAATTTTAGGTGAAGACCCCTAATTCACAAATTTATCTGGTATA 1953
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QY 1954 GTTTACGTTGACCGAATCGAATTTCTCCAGTAGTAGACATATGAGCGGACAGAT 2013
DB 1951 GTTTATATAGACCGAATCGAATTTCTCCAGTAGTAGACATATGAGCGGACAGAT 2010
QY 2014 TTAGAAGCAGCGAAGNAGCAGTGAAATGCTTGTGTTTACGAATACAAAAGATGGCTTACGA 2073
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QY 2614 CATGAGTCTCTATTTCTTATTTGATACAGGTGAATCGAATCAATGAATGAGGATG 2673
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QY 2674 TGGGTTGGATTTAAGATTACGACCCAGAGGGATGATGCAACACTCGGAAACCTAGAAATG 2733
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Db 3031 CAAACAGCGTGGATTTGTTATGATCAGCGAAATGCCATCAAAATGTTGTTTTCGAAAT 3090
QY 3094 GGGTTAAGTAATTTGGAATGCAACCGCTGCGGTAGAGTACAAACAAATCAATCATATCT 3153

Db 3091 GGGTTAAGTAATTTGGAATGCAACCGCTGCGGTAGAGTACAAACAAATCAATCATATCT 3150
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Db 3151 GTCCTTGTGATTTCCAAACCTGGGATGAGCAAGTTTCCAAACAGTTTACAGTTCAACCGAAT 3210
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RESULT 5

US-07-941-650A-1
; Sequence 1, Application US/07941650A
; Patent No. 6294184
; GENERAL INFORMATION:
; APPLICANT: Oyeda, Kendrick A.
; APPLICANT: Bradfisch, Gregory A.
; TITLE OF INVENTION: Process for Controlling Lepidopteran Pests
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/941,650A
; FILING DATE: 19920908
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/758,020
; FILING DATE: 12-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/658,935
; FILING DATE: 21-FEB-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/642,112
; FILING DATE: 16-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3471 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:

ORGANISM: Bacillus thuringiensis
STRAIN: kumamotoensis
INDIVIDUAL ISOLATE: P950C
IMMEDIATE SOURCE:
CLONE: E. coli NM522(pMYC1638), NRRL B-18751
US-07-941-650A-1

Query Match 50.0%; Score 1812.2; DB 4; Length 3471;

Best Local Similarity 72.2%; Pred. No. 0;

Matches 2504; Conservative 0; Mismatches 908; Indels 57; Gaps 9;

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QY 1 ATGAGTCCAAATAATCAAAATGAATATGAATATATAGATGCGACACCTTCTACCTTCTGTA 60
DB 1 ATGAGTCCAAATAATCAAAATGAATATGAATATATAGATGCGACACCTTCTACCTTCTGTA 60
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DB 61 TCCAGTGATTTCTACAGATACCTTTTGGGAATGAGCGCAACAGATGCGGTTACAAATATG 120
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QY 241 CTATCAGGTTTAGGGTCCCAATTTGTTGGGCGGATAGTGAATCTTATACCTTATTT 300
DB 238 CTAGGAGCTTTTAGGGGTTCCATTTGCTAGTCAGATAGTAGTTCTATAGTTTCAATGTT 297
QY 301 GATATTTCTGGCCCTTCAGGGGAAAAGAGTCAATGGGAAAATTTTATGGAACAAAGTAGAA 360
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QY 361 GAATCAATTAATCAAAAATAGCAGAAATATGCAAGGAATAAAGCGCTTTCGGAATTAAGA 420
DB 358 GAATCGTTGATCAAAAATAGAAAATATGTAAGAATAAAGGCTCTTGTGTAATTAATAA 417
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DB 898 CAACCTAACAGGAGTAGTATATACAGATCCAGATCCAGATCCAGATCCAGATCCAGATCCAGAT 957
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QY 1654 TTACAGTATATAAGAGTACTGTTCTGTAGGAACCTTATTTCTAGCTCGCATATGGCCTA 1713
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QY 1714 GCATTAAGAAAAGCAGGGAATATCTGTGTAAGACTCGAGATATGCTACTGATCGAGATATT 1773
DB 1720 TTAATCAACAAG-----ATATGTTGTAAGAAATTCGCTATGCTCTACACAGATTTT 1770
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QY 1834 CTGACATCTAAACCTTTTAAAGTTGCGAGATGCTATCAACCAATTTAAATTTAGCAACAGAT 1893
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QY 1894 AGTTGCTAGCATTTGAACAAATAATTTTAGGTGAAGACCTTAATTTCAACAATTTATCTGTATA 1953
DB 1891 TTCAGAGAAACACAAAGATAAAATACTCCTATCCATGGGTGATTTTAGCTCCGGTCAAGAA 1950
QY 1954 GTTTACGTTGACCGAATCGAATTTCAATCCAGTAGATGAGACATATGAAGCGGAAACAGAT 2013
DB 1951 GTTTATATAGACCGAATCGAATTTCAATCCAGTAGATGAGACATATGAGCGGAAACAGAT 2010
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STRAIN: japonensis
INDIVIDUAL ISOLATE: Buibu1
FEATURE:
NAME/KEY: CDS
LOCATION: 187..3636
US-07-915-203-1

Query Match 32.6%; Score 1180; DB 1; Length 3797;
Best Local Similarity 61.4%; Pred. No. 3.9e-248;
Matches 2094; Conservative 0; Mismatches 1230; Indels 86; Gaps 9;

Qy	1	ATGAGTCCAAATATCAAAATGAATATGAATATAGATGCGACACCTTCTACTTCTGTA	60
Db	187	ATGAGTCCAAATATCAAAATGAATATGAATATAGATGCGACACCTTCTACTTCTGTA	246
Qy	61	TCCATGATTTCAACAGATACCTTTTCGGATGAGCAACAAATGCGCTACAAATATG	120
Db	247	TCCGATAATTTCTATTAGATATCTTTAGCAACGATCAACAAATGATATACAAATC	306
Qy	121	GATTATAAGATTTATTAATAATGCTCGCGGAATGCTAGTGAATACCTCGTTTCACT	180
Db	307	AATTATAAGATTTCTGAAATGACCGAATCAACAAATGCTGAATGCTCGAATCC	366
Qy	181	GAACTACTTTAGCGGACAAATGAGCTAAGCGCGCAATTTGATATAGTAAATTA	240
Db	367	GGGACATTTATTAGTGGCAGGATCGGTTGGAACTGGAAATGATATTTAGTACTATA	426
Qy	241	CTATCAGGTTTAGGGTCCCATTTCTGGCCGATAGTAGTCTTTATCTCAACTATT	300
Db	427	ATAAGTGGTTTAGGATTTCCAGTGTCTGGGGAAGTCTTCTCAATTTCTGGGTTCT	486
Qy	301	GATATTTCTGGCCCTCAGGGGAAAAGAGTCAATGGGAAATTTTATGAAACAAAGT	360
Db	487	GGCTTATTGTGGCCGTCAAATTAATGAAATGTATGGCAATATTTATGATCGAGT	546
Qy	361	GAACTCATTAATCAAAATATGACAGATATGCAAGGAATAAAGCGCTTTCCGAA	420
Db	547	GAGCTAAATGATCAAAATATTTAGATTTCTGTAAGATCAAGAGCCATTGCGAGT	606
Qy	421	GGATTAGTAAATTAATCAATTTATCTAACTGCTGGCGATAGTAGTCTTTATCT	480
Db	607	AATCTAGAAATAGCTGTAGAGTACTATCAAAATGCACTTGAAGACTGGAGAA	666
Qy	481	AATGGTTCAAGAGCCTTACGAGATGCGAAATTCGATTTGAAATCTCGATAGTT	540
Db	667	CACATGACAGAGCGCAGCATTTGTAAGGAAAGATTTGGAAATGCCAAGCAAT	726
Qy	541	AGCAATATATGCCATCTTTTAGAGTGACAAATTTTGAAGTACCATTCCTTACT	600
Db	727	CGTACTAATCGGTTCAATTTCTCAACGAAATTTATGAGACTCCACTCTTAC	786
Qy	601	GCAATGGCAGCCAACTTCAATTTACTGTTTATTAAGGAGCGCTCAATTTTGG	660
Db	787	GCACAGGCGCCTCTCTGCAATTTGTTGTAATGAGGATGTTCAAAATTTAC	846
Qy	661	TGGGATGGTCAACAACTACTATTAATACTATTATGATCGTCAAAATGAACT	720
Db	847	TGGGATATCTCAAAATGATATGACCTATTTTATAAGAACAGTATCTTATAC	906
Qy	721	GAAATTTCTGATCATGTTGTAAGTGGTATGAACTGGTTTATAGCAAAATTA	780
Db	907	AGATATTCGATCAATTCGCTCAATGGTCAATGGTCAATGGTCTGGTTAAAT	966
Qy	781	ACCGCTAAACATGGTTGACTATATACCAATTTCCGTAGAGNAATGACATG	840
Db	967	GGTGTAAAGCAATGGGTGATATATAATCTGTTTCCGAGAGAAATGAATG	1026
Qy	841	GATGTTGTTGCTATTCTCCAAATATGACACAGCAGCTACCCCAATGAAAC	900
Db	1027	GATCTAGTTGCAATTTTCCAAACTACGATGCGCGTATATATCCATTTGAA	1086
Qy	901	CAACTAACAGGGAAGTATATACAGATCCACTGGGCGCGTAAACGTTCTCA	960

Db	1087	GAACTTACAAGAGAAATTTTTCACAGATCCTGTTGGAAGT-----TACGTAACTGGA	1137
Qy	961	TCCTGGTATGACAAAGCAGCCTTTCTTCGGAGTGTAGATAATCATCGTTATTTCGAC	1020
Db	1138	CAATCGAGTACCTTTATATCTTGTGATCGATATGATTCAGCAGCTCTCTCTTCA	1197
Qy	1021	CATGTAATTTGATATATAAAGCGGACTCACAGTGTATATACAAATCAAGAA	1080
Db	1198	ACGCTCGAAGAACCTTACTTAGAAAACCTGATTTCTTTACTTGTGCAAGAAAT	1257
Qy	1081	GCTCGCTATATAGACATTTGGCTGGTGCATCAATAGCTACCATCGTGTGAGT	1140
Db	1258	TATCAAGTTTTATAGCAAAACGGTACGATGGAATATTTATTAATTTGGGGAG	1317
Qy	1141	AGTAATCTTCAACAAATGATGGAACCTAAATCAAAATCTACACAGCCTAGT	1200
Db	1318	TTAACCTTTCTTATATCTATGTTCTCTCATTAATAATAG-----TGGGGT	1374
Qy	1201	TTTACGAATATGATATTTACAGACTCTATCAAAAGGATGAGTCTCTCTTGA	1260
Db	1375	GGTGTGAGGATATTTATCTCTGGGTCAAAATGATATTTACAGAGTTGTATG	1434
Qy	1261	TACCTCGTTATAGTATATTTTGGATGCGCAGAGTGGAGTTTTCATGTTAA	1320
Db	1435	ATAGGAAGGTACACGAATAGTCTGCTAGGAGTAAATCCAGTTACTTTTT	1483
Qy	1321	CAATTGAATATACACAGAAAGCGTTAAAGTATAATCCAGTTTCCAAAGAT	1380
Db	1484	-ACTTCAGTAAATATACAAAAAACCTTTTCGAAGCCAAACAAATTCGCGGT	1542
Qy	1381	AGTACAAGAGATTCGGAATTAGAATTTACCTCCAGAACTTCAGATCAACCA	1440
Db	1543	AAAACAAATGATTCGCGGGAAGATTTAACTTACGAAATTTCAATCTTATAG	1602
Qy	1441	TCATATAGCCATAGATTTATGTCATATCACAGTATTTCCGCGACGGGTAA	1500
Db	1603	GTAAGTTACATTTACATCTTTTGAATAAAGTA-----CCGGTGGTAC	1656
Qy	1501	TTAGTACCTGTATTTCTTGGACACATCGAATGTCAGATTTTAAACAATA	1560
Db	1657	GTAGTTCTTATTTTGGTTGGACGATAGTAGTGGCAGTCCCAATTAATTT	1716
Qy	1561	GATAAAATCACTCAAAATTCGCGCCGTTAA-----ATGTTGGGATAAT	1617
Db	1717	ACAAAATCTCACAAATCCCAATCAATAAGCAAGTAACTAGCGGTGGAGCG	1776
Qy	1618	GTGGTAAAGACCCAGGACATACAGAGGGGATTTTATACAGTATATAGAA	1677
Db	1777	AATTTCCAGGAAGGTTCTATATAATGGAGGACCTGTAAATGNAATTA	1836
Qy	1678	TCTGTAGGAACCTTATTTCTAGCTCGATAT-----GGGCT	1712
Db	1837	CAAGTAAATTAAGGTTGCGAAGGAGCAAGTCAAGAGATATCGTATT	1896
Qy	1713	AGCATTAGAAAAGCAGGGAATATCGTTAAGACTGAGATATGCTACTGATG	1772
Db	1897	AGAAATCAGATATGCTCTGATAGAGCGGTAAATTTACGATATCTTCCAG	1956
Qy	1773	TGTTATGATGTAAACGATGCTCAGATTCAGATGCCAAAACAAATGAAC	1832
Db	1957	AATCTGCAACCTATTCAGCTTCTATTGCTTATA-CAAAATACTGTCTCA	2015
Qy	1833	TCTGACATCTAAAACCTTTTAAAGTTGAGATGCTATCAACATTTAAAT	1892
Db	2016	TCTAACGTATAGTACTTTTGCATATGCAAGATCTGGCCCTATAAACTT	2075
Qy	1893	TAGTTTCGCTAGCAATTTGAAACATAATTTTAGTGAAGACCCCTAAT	1952
Db	2076	NAAGTTCAAGGACTTTTGTATATATCTATTACAAAAG-----AGCAG	2126
Qy	1953	AGTTTACGTTGACCAATTCGAATTCATCCAGTAGATGAGACATATGAAG	2012
Db	2127	CCTTTATATGATAGAAATTTTATTTTCCAGTTAATAGCTTTTATTTGA	2186

INDIVIDUAL ISOLATE: Buibui

FEATURE:
NAME/KEY: CDS
LOCATION: 187..3636
US-08-272-887-1

Query Match 32.6%; Score 1180; DB 1; Length 3797;
Best Local Similarity 61.4%; Pred. No. 3.9e-248;
Matches 2094; Conservative 0; Mismatches 1230; Indels 86; Gaps 9;

```
Qy 1 ATGAGTCCTCAATTAATCAAAATGAATATGAATATATAGATGCGACACCTTCTACTCTCTGTA 60
Db 187 ATGAGTCCTCAATTAATCAAAATGAATATGAATATATAGATGCTTTATCACCCACTTCTGTA 246
Qy 61 TCCAATGATTTCTAAACAGATACCTTTTGGCAATGAGCCAAACAAATGCGCTCACAATAATG 120
Db 247 TCCGATAATTTCTTAGATATCTTTAGCAACAGCATCAACGACACATTAACAACATG 306
Qy 121 GATTATAAGATTATTTAAATATGCTGCGGGAATGCTAGTAGAATACCTCGTTCACT 180
Db 307 AATTATAAGATTATCTGAAATGACCGAATCAACAAATGCTGAATGCTCGAAATCCC 366
Qy 181 GAAGTACTTGTAGCGCAAGATCAGCTAAGCGCGCAATTCATATAGTAGTAATTA 240
Db 367 GGGACATTTATTTAGTCGCGCAGATGCGGTTGGAACCTGGAATTTGATATGTTAGTACTATA 426
Qy 241 CTATCAGGTTTAGGGTCCCATTTGTTGGCCGATAGTAGTCTTTATATCTCAACTTAT 300
Db 427 ATAGTGGTTTAGGATTCAGTGTCTTGGGAAGTCTTCTCAATTCGGTTCATTAAT 486
Qy 301 GATATTTCTGTGCTTCAGGGGAAAAAGAGTCAATGGGAAATTTTATGGAACAAAGTAGAA 360
Db 487 GGCCTTATTGTGCGCGTCAAAATTAATGAATGATGCAAAATATTTATGAATCGAGTGGAA 546
Qy 361 GAATCTTAATTAACAAAATAGCAGATATGCAAGGAATAAGCGCTTTCCGNAATTAGAA 420
Db 547 GAGCTAAATGATCAAAAATATTTAGATCTCTGAAGATCAAGAGCCATTCAGATTTAGCT 606
Qy 421 GGATTAGGTAAATTAATCAATTTATATCTAACTGCGCTTTGAAGATGGGAAGAAATCCA 480
Db 607 AATTCAGATAGTGTAGAGTACTATCAAAATGCACTTGAAGACTGGAGAAACCA 666
Qy 481 AATGTTCAAGAGCCTTAACAGATGTCGAAATCGAATTTGAAATCCTGGATAGTTTATTT 540
Db 667 CACAGTACACGAAGCGCAGCACTTGTAAAGGAAAGATTTGGAAATCGAAGCAATTTTA 726
Qy 541 ACGCAATATGCCATCTTTTAGAGTGACAAATTTTGAAGTACCAATCTTACTGTATAT 600
Db 727 CGTACTAATGGGTTTCAATTTCTCAACGAAATTTAGAGACTCCACTCTTACCACATAT 786
Qy 601 GCAATGGCAGCAACCTTCATTTACTGTTTATTAAGAGCGCGTCAATTTTGGAGAAGAA 660
Db 787 GCACAGCCGCTCTCTGATTTGCTTGTAAAGAGGATGTTCAATTTACGGGAAGGA 846
Qy 661 TGGGATGTCACAACTACTATTAATACTATATGATCGTCAAAATGAAACTTACTGCA 720
Db 847 TGGGGATATCCTCAAAATGATATGACCTATTTTATAAAGAACAACTATCTTATACGGCT 906
Qy 721 GAATATTCTGATCACTGTGTAAGTGGTATGAACTGGTTTAGCAAAATTAAGAGCAG 780
Db 907 AGATATTCGATCATTTGCGTCCAAATGGTCAATGCTGGTTTAAATTAATTAAGAGGACG 966
Qy 781 ACGGCTAAACAAATGGGTTGACTATATAACCAATTCGCTAGAGAAATGACACTGGCGGTTTA 840
Db 967 GGTGCTAGCAATGGTGGATATATATCGTTTCCGAAGAGAAATGAATGATGATGTTG 1026
Qy 841 GATGTTGTTGCAATTTCCCAATTAATGACACGACGCTACCCAAATGGAACCAAGCA 900
Db 1027 GATCTAGTTGCAATTTTCCAACTACGATGCGCGTATATATCCACTTGGAAACAAATGCA 1086
Qy 901 CAACTAACAGGGAAGTATATACAGATTCACATCGGCGCGGTAAACGTGCTCAATTTGGT 960
Db 1087 GAACTTACAAGAGAAATTTTCAAGATCTCTGTGGAAGT-----TACGTAACCTGGA 1137
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Qy 961 TCCTGGTATGACAAAGCACCTTCTTTCCGAGTGATAGAAATCATCCGTTATTTCGACCAACC 1020
Db 1138 CAATCGAGTACCCTTATATCTTGGTACGATATGATTCAGCAGCTCTTCCCTCATTTTCA 1197
Qy 1021 CATGTATTTGATATATAAACGGGACTCAAGTGTATACAAATCAAGAAAGCAATTTCTCC 1080
Db 1198 ACGCTCGAAGAACCTACTATTAGAAAACCTGATTTCTTTACTTTGCTGCAAGAAATAGAATG 1257
Qy 1081 GCTCGCTATATAAGACATTTGGGCTGGTCAATCAAAATAAGCTACCATCGTGTCTAGTAGGGT 1140
Db 1258 TATACAGGTTTATAGCAAAACGGTACGATGAATATTAATAATTTATGGGAGGACAAAGG 1317
Qy 1141 AGTAATCTTCAACAAATGATATGGAATCAATCAAAATCTACACAGCACTAGTACCTTTTAT 1200
Db 1318 TTAACCCCTTCTTATATCTATGTTTCTCAATCAATAAATATAG---TGGGGTCTTTGCC 1374
Qy 1201 TTTAGCAATATGATATTTACAGACTCTCTCAAGGATGCGAGTACTCTCTTGATATTTGTT 1260
Db 1375 GGTGCTGAGGATATTTATCTCTGTTGGGTCAAAATGATATTTACAGAGTTGTATGGAATTTAT 1434
Qy 1261 TACCCTGGTTTATACGTATATATTTTTCGAATGCCAGAAAGTCGAGTCTTTTTCATGGTAAAC 1320
Db 1435 ATAGGAAGGTACCAANTAGTCTGCTAGAGTAAATCCAGTTACTTTTTF----- 1483
Qy 1321 CAATTTGAATTAATACCAAGAAAGACGTTAAAGTATATATCCAGTTTCCAAAGATATTTATAGCG 1380
Db 1484 -ACTTCAGTAAATATACACAAAATCTTATTCGAAGCCAAAACAAATTCGGGGTGAATA 1542
Qy 1381 AGTACAAGAGATTCGGAATTTAGAAATTAATCTCCAGAAATCTTCAGATCAACAAATATATGAG 1440
Db 1543 AAAACAAATTTGATTCGGGCGAAGAAATTAATCTACGAAATTTATCAATCTTATAGTACAGG 1602
Qy 1441 TCATATAGCCATAGATATGTCATATCAACAGTATTCGCGGACGGGTAAACTACCTACCGGA 1500
Db 1603 GTAACTTACATTTACATCTTTTGAATTAAGAAAGTA-----CGGGTGGTACAGTATTAGGA 1656
Qy 1501 TTAGTACCTGTATTTTCTTGGACACATCGAAGTCAGATTTTAAACAATACAATATATTTCA 1560
Db 1657 GTAGTTCCTATATTTGTTTGGAGCATAGTAGTGCAGTCGCAATAAATCTTTATTTACGCA 1716
Qy 1561 GATAAATACATCAAAATTCGGGCCGTTAA---ATGTTGGGATAAATTTACCGTTTGTTCGA 1617
Db 1717 ACAAATATCTCAAAATCCCAATCAATTAAGCAAGTAGAAGTACGCGGTGGAGCGGTTTGG 1776
Qy 1618 GTGGTAAAGGACACAGGACATACAGSAGGGATTTTATACAGTATAATAAGAGTACTGCT 1677
Db 1777 AATTTCCAGGAAGGTCTATATATGAGGAACCTGTATGAATATCTGGGTCTGGTTCC 1836
Qy 1678 TCTGTAGGAACCTTATTTCTAGCTCGATAT-----GGCCT 1712
Db 1837 CAAGTAAATAAATCTTAAGGTTCGCAACAGATGCAGGAGCAAGTCAAGATATCGTAT 1896
Qy 1713 AGCATTAGAAAAGCAGGGAATATCGTGTAAAGACTGAGATATGCTATGATGCGAGATAT 1772
Db 1897 AGAATCAGATATGCTCTGATAGAGCGGTAATTTAAGATATCTTCCAGATCTCCAGAG 1956
Qy 1773 TGTATTGATGTAAGACGATGCTCAGATTCAGATGCCAAAACAATGAACCCAGGTGAGGA 1832
Db 1957 AATCTGCAACCTTATTCAGCTTCTATGCTTATA-CAAACTACTATGCTACAAATGCTTTC 2015
Qy 1833 TCTGACATCTAAAACTTTTAAAGTTGCGAGATGCTATCAACAATTTAAATTTAGCAACAGA 1892
Db 2016 TCTAAGTATAGTACTTTTGCATATGCAAGATCTGCGCCCTATAAATCTTAGGAGTTCCGG 2075
Qy 1893 TAGTTCCGCTAGCAATTTGAACATAAATTTAGGTGAAGACCCCTAAATCAACATATCTGGTAT 1952
Db 2076 AAGTTCAAGGACTTTGATATATCTATTACAAAAGA-----AGCAGGTGCTGCTAA 2126
Qy 1953 AGTTTACGTTGACCAATCGAATTTCCAGTAGATGAGCATATGAGCCGACCAACAGA 2012
Db 2127 CCTTTATTTGATGAATTTTATCCAGTTTATTTCCAGTTTATTTGAGAGCAAGAGA 2186
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QY 2013 TTTAGACGAGGAGAAAGCGATGAAATGCTTGTGTACGAATAAAGAGATGGCTTACG 2072
Db 2187 CCTAGATGGCAAGAAAGCTGTGAATGGCTTGTGTACGAATGAAGAGATGCTTACA 2246
QY 2073 ACCAGGCGTAAACGATTAAGTGAATCAAGCGGCAAACTTAGTGGATGCTTACGA 2132
Db 2247 GACAGTGTAAACGATTAAGTGAATCAAGCGGCAAACTTAGTGGATGCTTACGA 2306
QY 2133 TGATTTGTATCAATGAAGAAACGATTTGATTTGATGCAAGTGAAGAGGCAAAACGCT 2192
Db 2307 TGATTTATACCAATGAAGAAACGATTTGATTTGATGCAAGTGAAGAGGCAAAACGCT 2366
QY 2193 CAGTGAGGCAATTAATTTGCTTCAAGATCCAGATTTCAAGAGATTAATGAAGAAATGG 2252
Db 2367 TGTTCAAGGCAATTAATTTGCTTCAAGATCCAGATTTCAAGAGATTAATGAAGAAATGG 2426
QY 2253 CTGAGCGCAAGTACGGAATTTGAGTTATAGAGGGGATGCTTTATTTCAAGGGCGTTA 2312
Db 2427 ATGACGGGAAGTACGGAATTTGAGTTATAGAGGGGATGCTTTATTTAAAGATCGTTT 2486
QY 2313 TCTACGCTACACGAGTGCAGAGAAATAGATACGGAACGATTCACACGCTATCTGTATCA 2372
Db 2487 GCTTGGTTGACAGTGCAGAGAGATTTGATACAGAAATATCCAGATATCTCTATCA 2546
QY 2373 AAAAGTAGAGGAGGTGATTAATAACCATACACAGATATAGATTTAGAGGGTGTTCGG 2432
Db 2547 ACAATAGATGAATCGCTTTTAAACCATATACAGATATTAACCTTAAAGGTTTATAGG 2606
QY 2433 AAGCAGTCAAGGATTTGGAATTTTCAACATTCGTCATCAAGCAACCAATTTGTAAGAAA 2492
Db 2607 AAGTAGTCAAGATTTAGAGATTTAAATTAATAGCTCATCGGGCAATCAAAATCGTCAAAA 2666
QY 2493 TGTACCGGATGATTTGCTGCGAGATGATCTCTGTTAACTCGGATGTAGTATCAATCG 2552
Db 2667 TGTACCAAGATATCTTGGCCAGATGATCGGCTGTCAATCTTGTGTGAGTGCATCG 2726
QY 2553 ATGACGGAACAAAGTATGGAATAGCGGTTTGAAGTAGAAGAACCGT----- 2601
Db 2727 CTGAGTGAACAAAGTATGATAGACGGAATTTAGCACTCGAAGAAATGGAAGAAATGG 2786
QY 2602 -----TCTGTCAGGCGATGAGTCTCTATCTTATCTATGATACAGTGAATCGATTA 2654
Db 2787 AAATATGCTTCTGATTCCTCCATGCAATTTCTTCCATATGATACGGGTGAATAGATTT 2846
QY 2655 CAATGAAGAAATGACGAATATCGGTTGGAATTAAGATTAAGCAACCCAGAGGATATGCAAC 2714
Db 2847 GAATGAAGAAATACAGAAATTTGATGCTATTAATAATTCGCAACAAATGGAAGCGCAAC 2906
QY 2715 ACTCGGAACCTAGAAATTTGGTTCGAAGAGGGACCTTTATCAGGAGACGATTAGAACGCTT 2774
Db 2907 ACTAGGAATCTTGAATTTGTAGAAGAGGGGCCATTTGTACGGGAAACATTAGAATGGC 2966
QY 2775 GCAAGAGAGAGAAACAAAGTGGAGATTCATATGCAAGAGAGAGTGAAGAAACGATAG 2834
Db 2967 CCAACAAAGAAACAAAGTGGCAAGCAAAATGCAAGAAACGTCAGCATCAGAAA 3026
QY 2835 AAGTATATGCGATCGAAACAAAGCGGTAGATGCTTTATGCGGATATCAGGATCAGCA 2894
Db 3027 AACATATATGCAAGCAAGCAAGCAATGATGCTTTATGCGAGATTAAGAACCAAAA 3086
QY 2895 ACTGAATCTGATAGAGATTAAGATCTTTATCTGCGGCCCAAGATCTGATACAGTCCAT 2954
Db 3087 ACTTAATCTGCTGTAGAAATGTAGATTTGTTGTCAGGCCCAAAACCTTTGTACAGTCCAT 3146
QY 2955 TCCTTAGGTATATACGAATTTCCCGAAGAAATACAGGAGATGAATATAGCAAGTTTAC 3014
Db 3147 TCCTTAGGTATATAGTATGCGGTTTACCGGAATCCCTGGAATGAATATAGCAGTTTAC 3206
QY 3015 AGAATTAACAGATCGATCTCAACAAAGCGGTGAGTTGTTGATGATCAGCGAAATGCCATACC 3074
Db 3207 AGAGTTAAACAAATAGATCTCAACAAAGCATGGAATTTGATGATCTTCAAAACGCTATACC 3266
QY 3075 AAATGGTGAATTTTCAAAATGGTTAAGTAAATGGAATGCAACGCTGCGGTAGAAGTACA 3134

Db 3267 AAATGGAGATTTTCAAAATGGAATTAAGTAAATGGAATGCAACATCAGATGTAAATGTCCA 3326
QY 3135 ACAATCAATCATACATCTGCTTGTGATTCGAACTGGGATGAGCAAGTTTTCGCAACA 3194
Db 3327 ACAATAGCGATACATCTGCTTGTGATTCGAACTGGGATGAGCAAGTTTTCGCAACA 3386
QY 3195 GTTTACAGTTCCAACCGCAATCAAGATATGCTTACGAGTTACTGCGAGAAAGAGGGGT 3254
Db 3387 ATTTACAGTTCACCGCAATTAAGATATGCTTACGAGTTACTGCGAGAAAGAGGGAGT 3446
QY 3255 AGGAATGGAATGATTAAGTATCCGTGATTCGAGTGGGAAATCAAAACAGAAACGCTTACTTTTAG 3314
Db 3447 AGGAGCGGATATGATGATCATCCGTGATGGTGGCAATCAGACAGAAACACTCACAATTAA 3506
QY 3315 TGCAGCGATATGATCAAAATGGAATGGAATGATATACGCAAGTGTCCCAATA 3364
Db 3507 TATATGTGATGATGATACAGGTGTTTATCTACTGATCAAACTAGCTATA 3556

RESULT 8

US-08-789-449-1
; Sequence 1, Application US/08789449
; Patent No. 5824878
; GENERAL INFORMATION:
; APPLICANT: Ohba, Michio
; APPLICANT: Iwahana, Hidenori
; APPLICANT: Sato, Reiichi
; APPLICANT: Suzuki, No. 5824878ukazu
; APPLICANT: Ogiwara, Katsutoshi
; APPLICANT: Sakanaka, Kazunobu
; APPLICANT: Hori, Hidetaki
; APPLICANT: Asano, Shouji
; APPLICANT: Kawasaki, Tadaaki
; TITLE OF INVENTION: No. 5824878el Microorganism and Insecticide
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/789,449
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,887
; FILING DATE: 08-JUL-1994
; APPLICATION NUMBER: US 07/915,203
; FILING DATE: 23-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: M/K 301
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3797 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis

STRAIN: japonensis
INDIVIDUAL ISOLATE: Buibui
FEATURE:
NAME/KEY: CDS
LOCATION: 187..3636
US-08-789-449-1

Query Match 32.6%; Score 1180; DB 1; Length 3797;
Best Local Similarity 61.4%; Pred. No. 3 9e-248; Indels 86; Gaps 9;
Matches 2094; Conservative 0; Mismatches 1230;

QY 1 ATGAGTCCAAATATCAAAATGAATATGAATATATAGATCGCACACTTCTTCTCTGTA 60
DB 187 ATGAGTCCAAATATCAAAATGAATATGAATATATAGATCGCACACTTCTTCTCTGTA 246
QY 61 TCCAAATGATTTCAACGATACCTTTTCCGAATGAGCGCAACAATGGCTGACAAATATG 120
DB 247 TCCGATAATTTCTATAGATATCTTTAGCAACGATCAAAACGACATTAACAACATG 306
QY 121 GATTATTAAGATTTATTAATAATGCTCGGGAAATGCTAGTAGTAATACCTGGTTACCT 180
DB 307 AATTATTAAGATTTATCTGAATAATGACCGAATCAACAATGCTGAATGCTCGAATCCC 366
QY 181 GAAGTACTTCTTAGCGGACAGATGCAAGTAAAGCCGCAATTTGATATAGTAGGTAATTA 240
DB 367 GGACATTTATAGTGGCAGGATGCGGTTGGAATGGAATTTGATATTTAGTACTATA 426
QY 241 CTATCAGTTTATGGGTCCTATTTGTTGGCCGATAGTAGTCTTTATATCTCACTTTAT 300
DB 427 ATAAATGGTTAGGATTTCCAGTCTTGGGGAAGTCTTCTCAATTTCTGGGTTCAATTA 486
QY 301 GATTATCTGTGGCTTCAGGGAAAGAGTCAATGGGAATTTTATGGAAACAGTAGAA 360
DB 487 GGCTTATTTGGGCGTCAAAATATGAATAATGGAATGATGGCAATATTTATGAATCGAGTGAA 546
QY 361 GAATCAATTAATCAAAATATAGCAGAAATATGCAAGGAATTAAGAGCTTTCCGAATTAAGAA 420
DB 547 GAGTAAATGATCAAAATATATAGATTTCTGTAAGATCAAGAGCCATTTGACATTTAGCT 606
QY 421 GGATAGGTAATTAATACCAATTTATCTAATCTGCTGCTGAGATGCGGAAGAAATCCA 480
DB 607 AATTCTAGAATAGCTGTAGAGTACTATCAAAATGCATTTGAAGCTGGAGAAACCCCA 666
QY 481 AATGGTTCAAGAGCTTACAGATGTCGAAATCGATTTGAAATCCTGGATAGTTTATTT 540
DB 667 CACAGTACAGAGCGCAGCATTTGTAAGAAAGATTTGGAATGCAAGAGCAATTTTA 726
QY 541 ACGCAATATATGCCATCTTTTAGAGTGACAAATTTTGAAGTACCATCTTCTTCTGTATAT 600
DB 727 CGTACTAACATGGGTTCAATTTCTCAACGAAATTTAGACTCCACTTTACCCACATAT 786
QY 601 GCAATGCGACCAACCTTCAATTTACTGTTATTAAGAGCGGCTCAATTTTGGAGAGAA 660
DB 787 GCACAGCGCGCTCTCTGCAATTTGCTGTAATGAGGATGTTCAAAATTTACGGGAAGAA 846
QY 561 TGGGATGGTCAACACTACTATTAATAATCTATTTATGATGCTCAATGAAATTTACTTCCA 720
DB 847 TGGGGATATCTCAAAATGATATTTGACCTATTTTATAAAGAACCAAGTATCTTTATACGGCT 906
QY 721 GAATATTTCTGATCACTGTATAAGTGTGTGAAATCTGGTTTATGCAAAATTAAGAGGCAAG 780
DB 907 AGATATTTCCGATCATTTGGTCCATTTGTAATGTAATTTAAATTAATTAAGAGGAACG 966
QY 781 AGCGTAAACAAATGGGTTGACTATAACCAATTCGCTAGAGAAATGACACTGGCGGTTTAA 840
DB 967 GGTCTTAAGCAATGGGTTGATTAATAATCGTTTCCGAAGAGAAATGAATGTGATGTTATG 1026
QY 841 GATGTTGTTGATTTATTTCCAAATTTATGACACGCGAGTACCCCAATGGAAACGAAAGCA 900
DB 1027 GATCTAGTTGCAATTTATTTCCAAATCTACGATGCGGCTATATATCCACTGGAAACCAATGCA 1086
QY 901 CAATCAACGAGGAGATATATACAGATCCACTGGGCGGGTAACGCTGCTTCAATTTGGT 960

DB 1087 GAACCTTACAAGAGAAATTTTTCACAGATCCTGTGTGAAGT-----TACGTAACTGA 1137
QY 961 TCCTGTATGACAAAGCACCTTCTTTTCGGAGTGATAGAAATCATCTCGTTATTTCGACACCC 1020
DB 1138 CAATCGAGTACCTTATATCTTGGTACGATATGATTCGACGAGCTCTTCCITCAITTTCA 1197
QY 1021 CATGTATTGATTTATTAACGGGACTCAAGTGATATACAAATCAAGAAAGCAATTTCTTCC 1080
DB 1198 ACGCTCGAGAACCTACTTTAGAAAACCTGATTTCTTTTACTTTGCTGCAGAAATTAAGAATG 1257
QY 1081 GCTCGCTATATAAGCATTTGGCTGGTCTCATCAATAAGTACCATCGTCTAGTAGGGT 1140
DB 1258 TATACAAGTTTATAGACAAACGGTAGATTAATTAATTAATTTATTTGGGGAGGACAAAGG 1317
QY 1141 AGTAATCTTCAAAATGATGGAATAATCAAAATCTACACAGCACTAGTACCTTTGAT 1200
DB 1318 TTAAACCTTTCTTATCTATGTTCTCTCAATTCATTAATATAG---TGGGGTCTTGGC 1374
QY 1201 TTTACGAATTTATGATTTTACAAGACTCTATCAAAAGGATGCAAGTACTCTTGTATTTGT 1260
DB 1375 GGTGCTGAGGATATTTCTCTGGGTCAAAATGATATTTACAGAGTTGTATGAGACTTAT 1434
QY 1261 TACCTGGTTATACGATATATTTTTTGGATGCGCAAGTCAAGTCTTTCATGTTAAAC 1320
DB 1435 ATAGGAAGGTACACGAATAGTCTGCTAGGATTAATTCAGTTTACTTTTT- 1483
QY 1321 CAATTAATAATACAGAAAGAGTAAAGTATATCCAGTTTCCAAAGATATATATAGCG 1380
DB 1484 -ACTTCAGTAATAATACACAAAAACCTTATTCGAAGCCAAACAAATTCGCGGTGGAATA 1542
QY 1381 AGTACAAGAGATTCGGAATTTAGAAATTTACCTCCAGAAACTTTCAGATCAACCAATTTATGAG 1440
DB 1543 AACAATTTGATTCGCGGAGAAATTAATCTTACGAAATTTATCAATCTTATAGTACAGG 1602
QY 1441 TCATATAGCAATAGATTTATGTCATATCAAGATTTCCCGGAGCGGTAACTACCGGA 1500
DB 1603 GTAAGTTACATTTACATCTTTTGAATAAAGTA-----CCGGTGTGACAGTATTAGGA 1656
QY 1501 TTAGTACCTGTATTTTTCGGACACATCGAAGTGCAAGTTTAAACAATACAATATATTC 1560
DB 1657 GTAGTTCTTATTTTGGTTGGACGCAATAGTAGTCCGATGCGCAATATTTTATTAGGCA 1716
QY 1561 GATPAAATCACTCAAAATTCGCGCGTTAA---ATGTTGGGATAATTTTACCGTTTGTTC 1617
DB 1717 ACAAATCTCAAAATCCCAATCAATAAAGCAAGTAGAAGTACGCGGTGAGCGGTTGG 1776
QY 1618 GTGGTAAAGGACCGAGACATACAGAGGGGATTTATACAGTATTAATAGAGTACTGGT 1677
DB 1777 AATTTCCAAGAGGTCTATATAATGAGGACCTGTAATGAATTTATCTGGGTCTGGTTCC 1836
QY 1678 TCTGTAGGAACCTTATTTCTAGCTCGATAT-----GGCCT 1712
DB 1837 CAAGTAAATAACTTAAGGGTTCGCAACAGATGCAAGGGAGCAAGTCAAAAGATATCGTATT 1896
QY 1713 AGCATTTAGAAAAGAGCGGAAATATCTGTAGACTGAGATATGCTACTGATCGAGATAT 1772
DB 1897 AGAATCAGATATGCTCTGATAGAGCGGTAAATTTACGATATCTTCCAGATCTCCAG 1956
QY 1773 TGTATTGCAATGTAACGATGCTCAGATTCAGATGCCAAAACAATGAACCCAGGTGAGGA 1832
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QY 1833 TCTGACATCTAAAACCTTTTAAAGTTGCAAGTGTCTATCAACAAATTAATTTAGCAACGA 1892
DB 2016 TCTAACGTATAGTACTTTTGCATATGCAAACTCTGCGCTTATAAACTTAGGGATTTCCGG 2075
QY 1893 TAGTTGCTAGCAATGGAACATAAATTTAGGTGAAGACCCCTAAATTCACATTTATCTGTAT 1952
DB 2076 AAGTTCAAGCACTTTTGTATATCTATTAACAAGA-----AGCAGGTCTGTCTAA 2126
QY 1953 AGTTTACGTTGACCGAATCGAATTTCTCCAGTAGTAGACATATGAAGCGGAACAGA 2012
DB 2127 CCTTTATTTGATGAATTTGAATTTATTTCCAGTTTATACGTTTATTTGAAGCAGAGAAGA 2186

QY 2013 TTTAGAGCAGCGAAGAAAGCAGTGAATGCTTGTACGAATACAAAGAGTGCCTTACG 2072
DB 2187 CCTAGATGTGCGAAGAAAGCAGTGAATGCTTGTACGAATACAAAGAGTGCCTTAC 2246
QY 2073 ACAGGCGTAAACGGATATGAAGTGAATCAAGGCGCAAACTTAGTGAATGCCCTATCGGA 2132
DB 2247 GACAGGTGAACGGATATCAAGTCAATCAAGGCGCAAACTTAGTGAATGCCCTATCGGA 2306
QY 2133 TGATTTGTATCCAAATGAAAGAGATTTATTTATGATGCGAGTGAAGAGCGCAAAAGCGCT 2192
DB 2307 TGATTTATACCAATGAAAGAGATTTATTTATGATGCGAGTGAAGAGCGCAAAAGCGCT 2366
QY 2193 CAGTGAAGCGATTAATTTGCTTCAAGATCCAGATTTTCAAGAGATTAATGCAAGAAATGG 2252
DB 2367 TGTTCAAGCAGTAACTTCTCAAGATACAGGCTTTAATAGGATTAATGCAAGAAACGG 2426
QY 2253 CTGACGCGAAGTACGGGAATGAGGTATAGAGGGGATGCTTTATTCAAAGGGCGTTA 2312
DB 2427 ATGACGCGGAAGTACGGGAATCGAGGTGTGGAAGGAGATGTTCTGTTTAAAGATCGTTC 2486
QY 2313 TCTACGCTTACAGGTGCGAGAGAAATAGATACGGAACGATCCCAAGTATCTGTATCA 2372
DB 2487 GCTTCGTTTGAAGTCCGAGAGAGATTTGATACAGAAACATATCCCAAGTATCTGTATCA 2546
QY 2373 AAAAGTAGAGGAAGGTGTTATTAACCAATACACAGATATAGATTTAGAGGGGTTTGTGCG 2432
DB 2547 ACAATAGATGATCGCTTTTAAACCAATATACAGATATTAACCTAAAGGTTTATAGG 2606
QY 2433 AGCAGTCAAGATGGAATTTTCAAAATTCGTATCAACCAAGCAACGAATGTTGAAAGAA 2492
DB 2607 AGTAGTCAAGATTTAGAGATTAATTAATACGTCATCGGCGCAAAATCAATCGTCAAAA 2666
QY 2493 TGTACCGATGATTTGCTGCGAGATGATCTCTGTTAACTCGAGTGTAGTATCAATCG 2552
DB 2667 TGTACAGATAATCTCTTGGCCAGATGATCGCCCTGTCAATTTCTGTTGGAGTGTGATCG 2726
QY 2553 ATGACGCGCAACAAAGTATGTAATAGCCTGTTAGAGTATGAAACCGT----- 2601
DB 2727 CTGCACTGAACACAGATGTAAGCGGAATTTAGCACTCGAAGAAATGGAAGAAATGG 2786
QY 2602 -----TCTGGTGAAGCGCATAGTTTCTTATTCCTATTGATACAGGTGAATCGATTA 2654
DB 2787 AAATATGCTCTGATCCCATGCAATTTCTTCCATATTGATAGGGTGAATAGATTT 2846
QY 2655 CAATGAATGCAAGATATGCTGATTTAGATTTACGACCCAGAGGAGATGCAAC 2714
DB 2847 GAATGAATAACAGGAATTTGGATCGTATTTAAATTTCCGACCAACAAATGGAACCGCAAC 2906
QY 2715 ACTCGGAACCTAGAAATTTGTCGAAGAGGACCTTTATCAGGAGACGCAATTAGAACGCTT 2774
DB 2907 ACTAGGAATCTTGAATTTGTAAGAGGGGCCATTTCTAGGGGAACATTAGATGGC 2966
QY 2775 GCAAGAGAGAAACACAGTGGAGATTTCAATGCAAGAGAGCGTGAAGAAACAGATAG 2834
DB 2967 CCAACCAAGAAACAAATGCGAGACAAATTTGGCAAGAAACGTCAGCATCAGAAA 3026
QY 2835 AAGGTATGCGATCGAACAAGCGGTAGATCGTTTATATGCCGATTTATCAGATCAGCA 2894
DB 3027 ACATATTTAGCGCAAGCAAGCCATTTGATCGTTTATTCGCAATTTATCAGACCAAAA 3086
QY 2895 ACTGAATCTGATGTAGATTTACAGATCTTACTGCGGGCCCAAGATCTGTATACAGTCCAT 2954
DB 3087 ACTTAATCTGGTGTGAATGTGATTTGTTGGGAGCCCAAACTTGTACAGTCCAT 3146
QY 2955 TCTTACGTATATACGAATTTTCCAGAAATACCAAGGATGAATATACGAAGTTTAC 3014
DB 3147 TCTTACGTATATATGATCGTTTACCGGAATCCCTGGATGAACTATACGATTTTAC 3206
QY 3015 AGAATTAACAGATCGACTCCAAAGCGGTGAGTTTGTATGATCAGCGAAATGCCATACC 3074
DB 3207 AGAGTTAAACAAATAGACTCCAAAGCATGGAATTTGTATGATCTTCAAAAGCGTATACC 3266

QY 3075 AAATGGTGAATTTTCGAAATGGGTTAAGTAAATGGAATGCAACGCCCTGGCTAGAGTACA 3134
DB 3267 AAATGGGATTTTCGAAATGGGTTAAGTAAATGGAATGCAACGCCCTAGATGTAATGTGCA 3326
QY 3135 ACAATCAATCAATCAATCTGCTCTGATTTCAAACTGGGATGAGCAAGTTTTCGCAACA 3194
DB 3327 ACAATCAAGCGATACATCTGCTCTGATTTCCAACTGGAATTTCTCAAGTGTCAACAACA 3386
QY 3195 GTTACAGTTCACCGAATCAAGATATGTTTACGAGTGTACGAGTGTGCGAGAAAGAGGGGT 3254
DB 3387 ATTACAGTTCACCGAATTTATAGATATGTTTACGTCACACAGCGAGAAAGAGGGAGT 3446
QY 3255 AGGAATGATATGTAAGTATCGGTATCGTGAATGGAATCAAACTGGAATCAAACTGTTTAC 3314
DB 3447 AGGAGCGGATGATGATCATCGGTATGTTGCAATCAGACAGAACTCACTCATTTAA 3506
QY 3315 TGAACGGATTTATGATACAAATGGAATGATATACGCAAGTGTCCAAATA 3364
DB 3507 TATATGATGATGATACAGGTGTTTATCTACTGATCAAACTAGCTATA 3556

RESULT 9

US-08-532-547-4
; Sequence 4, Application US/08532547
; Patent No. 5861543
; GENERAL INFORMATION:
; APPLICANT: LAMBERT, BART
; APPLICANT: JANSSENS, STEFAN
; APPLICANT: VAN AUDENHOVE, KATHRIEN
; APPLICANT: PEPEROEN, WERNIX
; APPLICANT: VAN RIE, JEROEN
; APPLICANT: VAN RARSSEN, ROEL
; TITLE OF INVENTION: NEW BACILLUS THURINGIENSIS STRAINS AND THEIR
; TITLE OF INVENTION: INSECTICIDAL PROTEINS.
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/532,547
; FILING DATE: 06-DEC-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: SVENSSON, LEONARD R.
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 2121-109P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4344 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 668..4141
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..4344
; OTHER INFORMATION: /note= "encompasses entire sequence"

OTHER INFORMATION: of SEQ ID NO (SID) 2: from nt position 474 to 2034
OTHER INFORMATION: in SID 4"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..4344
OTHER INFORMATION: /note= "also encompasses part of
OTHER INFORMATION: the sequence of SID 3: from nt position 2994 to
OTHER INFORMATION: 4344 in SID 4"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..4344
OTHER INFORMATION: /note= "SID 3 shows additional
OTHER INFORMATION: nucleotides, located 3' from the sequence shown in
OTHER INFORMATION: SID 4 (1352-1554 in SID 4)"
US-08-532-547-4

Query Match 24.4%; Score 883.4; DB 2; Length 4344;
Best Local Similarity 56.6%; Pred. No. 1.5e-183;
Matches 1936; Conservative 0; Mismatches 1386; Indels 101; Gaps 12;

QY 1 ATGAGTCCAAATATCAAAATGAATATGAAATATAGATGCGACACCTTCTACTCTGTA 60
DB 668 ATGAATCGAAATATCAAAATGAATATGAAATATGATGCGCCCAATGTTGGGTGTC 727
QY 61 TCCAAATGATTTCAACAGATACCCCTTTTCGGAATGAGCCAAACAAATGCGCTACAAATATG 120
DB 728 TCAGATGACGATGAGATATCTTTTGGCAATGACCCAAATGCGCTTACAAATATG 787
QY 121 GATTATAAAGATATTTAAATATGTCGCGGAAATGCTAGTGAATACCCCTGGTTCACCT 180
DB 788 AACTATAAAGATATCTTACAAATGACAGATGAGGACTACACTGATTTCTATATAAATCCT 847
QY 181 GAAGTACTTTAGCGGACAGATGCGCTAGGCGCAATGATATAGTATAGTAAATTA 240
DB 848 AGTTATCTATTTAGTGGTAGAGATGAGTTCAGATGCGCTTACTGCTGCTTATGAGGAGA 907
QY 241 CTATCAGGTTTGGGGTCCCAATTTGTTGGGCGATGATGAGTCTTTTATCTCAACTTAT 300
DB 908 CTCGGGCTTTAGGTGTTCCGTTTCTGGAACAATGATGAGTTTATCAATTCCTTTTA 967
QY 301 GATATTCGTGCGCTTCAGGGGAAAGAGTCAATGGGAAATTTTATGGAAACAAGTAGAA 360
DB 968 AATACACTGTGCGCAGTTAATGATACAGCTATATGGGAAGCTTTTCATGCGACAGTGAG 1027
QY 361 GAATCTAATATCAAAATATGACAGAAATATGCAAGGAATGAGCGCTTTCGGAATTAGA 420
DB 1028 GAATCTGCAATCAACAAATATGCAAGAAATTTGCAAGAAATTCAGGCAATTCGAAGATTG 1087
QY 421 GGATTAGTAATAATTACCAATTTATCTAACTGCGCTTGAAGATGGAAGAAATCCA 480
DB 1088 GGATTAGAGACTCTTTTAAATGATATCAACGTTCCCTTCAAAATTTGGTGGCTGATCGA 1147
QY 481 AATGGTTCAAGAGCCTTACGAGATGTGCGAAATCGATTGGAATCCTGGATGTTTATTT 540
DB 1148 AATGATACACGAAATTTAAGTGTGTTCTGCTCAATTTATAGCTTTAGACCTTGATTTT 1207
QY 541 ACGCAATATATGCCATCTTTTAGAGTGACAAATTTTGAAGTACCAATTCCTTACTGTATAT 600
DB 1208 GTTAATGCTATTCCTATGTTTTCGCAATAATGGACAGCAGGTTCCCAATTTACTGTCA 1267
QY 601 GCAATGGCAGCAACCTTCTATTCTATGTTTAAAGGAGCGCTCAATTTTGGAGAGAA 660
DB 1268 GCACAGCTGTGAATTTACATTTGTTATTTTAAAGATGCAATCTCTTTTGGAGAGAA 1327
QY 661 TGGGGATGGTCAACAACTACTATTAAATCACTATTTATGATCGCTCAATGAAATCTTACTGCA 720
DB 1328 TGGGGATTCACACAGGGGGAATTTCCACATATTTATGACCGTCAATTCGGAATCAACCGCT 1387
QY 721 GAATATTCGATCACTGTGTAAGTGGTATGAACTGGTTAGCAAAATTTAAAGGACAG 780
DB 1388 AAGTACACATAATTAAGTGAACCTTGGTATATAACAGGTTTATAGATCGTTTAAAGAGAA 1447
QY 781 AGCGCTAAACAAATGGGTTGACTATATACCAATTTCCGTAGAGAAATCACTACTGCGGTTT 840

DB 1448 AATACTGAAAGTTGGTTAAGATATCATCAATTCGTTAGAGAAATGACTTTAGTGGTATTA 1507
QY 841 GATGTTGTTGCAATTTATCCCAATTTATGACACAGGACAGTACCAATGGAAACGAAGCA 900
DB 1508 GATGTTGTTGCGCTATTTTCCATATTTATGATGATAGCTTTTATCCACGGGATCAACCCCA 1567
QY 901 CAACCTAACAGGGAAGTATATACAGATCCACTGGCGCGGTAAACGTTCTTCAATTG- 958
DB 1568 CAGCTTACAGTGAGGTATATACAGATCCGATTTGTTTATCCACAGCTAATGTTGGA 1627
QY 959 -----GTTCTCTGATGACAAAGCACCTTTCTTTCCGAGTGATAGATCAATCCGTT 1008
DB 1628 CTTTGGCCGAGTTGGGGTACTTAATCCCTATAATACTTTTCTGAGCTCGAAATGCCCTTC 1687
QY 1009 ATTGACACACCCCATGTTTGTATATTAACGGGACTCAGAGTGTATACAAATCAAGA 1068
DB 1688 ATTGCGCCACACATCTTTTGTAGCTGAATAGCTTTAACAATCAGCAGTAATCGATTT 1747
QY 1069 AGCATTTTCTCCGCTCGCTATATAGAATTTGGGCTGCTCATCAAAATAAGCTACCATCGT 1128
DB 1748 CCAGTTTCACTAAT-----TTTATGGATTTTGGTTCAGACATAGCTTACGCCGTAGTTAT 1804
QY 1129 GTCAGTAGGGGTAGTAACTTTTCAACAAATGTATGGAATTAATCAAAATCTACACAGCACT 1188
DB 1805 CTGAACGATTCAGCAGTACAAAGAGATGTTATGG-----CCTAATTCACACCACAAGA 1858
QY 1189 AGTACCTTTGATTTTTCGAATTTATGATTTTCAAGACTCTATCAAAAGGATGAG-TACT 1247
DB 1859 GCAACAATTAATCCCGGAGTTGATGGAACAAACCCGATAGAGTCAACGGCAGTAGATTTT 1918
QY 1248 CTTTGAATTTGTTTACCCTGTTATAGCTATATATTTTGGATGCGCAGAGTCGAGTT 1307
DB 1919 CGTTCTCGATTTGATGATATATATGCGGTGAATAGACTTCTTTTGGCCAGGAGGCTTG 1978
QY 1308 TTTTCATGTTAAACCAATTTGAATATATACCAAGAAAGACGTTTAAAGTATATATCCAGTTTCCAA 1367
DB 1979 TTTAATGCT-----ACGACTTCTCTCTAATGGAGGATGAG 2016
QY 1368 AGATATTTATAGCGAGTACAAGAGATTCGGAATTTAGAAATTCCTCCAGAACTTCAGATCA 1427
DB 2017 AGATCTCTATGATACAAATGATGAATTTACCACAGATGAAAGTACCAGAGTTTCAACCCA 2076
QY 1428 ACCAAATATGAGTCATATAGCCATAGATTTATGTCATATCACAGTATTTCCCGGACGGG 1487
DB 2077 TAGACTATCTCATGTTTACTTTTACTTTT-----TCAAACCTAATCAGGCTGATCTAT 2130
QY 1488 TAACACTACCGGATTTAGTACTGTTATTTTCTTGGACACATCGAAGTGCAGATTTTAAACAA 1547
DB 2131 AGCTAATGCGAGGAGTGTACTTATTTGTTGGACCGCTGCTGATGTTGGACCTTATTA 2190
QY 1548 TACAATATATTCAGATAAATCACTCAAAATTCGCGCGCTTAAATTTTGGGATATTTTACC 1607
DB 2191 TACGATTTACCCCAATTAAGAAATTAACAATTTACCAATTTGTAAGGCACTCTGCACTGTTTC 2250
QY 1608 GTTTGTTCCAGTGTGTAAGAGCAACAGGACATACAGGAGGGAATTTATACAGTATATATAG 1667
DB 2251 GGGTACTACGGTCTTAAAGGTTCCAGGATTTACAGGAGGGGTATATCTCC---GAAGAAC 2307
QY 1668 AAGTACTGTTCTGTAGGAACCTTTATTTCTAGCTCGATATGCGCTAGCATTTAGAAAAAGC 1727
DB 2308 AACTAATGGCACATTTGGAACGTTAAGAGTAAACGTTAATTTACCATTTACACAACTATA 2367
QY 1728 AGGGAATATCGTGTAAAGACTGAGATATGCTACTGATGCGAGATTTGTTATGCAATGTAAA 1787
DB 2368 TCGCTTAAGAGTTCGTTTTCCTCAACAGGAAATTTTCAGTATATAGGTTACTCCGTGGAGG 2427
QY 1788 CGATGC-----TCAGATTCAGATGCGCAAAACAAATCAATGAAACCGAGGTGAGGATCTGACATC 1841
DB 2428 GGTTCCTATCGGTGATGTTAGATTAGGGAGCAATGAACAGAGGGCAGGAATCAACTTA 2487
QY 1842 TAAACCTTTTAAAGTTTCAGATGCTATCAACA-----TTAAATTTAGCAACAGATAG 1895

Db	2488	CGAATCCCTTTTTCACAAGAGGTTTACTACTACTGCTCGTTTCAATCCGCCCTTTTACATT	2544
Qy	1896	TTCCCTAGCATTTGAACATAAATTTAGGTGAAGACCCTTAATTCAAATTAATCTCGGTATAGT	1955
Db	2548	TACAACAGCTCAAGAGATTCTAACAGTGAATGCAGAAGGTGTAGCACCGGTGGTGAATA	2607
Qy	1956	TTACGTTGACCGGAATCGAATTCATCCAGTAGTAGAGACATATGAAGCGGGAACAGATTT	2015
Db	2608	TTATATAGTAGAATTTGAATTTGCTCCCTGTGAATCCGGCACAGAGAAGCGGAAGAGATTT	2667
Qy	2016	AGAACGACCGGAAGAAAGCAGTGAATGCCCTTGTATTACGAATACAAAAGATGCTTACGACC	2075
Db	2668	AGAACCGCGAAGAAAGCGTGGCGAGCTTTTATACGTAACAGGAGCGATTAACAGGT	2727
Qy	2076	AGCGGTAAACGGATTTATGAAGTGAATCAAGCGGCAAACTTTAGTGGAAATCCCTATCGAGTGA	2135
Db	2728	AAATGTGACAGATTTATCAAGTGCACCAAGCGGCAAAATTTAGTGTCAATGCTTATCCGATGA	2787
Qy	2136	TTTGTATCCAAATTCMAAAACGATGTGTATTTGATGCAAGTGAGAGAGGCAAAACGCTCAG	2195
Db	2788	ACAAATATGGGCATGACAAAAGATGTTATTTGAAGCGGTAAAGAGCGGCAAAACGCTCAG	2847
Qy	2196	TGAGGCACGTAAATTTGCTTCAAGATCCAGATTTTCAAGAGATAAAT-----CGAGAAA	2249
Db	2848	CCGCGAAGCGCACTTACTTCAAGATCCAGATTTTAAATCAATCAATAGTA CAGAAGAGAA	2907
Qy	2250	TGGCTGGAACGCAAGTACCGGAAATGAGGTATAGAGGGGATGCTTTATTTCAAAGGCG	2309
Db	2908	TGGCTGGAAGCAAGTAAACGGTGTACTATTAGCGAGGGCGGTCAATCTTTAAAGGTG	2967
Qy	2310	TTATCTACGGCTACAGGTGCGAGAGAAATAGATACGGAAAGTATCCAAAGTATCTGTA	2369
Db	2968	TGCATTTCACTTAGCAAGCGCAGA-----GAAAAATATCCAAATACATTTA	3015
Qy	2370	TCAAAAAGTAGAGAAAGGTCTATTAAAAACATACACAGATATAGATTCAGAGGGTTGT	2429
Db	3016	TCAAAAAGTAGATGCATCGGTGTTAAGCCTTATACCGCTATAGACTAGATGGAATTTGT	3075
Qy	2430	CGGAAGCAGTCAAGGATTTGAAATTTTCAAAATTCGTCTCATCAAAACCAACCGAAATGTAAA	2489
Db	3076	GAAGAGTAGTCAAGATTTAGAAATTCATCTCATCCACCATCATAAAGTCCATCTTGTAAA	3135
Qy	2490	AAATGTACCGGATGATTTGCTGCGAGATGTATCTCTGTTTAATCTCGGATGTTAGTATCAA	2549
Db	3136	AAATGTACCAAGATAATTAGTATCTCATCTTACTCAGATGGTCTTCAGCGGNAATCAA	3195
Qy	2550	TCCATGCAAGCGCAACAAAGTATGTGAATAGCCGTTTGAAGTGAAGNAACCGT-----	2601
Db	3196	CCGTTGTGATGAACAGCATCAGGTAGATATGAGCTAGATGCGGAGCATCATCAATGGA	3255
Qy	2602	-----TCTGGTGAACGCGATGAGTTCTTATTCCTATTGATACAGGTGAATTCGA	2651
Db	3256	TTGCTGTGAACCGCTCAACACATGATTTCTTCCTATTAATATACGGGGATCTAAA	3315
Qy	2652	TTACAATGAATAATTCGAGGAATATGGGTTGGATTTAAGATTAACGGACCCAGAGGATATGC	2711
Db	3316	TGCAAGTGTAGATCAGGGCATTTGGGTTGCTATTAATAAGTTTCGAAACAACAGATGGGTATGC	3375
Qy	2712	AACACTCGGAAACCTAGAAATGGTCCAAAGAGGACCTTTATCAGGAGACGATTTAGAACG	2771
Db	3376	GACGTTAGGAAATCTTGAATTTGGTAGAGGTTGGGGCATTTATCGGGTGAATCTCTAGAACG	3435
Qy	2772	CTTGCAAAAGAGAGAAACAAACAGTGAAGATTCMAATGACAGAAGACGTGAAGAAAACAGA	2831
Db	3436	GGAAACAAGAGATAATTCGNAATGGNAATCCAGCTAGGAGAGAAACGTGCGAANAATAGA	3495
Qy	2832	TAGAAGGTATATGGCATTCGAAACAAACGCGGTAGATCGTTTATATGCCGATTAACAGATCA	2891
Db	3496	TCGTGTGTATTTAGCTCGGAAACAAAGCAANTTAATCATCTGTTTGTAGACTATCAAGATCA	3555
Qy	2892	GCAACTGMAATCCTGATGTAGAGATTAACATCTTATCTCGGGCCCAAGATCTGATACATGC	2951
Db	3556	ACAAATTAATTCAGAAATTTGGGCTAGCAGAAATTAATGAAGCTTCAAACTCTGTAGAGTC	3615

Qy	2952	CATTCTTTACGTTATATAACGAAATGTTCCCGAGAAATACACAGGATGAACACTATACGAAAGTT	3011
Db	3616	AAATTTCGGGTATATATAGTGATACACTATTAACAGATTCCTGGGATTAACACTACGAAATTTA	3675
Qy	3012	TACAGAAATTAACAGATCGACTCCCAACGCGTGGAGTTTGTATGATCAGCGGAATGCCAT	3071
Db	3676	CACAGAGTTATCCGATCGCTTACACAGCATCGTATCTGTATAGCTCTAGAAATGCGGT	3735
Qy	3072	ACCAATGGGTGATTTTCGAAATGGGTAAAGTAAATGGAAATGCAACGCGCTGGCGTAGAAGT	3131
Db	3736	GCAAAATGGAGACTTTTAAACAGTGGTCTAGATAGTTGGAAATACAACTATGGATGCATCGGT	3795
Qy	3132	ACACAATCAATCAATCATCATCTGTCCTTGTGATTCCAAATCGGAGTAGCAAGTTTCGCA	3191
Db	3796	TCACAAGATGGCAATGATGATTTCTTAGTTCTTTCCGCAATGGGATGCACAAGTTTCCCA	3855
Qy	3192	ACAGTTTACAGTTTCAACCGCAATCAAAAGATATGTGTTACGAGTTACTGCGGAGAAAAGAGG	3251
Db	3856	ACAATTGGAGTAAATCCGNAATGTAAAGTATGTTCTTACGTGTGACAGCAAGAAAGTAGG	3915
Qy	3252	GGTAGGAAATGGATATGTAAGTATCCGTATCCGTGGTGGAAATCAAACAGAGAAACGCTTACTTT	3311
Db	3916	AGGCGAGATGGATAGCTACAAATCCGAGATGGCGCTCATCACCAAGAACTCTTTACATT	3975
Qy	3312	TAGTGCACAGCGATATGATACAAATGGAAATGATTAATAGCGCAAGTGTCCAATACAAATGG	3371
Db	3976	TAAATGCATGTGACTACGATGTAAATGGTAGTATGTCAATGACAAATTCGTATATAACAGA	4035
Qy	3372	ATA 3374	
Db	4036	AGA 4038	

RESULT 10
 ; Sequence 4, Application US/08379656B
 ; Patent No. 5885571
 ; GENERAL INFORMATION:
 ; APPLICANT: Lambert Bart
 ; APPLICANT: Jansens, Stefan
 ; APPLICANT: Van Audenhove, Katrien
 ; APPLICANT: Peferoen, Marnix
 ; TITLE OF INVENTION: NEW BACILLUS THURINGIENSIS STRAINS AND
 ; TITLE OF INVENTION: THEIR INSECTICIDAL PROTEINS
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
 ; STREET: 8110 Gatehouse Road, Suite 500 East
 ; CITY: Falls Church
 ; STATE: Virginia
 ; COUNTRY: U.S.A.
 ; ZIP: 22042
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/379,656B
 ; FILING DATE: 23-MAR-1995
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/EP93/01820
 ; FILING DATE: 12-JULY-1993
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: EP 93400949.9
 ; FILING DATE: 09-APR-1993
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: EP 92402358.8
 ; FILING DATE: 27-AUG-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Svensson, Leonard R.
 ; REGISTRATION NUMBER: 30.330

QY 1608 GTTGTCTCCAGTGGTAAAGAGCCAGGACATACAGAGGGGATTTATTACAGTATAATAG 1667
DB 2251 GGGTACTACGGTCTTAAAGGTCAGGATTTACAGAGGGGGTATCTCC---GAAGAAC 2307
QY 1668 AAGTACTGCTCTGAGGACCTTATTTCTAGCTCGATATGCGCTAGCATTTAGAAAAGC 1727
DB 2308 AACTAATGGCAATTTGGAACGTTAAGAGTACGGTTAATTCACCATTAACACACATTA 2367
QY 1728 AGGGAATATCGTGTAAAGCTAGATATGCTACTGATGCAGATATTTGTTATTCATGTAAA 1787
DB 2368 TCGCTTAAGAGTTCTGTTTGGCTCAACAGGAATTTTCAATTAAGGGTACTCCGTGGAG 2427
QY 1788 CGATGC-----TCAGATTCAGATGCCAAAACAATGAACCCAGGTGAGGATCTCACATC 1841
DB 2428 GGTTCCTATCGGTGATGTTAGATTAGGAGCACAATGAACAGAGGGCAGGAACCTAATTA 2487
QY 1842 TAAACCTTTTAAAGTTGAGATGCTATCACACA-----TTAAATTTAGCACAGATAG 1895
DB 2488 CGAATCCCTTTTTCACAGAGAGTTTACTACTCGGTCCGTTCATCCGCCCTTTTACATTT 2547
QY 1896 TTCGTAGCATTTGAAACATAATTTAGGTGAAGACCCCTAATTCACATTTATCTGGTATAGT 1955
DB 2548 TACACAGCTCAAGAGATTTCAAGGTGAGTGCAGAGGTGTAGCACCGGTGGTGAATA 2607
QY 1956 TTAGCTGACCGAATCGAATTCATCCAGTAGAGACATATGAAGCGGAAACAAGATTT 2015
DB 2608 TTAATAGATAGAAATTGAATTTGCTGTGAATCCGCGCAGCAGAGGCGGAAGGATTT 2667
QY 2016 AGAGCGAGGAGAGAGCAGTGAATGCTTTTACAGTATCAAAAAGATGGCTTAGGACC 2075
DB 2668 AGAAGCGCGAAGAAAGCGGTGGCGAGCTGTTTACAGCTACAGGCGGAGATTAACAGT 2727
QY 2076 AGGGCTTAACGGATTTAGAGTGAATCAAGCGGCAACTTTAGTGAATGCTATCGATGA 2135
DB 2728 AAATGTGACAGATTTCAAGTGGACCAAGCGGCAATTTAGTGTCAAGCTTATCCGATGA 2787
QY 2136 TTTGTATCAAAATGAAAACGATTTGATTTGATGACGAGAGAGGCAAAACGCTCAG 2195
DB 2788 ACAATATGGCGATGACAAAAGATGTTATGGAAGCGGTAGAGCGGCAAAACGCTCAG 2847
QY 2196 TGAGCGAGTATTTGCTTCAAGTCCAGATTTTCAAGAGATAAT-----GGHAAAA 2249
DB 2848 CCGGAGAGCGCACTTACTTCAAGATCCAGATTTTATTAACAATAGTACAGAGAGAA 2907
QY 2250 TGGCTGAGCGCAAGTACGGCAATTTGAGGTTATGAAGGGGATGCTTTATTCAGAGGGG 2309
DB 2908 TGGCTGAGAGCGAAGTACCGGTGTTACTATTAGCGAGCGGTCCATCTTTTAAAGGTCG 2967
QY 2310 TTATCTACGCCCTACAGGTGCGAGAGAAATAGATACGGAAACGTATCCAAAGTATCTGTA 2369
DB 2968 TGCACCTTCAGTTAGCAAGCGCAAG-----GAAATTTATCCACATACATTTTA 3015
QY 2370 TCAAAAGTAGAGGAGGTGTTAAACCATACACAGATATAGATTGAGAGGGTTTGT 2429
DB 3016 TCAAAAGTAGATGATCGGTGTTAAAGCCTTTATACAGCTATAGACTAGATGATTTGT 3075
QY 2430 CGGAAGCAGTCAAGATTTGGAATTTTTCACAACTGCTCATCAACCGAATTTGTTAA 2489
DB 3076 GAAGAGTAGTCAAGATTTAGAAATTTGATCTCATCCCATCATAAAGTCCATCTTTGTA 3135
QY 2490 AAATGTACCGGATGTTTGTGCGCAGATGTTATCTCTGTTAACTCGGATGGTAGTATCA 2549
DB 3136 AAATGTACCAATAATTTAGTATCTGATCTTACTCAGATGGTTCTTCAGCGGAATCAA 3195
QY 2550 TCGATGACGCAACAAAGTATGTAATAGCGGTTTAGAAGTAGAATAACCGT----- 2601
DB 3196 CCGTTGTGATGAACAGCATCAGGTAGATATGCGAGTAGATGCGGAGCATCATCCAATGGA 3255
QY 2602 -----TCTGTGAGCGCATGAGTTCTTCTATTCTTATTGATACAGGTGAATCGA 2651
DB 3256 TTGCTGTGAGCGGCTCAACACATGAGTTTCTTCTCTATTAATACAGGGGATCTAAA 3315
QY 2652 TTAACAATGAAAATGAGGAATATGGGTTTGAATTTAAGATTACGGACCCAGAGGGATATGC 2711

DB 3316 TGCAAGTGTAGATCAGGGCATTTTGGTTGTATTATAAAAGTTTCGAACAACAGATGGGTATGC 3375
QY 2712 AACACTCGGAAACCTAGAAATTTGGTTCGAAGAGGAGCCCTTTATCAGGAGACGCAATTAGAACG 2771
DB 3376 GACGTTTAGGAAATCTTGAATTTGGTAGAGGTTGGGCCAATATTCGGGTGAATCTCTAGAACG 3435
QY 2772 CTTTCAAGAGAGAACAAACAAGTGAAGATTTCAATGCAAGAAGACGTTGAAGAAACAGA 2831
DB 3436 GGAACAAAGAGATTAATCGGAATTTGGAATGCAGAGCTAGGAAGAAAACGTCGAGAATAGA 3495
QY 2832 TAGAAGGTATATGGCATCGAAACAAGCGGTAGATCGTTTATATCCCGATTTATCAGGATCA 2891
DB 3496 TCGGTGTATTTAGTCTCGAAAACAAGCAAATTAATCACTCTGTTGTAGACTATCAAGATCA 3555
QY 2892 GCAACTGAATCTCTGATAGAGATTACAGATCTTACTTCGGGCCCAAGATCTGATACAGTC 2951
DB 3556 ACAATTAATCCAGAAATTTGGGCTAGCAGAAATTAATGAAGCTTTCAATCTTTAGATGC 3615
QY 2952 CATTCCTTACGTATATAACGAATTTTCCAGAAATACCAGGGATGAATATATACGAAGTT 3011
DB 3616 AATTCGGGTGTATATAGTATGATACACTATTACAGATTTCTGGGATTAACCTACGAATTTA 3675
QY 3012 TACAGAAATTAACAGATCGACTCCAAACGAAGCGGTGGAGTTTGTATGATCAGCGAAATGCGAT 3071
DB 3676 CACAGAGTTTACCGATCGCTTACAAACAGCATCGTATCTGTATACGCTCTAGAAATCGGT 3735
QY 3072 ACCAAATGGTGTATTTCCGAATTTGGTTAAGTAATTTGAATGCAACGCTGGCGTAGAAGT 3131
DB 3736 GCAAAATGGAGACTTTAAACAGTGGTCTAGATAGTTGGAATACAACTATGATGATCGGT 3795
QY 3132 ACAACAAATCAATCATCATCTGCTCTGTTGATTCCAAACCTGGGATGAGCAAGTTTCGCA 3191
DB 3796 TCACAGATGCGCAATATGCAATTTCTTAGTCTTTCCATTTGGGATGCAACAGTTTCCCA 3855
QY 3192 ACAGTTTACAGTTTCAACCGAATCAAGATATGTTTACGAGTTACTCGGAGAAAAGAGG 3251
DB 3856 ACAATTCAGAGTAAATCCGAATTTGTAAGTATGCTTACGTTGTGACAGCAAGAAAAGTAGG 3915
QY 3252 GGTAGGAATGGATATGATATGATATCCGTGATGTTGGAAATCAACAGAAACGCTTACTTT 3311
DB 3916 AGCGGAGATGGATACGCTCAATCCAGATGGCGCTCCTACCCAGAAAACCTTTTACAT 3975
QY 3312 TAGTGAAGCGATTTATGATACAAATGGAATGTATAACGCAAGTGTCCCAATACAAATGG 3371
DB 3976 TAATGCATGTGACTACGATGTAATGTTAGTATGTCATGCAATTCGTATATACAGA 4035
QY 3372 ATA 3374
DB 4036 AGA 4038

RESULT 11
US-08-455-838-4
; Sequence 4, Application US/08455838
; Patent No. 6028246
; GENERAL INFORMATION:
; APPLICANT: Lambert Bart
; APPLICANT: Jansens, Stefan
; APPLICANT: Van Audenhove, Katrien
; APPLICANT: Peferoen, Marix
; TITLE OF INVENTION: NEW BACILLUS THURINGIENSIS STRAINS AND
; THEIR INSECTICIDAL PROTEINS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 8110 Gatehouse Road, Suite 500 East
; City: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/455,838

FILING DATE: 31-MAY-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP93/01820

FILING DATE: 12-JULY-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 93400949.9

FILING DATE: 09-APR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 92402358.8

FILING DATE: 27-AUG-1992

ATTORNEY/AGENT INFORMATION:

NAME: Svensson, Leonard R.

REGISTRATION NUMBER: 30,330

REFERENCE/DOCKET NUMBER: 2121-106P

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 205-8000

TELEFAX: (703) 205-8050

TELEX: 248345

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 4344 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: 668..4141

FEATURE:

NAME/KEY: misc feature

LOCATION: 1..4344

OTHER INFORMATION: /note= "encompasses entire sequence"

OTHER INFORMATION: of SEQ ID NO (SID) 2: from nt position 474 to 2034 in SID 4"

FEATURE:

NAME/KEY: misc feature

LOCATION: 1..4344

OTHER INFORMATION: /note= "also encompasses part of"

OTHER INFORMATION: the sequence of SID 3: from nt position 2994 to 4344 in SID

OTHER INFORMATION:

OTHER INFORMATION: 4"

FEATURE:

NAME/KEY: misc feature

LOCATION: 1..4344

OTHER INFORMATION: /note= "SID 3 shows additional"

OTHER INFORMATION: nucleotides, located 3' from the sequence shown in SID 4

OTHER INFORMATION:

OTHER INFORMATION: (1352-1554 in SID 4)"

US-08-455-838-4

Query Match 24.4%; Score 883.4; DB 3; Length 4344;

Best Local Similarity 56.6%; Pred. No. 1.5e-183;

Matches 1936; Conservative 0; Mismatches 1386; Indels 101; Gaps 12;

QY 1 ATGAGTCCAAATTAATCAAAATGAATGAAATATAGATGCGACACCTTCTACTTCGTA 60

DB 668 ATGATCGAAATTAATCAAAATGAATGAAATATAGATGCGACACCTTCTACTTCGTA 727

QY 61 TCCAATGATCTTAACAGATACCTTTTGGCAATGAGCGCAACAATGCGCTACAAATATG 120

DB 728 TCAGATGACGATGAGGTATCTTTGGCAAGTGAACCAATGACGCGTTACAAATATG 787

QY 121 GATTATTAAGATTATTTAAATAATGCTGCGGGAATCTAGTGAATACCTCGGTACCT 180

DB 788 AACTATAAAGATTCTTACAAATGACAGATGAGACTACTGATCTTATATAATCCT 847

QY 181 GAAGTACTTTGTCGCGCAAGATGACAGCTAAGCGCAATTTGATATAGTAGGTAATTA 240

DB 848 AGTTTATCTATTAGTGTAGAGATGCAAGTTCAGACTCGGCTTACTGTTGTTGGGAATA 907

QY 241 CTATCAGGTTTAGGGTCCCATTTGTTGGCGCGATAGTAGTCTTTATCTCAACTTATT 300

Db	908	CTCGGGCTTTAGGTGTTCCGTTTCTGGACAAAATAGTAGTGTATCAATTCCTTTTA	967
QY	301	GATATTCGTGCGCTTCAGGGGAAAAGAGTCAATGGGAAAATTTTATGGAAACAAGTAGAA	360
Db	968	AATACACATGTCGCCAGTTAATGATACAGCTATATGGGAAGCTTTTCATGCGACAGGTGAG	1027
QY	361	GAACTCATTAAATCAAAAATATGCAAGAAATGCAAGAAATATAAGCGCTTTCGGAATTAGAA	420
Db	1028	GAACTTGTCAATCAACAATAACAGAAATTTGCAAGAAATCAGGCACCTTCAAGATTGCAA	1087
QY	421	GGATTAGGTAAATTAATCAATTTATATCTTAATCTGCGCTTGAAGAATGGGAAGAAATCCA	480
Db	1088	GGATTAGGAGACTCTTTTAAATGATATCAACGTTCCCTTCAAAAATTTGGTTGGCTGATCGA	1147
QY	481	AATGGTTCAGAGCCCTTAGCAGATGTGCAAAATCAATTTGAAATCTCGATAGTTTATTT	540
Db	1148	AATGATACACGAAATTTAAGTCTGTTGCTGCTCAATTTATAGCTTTAGACCTTGATTTT	1207
QY	541	ACGCAATATATGCCATCTTTTAGAGTGTGCAAAATTTTGAAGTACCATTCCTTACTGTATAT	600
Db	1208	GTTAATGCTAATTCATTTGTTTGCAGTAATGACAGCAGGTTCCATTACTGTCAGTATAT	1267
QY	601	GCAATGGCAGCCAACTTCATTTTACTGTTTATTAAGGACGCGTCAATTTTGGAGAAGAA	660
Db	1268	GCACAGCTGTGAAATTTACATTTGTTTATTAAGATGCACTCTTTTGGAGAAGGA	1327
QY	661	TGGGATGTCACAACTACTAATTAATTAATATGATCGTCAAAATGAACTTACTGCA	720
Db	1328	TGGGATTCACACAGGGGGAATTTCCACATATTTATGACCGTCAATTTGGAATTAACCGCT	1387
QY	721	GAATATTCGATCAGTGTGTAAGTGTATGAACTGCTTTAGTACCAAAATTAAGGACAG	780
Db	1388	AAGTACACTAATTTACTGTGAAAATCTGGTATAATACAGGTTTGTAGTCGTTTAAAGAGGA	1447
QY	781	AGCGCTTAAACAATGGGTTGACTATAACCAATTTCCGTAGAGAAATGACACTGGCGGTTTA	840
Db	1448	ATACTGAAGTTGGTGAAGATATCATCAATTCGCTAGAGAAATGACTTTAGTGGTATTA	1507
QY	841	GATGTTGTCATTTATCCCAATTAATGACACACGACGATCCCAATGGAACGAAAGCA	900
Db	1508	GATGTTGCGCGTATTTCCATATTTATGATGATGACACTTTATCCAACGGGATCAACCCA	1567
QY	901	CAACTAAGAGGAGTATATACAGATCCACTGGGCGCGGTAAACGTGTCTTCAATTG--	958
Db	1568	CAGCTTACACGTCGAGGTATATACAGATCCGATTTTAAATCCACCACTAATGTGGA	1627
QY	959	-----GTTCTGCTGATGACAAAGCACCTTCTTTCGGAGTGTAGTAATCATCCGTT	1008
Db	1628	CTTTGCGGAGTTGGGTTACTATCCCTATATATCTTTTCTGAGCTCGAAATGCTTTC	1687
QY	1009	ATTTCGACACCCCATGTTATTTGATTATATAACGCGGACTCACAGTGTATACACAATCAAGA	1068
Db	1688	ATTGCGCCACCATCTTTTGTATAGCTGTAATGCTTAAACAATCAGCAGTATCGATT	1747
QY	1069	AGCATTTCTTCGCTGCTATATAGACATTTGGGCTGGTCTCAATAAGTCTACCATCGT	1128
Db	1748	CCAGTTTCTCATTAAT---TTTATGGAATTTGCTCAGGACATACGTTACGCGCTAGTTAT	1804
QY	1129	GTCACTAGGGGTAGTAATCTTCAACAATAATGATGGAACCTAATCAAAATCTACACAGACT	1188
Db	1805	CTGAACGATTCAGCAGTACAAGAAGATAGTTATGG-----CTAATTAACAACCAAGA	1858
QY	1189	AGTACCTTTGATTTTACGAAATTTATGATATTTTACAGACTCTATCAAGGATGAG-TACT	1247
Db	1859	GCACAATTAATCCCGAGTTGATGGAACAACACCGCATAGATCAACGCGAGTAGATTTT	1918
QY	1248	CTTGTATGTTTACCTCGGTTATACGTATATATTTTGGAAATGCCAGAAGTCCAGTT	1307
Db	1919	CGTTCTGCAATGATAGGTATATATGCGGTGAATAGAGCTTCTTTTGTCCAGGAGCTTG	1978
QY	1308	TTTCACTGGTAAACCAATGAATTAATACAGAAAGAGCTTAAAGTAAATCACTCAGTTTCCA	1367

Db	1979	TTTAAATGGT-----ACGACTTCTCTCGCTAAATGAGGAGATGTAG	2015
Qy	1368	AGATATTATPAGCGAGTACAAGAGATTTCGGAATTAGAATTACCTCCAGAAACTTTCAGATCA	1427
Db	2017	AGATCTCTATGATACAAATGATGAATTTACCACCAGATGAAGTACCGGAAGTTTCACCCCA	2076
Qy	1428	ACCAAAATTATGAGTCATATAGCCATAGATATATGTCATATACAAGTATTTCCCGCGACGGG	1487
Db	2077	TAGACTATCTCATGTTTACCTTTTTTATGCTT-----TCAAACTAAATCAGGCTGGATCTAT	2130
Qy	1488	TAACTACTACGGATTAGTACCTGTATTTTCTTGGACACATCGAAGTGCAGATTTAAACAA	1547
Db	2131	ACGTATATGACGGAAGTGTACCTTATGTTTGGACCCGTCGTGATGTGACCTTAATAA	2190
Qy	1548	TACAAATATATTCAGATAAAATCACTCAAAATCCCGCGCGTTAAATGTTGGGATAAATTTACC	1607
Db	2191	TACGAATTACCCCAATAGAAATTACACAAATTACCAATTGTTAAAGGCATCTGCACCTGTTTC	2250
Qy	1608	GTTTGTTCAGTGGTTHAAAGGACGAGCAATACAGAGGGGGATTTATTAAGTATTAATAG	1667
Db	2251	GGGTACTACGGTCTTAAAGAGTCCAGGAATTTACAGGAGGGGGTATATCTCC--GAAGAAC	2307
Qy	1668	AAGTACTGCTGTCGTAGGAACCTTATTTCTAGCTCGATATGCGCTAGCATTAAGAAAGC	1727
Db	2308	AACTAATGSCAATTTGGAAAGCTTAAGAGTAAACGGTTAATTCACCAATTACACAAACATA	2367
Qy	1728	AGGGAATATTCGTGTAAAGACTCGAGATATGCTACTGATCGAGATATGTATTCATGTAAA	1787
Db	2368	TCGCGCTAAGAGTTCGTTTTTGCCTCAACAGGAAATTTTCAGTATTAAGGTACTCCGTGGAGG	2427
Qy	1788	CGATGC-----TCAGATTCAAGATGCAAAACAAATGAACCCAGGTGAGGATCTGATC	1841
Db	2428	GGTTTCTATTCGGTGTGTTTAGATTAGGGAGCACAATGAACAGAGGGCAGGAACCTAACTTA	2487
Qy	1842	TAAGAACTTTTAAAGTTGCAGATGCTATCAACA-----TTAAATTTAGCAACAGATAG	1895
Db	2488	CGAATCCTTTTTCAAGAGAGGTTTACTACTCTGTCGGTCCATTCGCGCTTTTACATT	2547
Qy	1896	TTTCGCTAGCATTTGMAACATAATTTAGTGTGAAGACCCCTAAATCAACATTAATCTGATATAGT	1955
Db	2548	TACACAGCTCAAGAGTTCTAACTGTGAATGCAGAAAGGTGTTAGCACCGGTGCTGAATA	2607
Qy	1956	TTACGTTGACCGAATTCGAATTCATCCAGTATGAGACATATGAAGCGGAAACAAGATTT	2015
Db	2608	TTATATAGATAGAAATTTGAATTTGTCCTCTGTGAATTCGGCACGAGGAAGCGGAAGGATTT	2667
Qy	2016	AGAAGCAGCGAAGAAAGCAGTGAATGCCCTGTTTACGAATACAAAAGATGGCTTACGACC	2075
Db	2668	AGAAACGGCGAAGAAAGCGGTGGCGAGCTGTTTATACGTACAAGGGAACGGATTAACGGT	2727
Qy	2076	AGCGCTAACCGGATTATGAAGTGAATCAAGCGGCAAACTTAGTGGAAATGCCCTATCGGATGA	2135
Db	2728	AAATGTGACAGATTATCAAGTGGACCAAGCGGCAAAATTTAGTGTCACTGCTTATCCGATGA	2787
Qy	2136	TTTGTTATCCAAATGMAAAACGAATGTTATTTGATCAGTGAAGAGGCGCAAAAACGCTTCAG	2195
Db	2788	ACAATATGGGCATGACAAAAGAGATGTTATTGGAAGCGGTAAAGAGCGGCAAAAACGCTTCAG	2847
Qy	2196	TGAGGCACGTAATTTGCTTTCAGATCCGAATTTCCAGAGATTAAT-----GGAGAAAA	2249
Db	2848	CCGCGAAACGCACTTACTTTCAAGATCCGAATTTTAACAATCANATGATACAGAAAGAA	2907
Qy	2250	TGGCTGGACGCGCAAGTACGGGAATTCAGGTTATAGAAAGGGGATGCTTTATTTCAAGGGCG	2309
Db	2908	TGGCTTGGAAAGGCAAGTAAACGGTGTACTATTACGAGAGCGCGTCCATTTCTTTAAGGTGCG	2967
Qy	2310	TTATCTTACGCGCTTACCAAGTGCAGAGAGAAATAGATACGGAAACGTTATCCACGTTATCTGTA	2369
Db	2968	TGCACCTTCAGTTAGCAAGCGCAAGA-----GAAATTTATCCAACATACATTTA	3015
Qy	2370	TCAAAAAGTAGAGGAAGGTGTATTAATAACATACAAAGATATAGATGTGAGAGGTTTGT	2429
Db	3016	TCAAAAAGTAGATGATCGGTGTTTAAAGCCTTATACGCTATAGACTAGAGAGGATTTGT	3075

QY	2430	CGGAGCAGCTCAAGGATTGGAAAATTTTCAAAATCGTCATCAACAGAAACCGAATTTGTAAA	2489
Db	3076	GAAGAGTAGTCAAGATTTAGAAAATTTGATCTCATCCACCATATAAAGTCCATCTTGTAAA	3135
QY	2490	AAATGTACCGGATGATTTGCTGCCAGATGTATCTCTGCTTAACTCGGATGGTAGTATCAA	2549
Db	3136	AAATGTACCGATTAATTTAGTATCTGATATCTTACTCAGATGGTCTTTCGACGGGAATCAA	3195
QY	2550	TCGATGCGACGGAACAAAAGTATGTGAATAGCCGTTTGTAGAAGTAGAAAACCGT-----	2601
Db	3196	CGGTTGTGATGAACAGCATCAGTAGATATGCAGCTAGATCGGAGCATCATCCAATGGA	3255
QY	2602	-----TCTGCTGAAGCCATGAGTCTCTATCTCTATTTGATACAGGTGAATTCGA	2651
Db	3256	TTGCTGTGAAGCGGCTCAAAACATGAGTTTTCTTCTATATTAATACAGGGGATCTAAA	3315
QY	2652	TTCAATGAAAAATGCAGGAATATGGTTGGATTAAAGATTACGGACCCAGAGGGATATGC	2711
Db	3316	TCCAGTGTAGATCAGGCATTTGGGTGTATTTAAAGTTTCGAAACAGATGGGTATGC	3375
QY	2712	AACACTCGGAAACCTAGAAATTTGGTCCAGAGGGAACCTTTATCAGGAGAGCCATTAGAACG	2771
Db	3376	GACGTTAGGAATCTTTGAATTTGGTAGAGTTGGGCCATTTATCGGGTGAATCTCTAGAACG	3435
QY	2772	CTTGCAAAAGAGAGAACAACTGCGAAGATTCAAATGACAAGAGACGTTGAAGAACAGA	2831
Db	3436	GGAAACAAAGAGATAATGCGAAATGGAATGACAGCTAGGAAGAAACCGTGCAGAAATAGA	3495
QY	2832	TAGAAGGTATATGGCATCGAAACAAAGCGGTAGATCGTTTATATGCCGATTTATCAGGATCA	2891
Db	3496	TCGTGTGATTTAGCTCGGAAACAGCAATTAATCATCTGTTGTAGACTATCAAGATCA	3555
QY	2892	GCAACTGAATCTGATGTAGAAATTAACAGATCTTACTCGGGCCCAAGATCTGATACAGTC	2951
Db	3556	ACAAATTAATCCAGAAATTTGGGCTAGCAGAAAATTAATGAAGCTTCAAACTCTGTGAGTC	3615
QY	2952	CATTCCTTACGTATATAACGAATGTTCCACAGAAATACCAGGGATGAATATACGAAGTT	3011
Db	3616	AATTTCCGGGTGATATATGTGTATACACTATTACAGATTCCTGGGATTAATCTAGAAATTTA	3675
QY	3012	TACAGAAATTAACAGATTCGACTCCAAACAGCGTGGAGTTTGTATGATCAGCGAAATGCCAT	3071
Db	3676	CACAGATTATCCGATCGCTTACAAACAGCATCGTATCTGTATACGCTCTAGAAATCGGT	3735
QY	3072	ACCAATGCTGATTTTCGAAATGGGTTAAGTAAATTTGGAATGCAACGCCCTGGGTAGAGT	3131
Db	3736	GCAAAATGAGACCTTTAAACAGTGGTCTAGATAGTTTGGAAATCAAACTATGSGATCGATCGGT	3795
QY	3132	ACAAACAAATCAATCATACATCTGCTCTGTGATTCCAAACCTGGGATGACCAAGTTTCGCA	3191
Db	3796	TCAGCAAGATGCAATATGCAATTTCTTAGTCTTTTCGCAATGGGATGCAACGATTTCCCA	3855
QY	3192	ACAGTTTACAGTTCAACCGAATCAAAAGTATGTGTTACGAGTTTACTCGAGAAAAGAGG	3251
Db	3856	ACAAATGAGAGTAAATCCGAATTTGAAAGTATGCTTTACGTTGACAGCAAGAAAAGTAGG	3915
QY	3252	GCTAGGAATGATATGTAAGTATCCGTGATCGTGGAAATCAACAGAAACGCTTACTTT	3311
Db	3916	AGCGGAGATGATACGTCACAAATCCGAGATGGCGCTCATCCAGAAACCTCTTACAT	3975
QY	3312	TAGTGCAGCGAATTAATGATACAAATGGAATGTATAATACGCAAGTGTCCAAATCAAAATGG	3371
Db	3976	TAATGCATGTGACTACGATGTAAATGGTAGCTATGTCAATGACAATTCGTATATACAGA	4035
QY	3372	ATA 3374	
Db	4036	AGA 4038	

RESULT 12
US-09-019-809-4
; Sequence 4, Application US/09019809

Patent No. 6143550
GENERAL INFORMATION:
APPLICANT: LAMBERT, BART
APPLICANT: JANSSENS, STEPAN
APPLICANT: VAN AUDENHOVE, KATRIEN
APPLICANT: PEPEROEN, MARNIX
APPLICANT: VAN RIE, JEROEN
APPLICANT: VAN AARSEN, ROEL
TITLE OF INVENTION: NEW BACILLUS THURINGIENSIS STRAINS AND THEIR
NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22040-0747

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/019,809
FILING DATE: 02-FEB-1998

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: SVENSSON, LEONARD R.

REGISTRATION NUMBER: 30,330

REFERENCE/DOCKET NUMBER: 2121-135P

TELECOMMUNICATION INFORMATION:

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TELEFAX: (703) 205-8050

TELEX: 248345

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 4344 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: 668..4141

FEATURE:

NAME/KEY: misc_feature

LOCATION: 1..4344

OTHER INFORMATION: /note= "encompasses part of

OTHER INFORMATION: the sequence of SID 3: from nt position 2994 to

OTHER INFORMATION: 4344 in SID 4"

FEATURE:

NAME/KEY: misc_feature

LOCATION: 1..4344

OTHER INFORMATION: /note= "SID 3 shows additional

OTHER INFORMATION: nucleotides, located 3' from the sequence shown in

OTHER INFORMATION: SID 4 (1352-1554 in SID 4)"

US-09-019-809-4

Query Match 24.4%; Score 883.4; DB 3; Length 4344;

Best Local Similarity 56.6%; Pred. No. 1.5e-183;

Matches 1936; Conservative 0; Mismatches 1386; Indels 101; Gaps 12;

1 ATGAGTCCAAATATCAAAATGAATATGAATATGAGATGGACACCTTCTACTTCTGTA 60

668 ATGAATCAAAATATCAAAATGAATATGAATATGAGATGGACACCTTCTACTTCTGTA 727

QY 61 TCCAAATGATCTAAACAGATACCCCTTTTGGCAATGAGCCAAACAAATGCGCTACAAAATATG 120
DB 728 TCAGATGACGATGTGAGGTATCTCTTTGGCAATGAGCCAAATGCGCTACAAAATATG 787
QY 121 GATTAATAAGATATTTAAATAATGCTGCGGGAATGCTAGTGAATACCTGGTTCACCT 180
DB 788 AACTATAAGATATCTTTACAAATGACAGATGAGGACTACACTGATCTTTATATAAATCCCT 847
QY 181 GAATGATCTGTTAGCGGACAGATGAGCTTAAGGCGGCAATTTATATGAGTAAATTA 240
DB 848 AGTTATCTATATGAGTGTAGAGATGAGTTCAGCTGCGCTACTGTTGTTGGAGATA 907
QY 241 CTATCAGTTTGGGGTCCCATTTGTTGGCCGATAGTCTTTATATCTCAACTTATT 300
DB 908 CTCGGGCTTTAGGTGTTCCGTTTCTGGAACAATAGTGAATTTTATCAATCTCTTTA 967
QY 301 GATATCTGTTGGCTTCAGGGGAAAGAGATCAATGGGAAATTTTATGGAACAAGTAGAA 360
DB 968 AATACACTGTGGCCAGTTAATGATACAGCTATATGGAAGCTTTTCATGCGACAGTGGAG 1027
QY 361 GAATCTAATTAATCAAAAATAGCAGATATGCAAGGAATAAAGCGCTTCGGAATTAGAA 420
DB 1028 GAATCTGATCAATCAAAATACAGAAATTTGCAAGAAATCAGGCACTGCAAGATGCA 1087
QY 421 GGATAGGTAAATTAACCAATTAATCTAACTGCGCTTGAAGAAATGGGAAGAAATCCA 480
DB 1088 GGATAGGAGACTCTTTTAAATGATATCAAGTTCCCTTCAAAATTCGTTGGCTGATCGA 1147
QY 481 AATGTTCAAGAGCTTACGAGATGTCGGAATTCGAAATCCCTGGATAGTTTATT 540
DB 1148 AATGATACACGAAATTTAAGTGTGTTGCTGCTCAATTTATAGCTTTAGACCTTTGATT 1207
QY 541 ACGCAATATATGCCATCTTTTAGAGTCACAAATTTTGAAGTACCATTCTTACTGTATAT 600
DB 1208 GTTAATGCTATTCATTTGTTGCAATTAATGGAACAGGTTCCATTTACTGTCTAGTAT 1267
QY 601 GCAATGGCAGCCAACTTCATTTACTGTTTAAAGGACGCTCAATTTTGGAGAAAGAA 660
DB 1268 GCACAAGCTGTGAATTTACATTTGTTTAAATTAAGATGATCATCTCTTTTGGAGAAAG 1327
QY 661 TGGGATGTTCAACACTACTATTAATACTATATGATCGTCAATGAATGAATTTACTGCA 720
DB 1328 TGGGATTTCAACAGGGGGAATTTCCACATATTTATGACCGTCAATTTGGAATCAACCG 1387
QY 721 GAATATTTCTGATCATCTGTAAAGTGTATGAATCTGTTTAGCAAAATTAABAGGACG 780
DB 1388 AATGATCACTAATTTACTGTGAACCTTGGTATTAATACAGTTTAGATCGTTTAAAGGAA 1447
QY 781 AGCGCTAAACAAATGGGTTGACTATAACCAATTCGTTAGAGAAATGACACTGGCGGTTTA 840
DB 1448 AATGATGAAAGTTGGTTAAGATATCATCAATTCGTTAGAGAAATGACTTTAGTGTATTA 1507
QY 841 GATGTTGTTGATTTATCCCAATTAATGACACAGCAGTACCAATGGAAACGAAAGCA 900
DB 1508 GATGTTGTTGCGCTTATTTCCATATTAATGATGATGATGATGATGATGATGATGATGAT 1567
QY 901 CAACATAACAGGAGAGTATATAGATCCACTGGGCGGCTAAACGCTGCTTCAATG-- 958
DB 1568 CAGCTTACAGGTGAGGTATATACAGATCCGATTTATTAATCCACAGCTAATGTTTGA 1627
QY 959 -----GTTCTGTTATGACAAAGACCTTCTTTTCGGAGGTAGATGATATCCGTT 1008
DB 1628 CTTTGGCGAGTTGGGTACTAATCCCTTAATAATCTTTTCTGAGCTCGAAATATGCTTTC 1687
QY 1009 ATTGCAACCCCATGTTATTTGATTAATTAACCGGACTCAAGTGTATATACAAATCAAGA 1068
DB 1688 ATTCGCCACCCACATCTTTTGTAGTGTGATGATGATGATGATGATGATGATGATGATG 1747
QY 1069 AGCATTTCTTCGCTCGCTATATAGACATTTGGCTGCTGATCAATTAAGTACCATCGT 1128
DB 1748 CCAGTTTCTCATTAAT---TTTATGGATTTATGGTCAGGACATAGCTTACGCGGTAT 1804
QY 1129 GTCAGTAGGGGTAGTAAATCTTCAACAAATGATGGAACAAATTAATCAAAATCTACACAGCA 1188

Db 1805 CTGAACGATTCAGAGTCAAGAGATAGTTATGG-----CTAATTACAACCAAGA 1858
Qy 1189 AGTACTCTTGATTTTACGAATTTATCATTTTACAGAGCTCTATCAAGGATCGAG-TACT 1247
Db 1859 GCAACAATTAATCCGGAGTTGATGGACAAACCGCATAGATCAACGGCATAGATTTT 1918
Qy 1248 CTTGATATGTTTACCCTGGTTATACGPATATATTTTTTGGAAATGCCAAGATCGAGTT 1307
Db 1919 GGTTCGTGATGATAGGTATATATCGGTGGAATAGAGCTTCTTTGTCCAGAGGCTTG 1978
Qy 1308 TTTCAATGTAACCAATTCGAATTAACCAAGAGAGGTTAAAGTATTAATCCAGTTCCNA 1367
Db 1979 TTTAATGTT-----ACGACTTCTCTCGCTTAATGGAGGATGAG 2016
Qy 1368 AGATATTATAGCGAGTCAAGAGATTCGGAAATTAGAAATTACCTCCAGAAATTCAGATCA 1427
Db 2017 AGATCTCTATGATACAAATGATGAATACCACAGATGAAGTACCGGAATTCACCCA 2076
Qy 1428 ACCAAATTATGATCATATAGCCATAGATTAATGTATATCAAGTATTTCCCGACGGG 1487
Db 2077 TAGACTATCTCATGTTACCTTTTATAGCTT-----TCAAACTAATCAGGCTGGATCTAT 2130
Qy 1488 TAACACTACCGGATTTAGTACCTGTATTTCTTTGGACACATCGAAGTGCAGATTTAAACA 1547
Db 2131 AGCTAATGCGAAGTGTACCTACTTATGTTTGGACCCGCTCGTGTATGTTGGACCTTTAATA 2190
Qy 1548 TACAATATATTACAGATAAAATCACTCAAAATTCGGCGGTTAAATGTGGGTAATTTTACC 1607
Db 2191 TAGCNATACCCNAATAGAAATTACAAATTAACNTTGGTAAGGCATCTGCACCTGTTTC 2250
Qy 1608 GTTTGTTCCAGTGGTAAAGGACAGAGACATACAGAGGGGATTTTATTAACAGTAAATAG 1667
Db 2251 GGGTACTACGGTCTTAAAGGTTCCAGGATTTTACAGAGGGGTA TACTCC---GAAGAAC 2307
Qy 1668 AAGTACTGTTCTGTAGGAACCTTATTTCTAGCTCGATATGCGCTTAGCAATTAAGAAAAAGC 1727
Db 2308 AACTAATGGCAATTTGGAAACGTTAAGAGTAAACGGTTAAATTCACCAATTAACAACAATA 2367
Qy 1728 AGGAAATATCGTGTAAAGTACAGATATGCTACTGATGCAGATATGTTATTCATGTAA 1787
Db 2368 TCGCTAAGATTCGTTTGGCTCAACAGGAATTTTCAGTATAAGGGTACTCCGTGGAGG 2427
Qy 1788 CGATGC-----TCAGATTCAGATGCCAAAAACAATGAACCCAGGTGAGGATCTGACATC 1841
Db 2428 GGTTCCTATCGGTGATGTTAGATTAGGAGCACAATGAACAGAGGCGCAGGACTAATCTTA 2487
Qy 1842 TAAACTTTTAAAGTTCAGATGCTATCAACA-----TTAAATTTAGCAACAGATAG 1895
Db 2488 CGAATCCCTTTTCAACAGAGAGTTTACTACTGCTCGGTTCATTCGCTTTTACATTT 2547
Qy 1896 TTCGCTAGCATTTGAACATAATTTAGGTGAAGACCCCTAATTCACATTTATCTGTTATAGT 1955
Db 2548 TACACAGCTCAAGAGATTCAAAGTGAATGCAGAGGTGTAGACCGGTGGTAATA 2607
Qy 1956 TTACGTTGACCGAATTCGAATTCATCCAGTATAGACATATGAAGCGGACCAAGATTT 2015
Db 2608 TTATATAGATAGATTGAATTTGCTCTGTTGATCCGCAACGAGAGCGGAGAGATTT 2667
Qy 2016 AGAAGCGGAAGAAAGCAGTGAATTCCTTGTGTTTACGAATACAAAGATGCGTTACGACC 2075
Db 2668 AGAAGCGCGAAGAAAGCGGTGGCGAGCTTGTTTACACGTAACAAGGACGATACAGGT 2727
Qy 2076 AGCGTAAACGATTTAGTGAATCAAGCGCAACTTAGTGGATGATCGCTATCGATGA 2135
Db 2728 AAATGTGACAGATTTATCAAGTGGACCAAGCGCAATTTAGTGTCTATTCGATGA 2787
Qy 2136 TTTGTATCCAAATGAAGACGATTTGTTATTTGATGTCAGTGAAGAGGCAAAACGCTCAG 2195
Db 2788 ACAATATGGCATGACAAAAGATGTTTATTTGAGCGGTAAAGCGGCAAAACGCTCAG 2847
Qy 2196 TGAGGCAGTAAATTTGCTTCAAGATCCAGATTTTCAAGAGATTAAT-----GGAGAAA 2249

Db 2848 CCGGAACGCAACTTACTTCAAGATCCAGATTTTAAATACAATCAATAGTACAGAAGAA 2907
Qy 2250 TGGCTGGACGCGCAAGTACGGGAATTGAGGTTATAGAGGGATGCTTTATTTCAAGGGCG 2309
Db 2908 TGGCTGGAGGCAAGTAAAGGTGTTACTATTAGCGGGCGGTCCATTTCTTTAAAGGTGG 2967
Qy 2310 TTATCTACGCCCTACCAGGTGCGAGAGAAATAGATACGGAAACGTATCCAAAGTATCTGTA 2369
Db 2968 TGCACCTTCAGTTAGCAAGCGCAAGA-----GAAAAATTATCCAAACATATTTA 3015
Qy 2370 TCAAAAGTAGAGAGAGGTGTTATTAACCAATACACAAGATATAGATTGAGAGGTTTGT 2429
Db 3016 TCAAAAAGTAGATCGATCGGTGTTTAAAGCCCTTATACACGCTATAGACTAGATGGAATTTGT 3075
Qy 2430 CCGAAGCAGTCAAGGATTTGGAAATTTTTCACAAATTCGTATCAAAACCAACCGAATTTGTA 2489
Db 3076 GAAGGTAGTCAAGATTTAGAAATTTGATCTCATCCACATCATAAAGTCCATCTTTGTA 3135
Qy 2490 AAATGTATCCGGATGATTTGCTGCCAGATGTATCTCTGTTAACTCGGATGGTAGTATCAA 2549
Db 3136 AAATGTATCCAGATAATTTAGTATCTGATACITTACTCAGATGGTTCTTGCAGCGGAATCAA 3195
Qy 2550 TCGATGCGAGCGAACAAAGTATGTGAATAGCCGTTTGAAGTAGAAGTAAACCGT----- 2601
Db 3196 CCGTTGTGATGAACAGCATCAGGTAGATATGACGTAGATCGGAGCATCATCCAATGGA 3255
Qy 2602 -----TCTGCTGAAGCGCATGAGTTCTCTATTCTTATTCATGATACAGGTGAATCGA 2651
Db 3256 TTGCTGTGAAGCGCTCAACACATGAGTTTCTTCTATATTATACAGGGGATCTAAA 3315
Qy 2652 TTACAATGAATAATCAGGAATATGGGTTGAGTTTAAAGATTACGGACCCAGAGGATATGC 2711
Db 3316 TGCAAGTGTAGATCAGGGCATTTGGGTTGTATTAAAGTTTCGAACAACAGATGGGTATGC 3375
Qy 2712 AACACTCGGAAACCTAGAAATTTGGTCGAAGAGGACCTTTATCAGAGACGCAATTAGAAGC 2771
Db 3376 GACGTTAGGAAATCTTGAATTTGGTAGAGTTGGGCCATTTATCGGGTGAATCTCTAGAAGC 3435
Qy 2772 CTTCCAAGAGAGAACAAACAAGTGCGAAGATTCAAATGACAGAGAGACGTGAAGAACAGA 2831
Db 3436 GGAACAAGAGATTAATGGAATGCAAGTACAGCTAGGAAGAAACCGTCAGAAATAGA 3495
Qy 2832 TAGAAGGTATATGGCATCGAAACCAAGCGGTAGATCGTTTATATCCGATTTATCAGGATCA 2891
Db 3496 TCGTGTGTTATTTAGCTCGAAACAAGCAATTTAATCACTCTGTTGTAGACTATCAAGTCA 3555
Qy 2892 GCAACTGATCTCGATGTAGATTAAGATTCAGATCTTACTCGGGCCCCAAGATCTGATACAGTC 2951
Db 3556 ACAATTAATCCAGAAATTTGGCTAGCAGAAATTAATGAAGCTTCAAAATCTTTGAGAGTC 3615
Qy 2952 CATTCCTTACGTATATAACGAATTTCCCAAGAAATACCGGGATGACTATACGAAGTT 3011
Db 3616 AATTTCCGGGTGTTATAGTGATACACTATTACAGATTCCTGGGATTAACACGAATTTTA 3675
Qy 3012 TACAGAAATTAACAGATCGACTCCCAACAGCGGTGGAGTTTGTATGATCAGCGCAATTCGCAT 3071
Db 3676 CACAGAGTTATCCGATCGCTTACAAACAGCATCGTATCTGTATACGTCTAGAAATTCGGT 3735
Qy 3072 ACCAAATGGTGATTTTCGAATGGTTAAGTAAATTTGGAATGCAACGCTGCGGTAGAAAT 3131
Db 3736 GCAAAATGGAGACTTTAAACAGTGGCTAGATAGTTGGAAATCAAACTATGGATGATCGGT 3795
Qy 3132 ACACAAAATCAATCATATCATCTGCTTGTGATTTCCAAACTGGGATGAGCAAGTTTCGA 3191
Db 3796 TCACCAAGATGGCAATATGCAATTTCTTAGTTCTTTTCGCAATTTGGGATGCAAAAGTTTCCA 3855
Qy 3192 ACAGTTTACAGTTTCAACCGAATCAAGATATGTTGACAGGTACTGCGAGAAAAGAGG 3251
Db 3856 ACAATTCAGAGTAAATCGGAATTTGTAAGTATGTTTACGTGTGACAGCAGAAAGTAGG 3915
Qy 3252 GGTAGGAAATGGATATGTAAAGTATCCGTTGATGTTGGAAATCAAAACAGAAACGCTTACTTT 3311
Db 3916 AGGGGAGATGGAATCGTCACAATCCGAGATGGCGCTCATCCCAAGAAACTCTTATCATTT 3975

Db 1568 CAGCTTTACAGCTGAGGTATATACAGATCCGATTCGATTTAATCCACGACGTAATGTTGGA 1627
Qy 959 -----GTTCTCGGTATGACAAAGCACCTTCTTTCGGAGTGATAGATCATCGGTT 1008
Db 1628 CTTTCCGAGCTTGGGTACTAATCCGTATATACCTTTCTGAGCTCGAAATGCGCTTC 1687
Qy 1009 ATTTCGACACCCCATGATTTGATATATATAACGGGACTCACAGTGATATACAAATCAAGA 1068
Db 1688 ATTGCGCCACCAATCTTTTGTAGAGCTGATATAGCTTAACATCAGCAGTATCGATTT 1747
Qy 1069 AGCATTTCTCCGCTCGCTATATAAGACATGCGGTGCTCATCAATATAAGCTACCATCGT 1128
Db 1748 CCAGTTTCTATCTAAT---TTTATGGAATTTAGTTCAGGACATACGTTTACGCCGTAGTTAT 1804
Qy 1129 GTCAGTAGGGGTAGTAACTTTCAACAAATGATGGAACCTAATCAAAATCTACACAGCACT 1188
Db 1805 CTGAACGATTCAGCAGTACAAAGAGATAGTTATGG-----CCTAATTAACACCAAGA 1858
Qy 1189 AGTACCTTTGATTTTACGAATATGATATTTACAAGACTCTATCAAGAGTGCAG-TACT 1247
Db 1859 GCAACAATTAATCCCGAGTTGATGGAACAACCGCATAGAGTCAACGGCAGTAGATTT 1918
Qy 1248 CTTTGATATTTGTTTACCTGGTTATACGTATATATTTTGGGAATGCCAGAAGTCGAGTT 1307
Db 1919 CGTTCTGCATTCGATAGTATATATGCGGTGAATAGAGCTTCTTTTGTCCAGGAGGCTTG 1978
Qy 1308 TTTTCAGTAAACCAATGATATATACCAGAAAGAGCTTAAGATATATCCAGTTTCCAA 1367
Db 1979 TTTAATGGT-----ACGATCTTCTCGCTTAATGGAGGATGTAG 2016
Qy 1368 AGATATATAGCGAGTACAAAGATTCGGAATTAGAATTAACCTCCAGAACTTCAGATCA 1427
Db 2017 AGATCTATGATACAAATGATGAATTAACACGATGAAGTACCGGAGTTCAACCCA 2076
Qy 1428 ACCAAATTAAGTCAATATAGCCATAGATTAATGTCATATACAAAGTATTCGCCGACGGG 1487
Db 2077 TAGACTATCTCATGTACCTTTTATGCTT-----TCAAACTAATCAGGCTGGAATCTAT 2130
Qy 1488 TAACACTACCGATTAGTACTGATTTTCTTGACACATCGAAGTGCAGATTTAAACAA 1547
Db 2131 AGCTAATGCAAGGAAGTGTACTTATGTTTGGACCGCTCGTGATGTGGACCTTAATA 2190
Qy 1548 TACAATATTTACAGATAAATCACTCAAAATTCGGCGGTTAAATGTTGGATATTTTACC 1607
Db 2191 TAGATATACCCAAATAGATTAACAAATTAACCATTCGTTAAGGCAATCTGCACCTGTTTC 2250
Qy 1608 GTTTGTTCCAGTGGTAAAGGACAGGACATACAGGAGGGGATTTATTAAGTATATAG 1667
Db 2251 GGGTACTACGCTCTTAAGGTCAGGATTTACAGNGGGGTATATCTCC---GAAGAAC 2307
Qy 1668 AGTACTGGTTCTGTAGGAACCTTATTTCTAGCTCGATATGGCTAGCATTAAGAAAGC 1727
Db 2308 AACTAATGGCACATTTGGAACGTTAAGAGTAAACGGTTAATTCACCTTAACACAAATA 2367
Qy 1728 AGGGAATATCGTGAAGTACGATATGCTACTGATGACAGATTTGTTATGCTATATA 1787
Db 2368 TCGCTTAAGAGTTGCTTTGCTTCAACAGGAATTTCAAGTATTAAGGGTACTCCGTGGAGG 2427
Qy 1788 CGATGC-----TCAGATTCAGATGCCAAACAAATGAACCCAGAGTGCAGATCTGCATC 1841
Db 2428 GGTTCATTCGGGTATGTTAGATTAGGAGCACATGACAGAGGCGGAGGACTTAATCTTA 2487
Qy 1842 TAAACCTTTAAAGTTGCGATGCTATCAACA-----TTAAATTTAGCAACAGATAG 1895
Db 2488 CGAATCCCTTTTCAAGAGAGTTTACTACTACTGCTCGCTTCAATCCGCTTTTACATT 2547
Qy 1896 TTCGCTAGCAATTGAACATATTTAGTGAAGCCCTTAATTCACATTTATCTGCTATAGT 1955
Db 2548 TACACAGCTCAAGAGATTTCTAATCAGTGAATGCAAGGTTGTAGCACCGGTGGTGAATA 2607
Qy 1956 TTACGTTGACCGAATCGAATTTCAATCCAGTATGACACATATGAAGCGGAACAAGATTT 2015

Db 2608 TTATATAGATAGATTGAATTTGCTCCTGTGAATCCGGCACGAGAAGCGGAAGAGATTT 2667
Qy 2016 AGAAGCAGCGAAGAAAGCAGATGAATGCCCTGTTTACGAATACAAAGATGGCTTACGACC 2075
Db 2668 AGAAGCGGGAAGAAAGCGGTGGCAGCTTGTTTACGTAACAGGGACGGATTTACAGGT 2727
Qy 2076 AGCGCTAACCGGATTTAAGTGAATCAAGCGGCAAACTTAGTGAATGCTTATCGGATGA 2135
Db 2728 AATGTGACAGATTTAAGTGGACCAAGCGGCAAAATTTAGTGTCTATCCGATGA 2787
Qy 2136 TTTGTATCAAAATGAAGAAACGATTTGTTATGCGAGTGAAGAGGCAAAACGCTCTAG 2195
Db 2788 ACAATATGGCATACAAAAGATGTTTGAAGCGGTGAAGCGGCAAAACGCTCTAG 2847
Qy 2196 TGAGCAGCTAATTTGCTTCAAGATCCAGATTTCCAGAGATTAAT-----GGAGAAA 2249
Db 2848 CCGCAAGCGCAACTTACTTCAAGATCCAGATTTTAATCAATCAATAGTACAGAAGAGAA 2907
Qy 2250 TGGCTGGACCGCAAGTACGGGAATTTAGGTTATAGAAGGGATGCTTTATTCAAAAGGCG 2309
Db 2908 TGGCTGGAAGCAAGTAAACGGTGTACTATTAGCGAGGGCGTCCATCTTTTAAAGTGG 2967
Qy 2310 TTATCTACGCCCTACAGGTGCGAGAGAAATAGATACGGAACGATCCAAACGTATCTGTA 2369
Db 2968 TGCACCTTCAGTTAGCAAGCGCAAGA-----GAAAATTTATCCAACTACATTTA 3015
Qy 2370 TCAAAAGTGAAGGAGGTGTTAATAAACCATACACAGATATAGATTGAGAGGGTTCGT 2429
Db 3016 TCAAAAAGTAGATGATCGGTGTTAAAGCCTTATACGCTATAGACTAGATGGATTTGT 3075
Qy 2430 CGGAAGCAGTCAAGGATTTGGAATTTTCAAAATTCGTCTATCAACGCAACCGGAATTTGTA 2489
Db 3076 GAAGAGTAGTCAAGATTTAGAAATTTGATCTCATCAACCATATAAGTCCATCTTTGTA 3135
Qy 2490 AAATGTACCGGATGATTTGCTGCCAGATGATCTCCTGTTAACTCGGATGGTAGTACAA 2549
Db 3136 AAATGTACAGATAATTTAGTATCTGATACCTACTCAGATGTTCTTTCAGCGGGAATCAA 3195
Qy 2550 TCGATGACGAGCAAAAGTATGTAATAGCGTTTAGAAGTAGAAGAACCGT----- 2601
Db 3196 CCGTTGTGATGAACAGCATCAGGTAGTATGAGCTAGATCGGAGCATCATCCAAATGGA 3255
Qy 2602 -----TCTGTGTAAGCGCATGAGTTCTCTATTCTCTATTGATACAGGTGAATCGA 2651
Db 3256 TTGCTGTGAAGCGGCTCAACACATGAGTTTCTTCTCTATATATACAGGGGATCTAAA 3315
Qy 2652 TTACAATGAATAATGAGGAATAATGGGTTTGAATTTAAGATTTACGGACCCAGAGGATATGC 2711
Db 3316 TGCAAGTGTAGATCAGGCAATTTGGGTTGTAATAAAGTTTCGAACAAACAGATGGGTATGC 3375
Qy 2712 AACACTCGGAAACCTTAGAATTTGGTCAAGAGGACCTTTATCAGGAGACGCAATTAGAAGC 2771
Db 3376 GACGTTAGGAATCTTGAATTTGGTAGAGGTTTGGGCAATTTATCGGGTGAATCTCTAGAAGC 3435
Qy 2772 CTTTGAAGAGAGAACCAACAGTGAAGATTTCAATGCAAGAACCGTGAAGAAACACA 2831
Db 3436 GGAACAAGAGATATAAGCAATGGAATGCAAGCTAGGAAGAAACCGTGCAGAAATAGA 3495
Qy 2832 TAGAAGGTATATGGCATCGAAACAAAGCGGTAGATCGTTTATATGCGGATTTACAGGATCA 2891
Db 3496 TCGTGTGTTATTAGCTGGAAACAGCAATTAATCATCTGTTTGTAGACTATCAAGATCA 3555
Qy 2892 GCACTGAATCTGATGATAGATTAAGATCTTACTGCGGCGCCCAAGATCTGATACAGTC 2951
Db 3556 ACAATTAATCCAGAAATTTGGGCTAGCAGAAATTAATGAAGCTTCAAAATCTTTGTAGAGTC 3615
Qy 2952 CATTCCTTACGTATATACGAATGTTCCCAAAATACAGGAGTCAACTATACCAAGTT 3011
Db 3616 AATTTCCGGGTGATATAGTATACACTATTAAGATTTCTCGGGATTAACCTACGAATTTA 3675
Qy 3012 TACAGAAATTAACAGATCGACTCCAAAGCGGTGAGTTTGTATGATCAGCGAAATGCCAT 3071
Db 3676 CACAGGTTATCCGATCGCTTACACAGCATCGTATCTGTATACGTCTAGAAATGCGGT 3735

Db 961 CTTTGGCAGCTTTGGGGTACTAATCCCTATAATACATTTTCTGAGCTCGAAAATGCGCTTC 1020
QY 1009 ATTTCGACCCACCATGATTTTGGATTATATAACGGGACTCACAGTGATATACATATCAGA 1068
Db 1021 ATTTCGACCCACCATGATTTTGGATTATATAACGGGACTCACAGTGATATACATATCAGA 1080
QY 1069 AGCATTTCTTCGCTCGCTATATAAGACATTTGGGCTCGTCAATCAAAATAGCTACCATCGT 1128
Db 1081 CCAGTTTCATCTAAT---TTTATGGATTATTTGGTCAGGACATAGCTTTACGCGGTAGTTAT 1137
QY 1129 GTCACTAGGGGTAGTAACTCTTCAACAAATGTATGGAAGTAACTCAAAATCTPACACAGACT 1188
Db 1138 CTGAACGATTTACGAGTACCAAGAGATAGTTATGG-----CCTAAATTACAACCAAGA 1191
QY 1189 AGTACCTTTGATTTTACGAAATTAATTTTACAGACTCTATCAAGAGTATCAAAATCTPACACAGACT 1247
Db 1192 GCACCAATTAATCTGGAGTTGATGGAAACAAACCGCATAGAGTCAACGGCAGTAGATTTT 1251
QY 1248 CCTTGATATTTGTTTACCTCGTTTATACGTATATATTTTGGAAATGCCAAGTTCGAGTT 1307
Db 1252 CGTTCTGCAATGATAGTATATATGGGTGAATAGACTTTCTTTTGTCCGAGAGGCTTG 1311
QY 1308 TTTCTGTGTAACCAATGTAATTAATACCAAGAGAGCTTAAAGTATATATCCAGTTTCCAA 1367
Db 1312 TTTAATGGT-----ACGACTTCTCTGCTAATGGAGGATGTAG 1349
QY 1368 AGATATTTATAGCAGTACAGAGATTCGGAAATTAGAAATTAGATTTACCTCCAGAACTTCAGATCA 1427
Db 1350 AGATCTCTATGATACAAATGATGAATTTACCAACAGATGAAAGTACCGGAAGTTTC---TA 1405
QY 1428 ACCAAATTTATGAGTCAATATAGCAGATTAATGTCTATATCAATCAAGTATTTCCCGCGAGGG 1487
Db 1406 CCATAGACTATCTCATGTTTACCTT---TTTATGTTTCAACTAATCAGGCTGATCTAT 1463
QY 1488 TAACTACCGGATAGTACTGTATTTCTTGGACACATTCGAAGTGCAGATTTAAACRA 1547
Db 1464 AGCTAATGCGAGGAGTGTACTACTTATGTTTGGACCGCTGCTGATGTGGACCTTAATAA 1523
QY 1548 TACAATATATTACAGTAATTAATCTCAATTTCCGGCGTTAAATGTTGGATATTTTACC 1607
Db 1524 TAGGATTAACCCAAATGAAATTAACAATTTACCAATTTGGTAAAGGCATCTGCACCTGTTTC 1583
QY 1608 GTTTGTTTCAGTGGTAAAGGACGAGACATACAGGAGGGGATTTTATACAGTATATATAG 1667
Db 1584 GGGTACTACGGTCTTAAAGGTCAGGATTTACAGGAGGGGTATATCTCC---GAAGAAC 1640
QY 1668 AAGTACTGTTCTGTAGGAACCTTTATTTCTAGCTCGATATGGCTAGCATTTAGAAAAGC 1727
Db 1641 AACTAATGGCACATTTGGAACTGTAAGAGTAAACAGTTAATTCACCATTAACACAAAGATA 1700
QY 1728 AGGGAATATCGTGAAGTACAGATATGCTACTGATGCGAGATTTGTATGTGATGTAA 1787
Db 1701 TCGGTGAAGATTCGTTTGTCTTCATCAGGAATTTTTCAGCATTAAGGATTAATCTGCGTGAAA 1760
QY 1788 CGATGCTCAGATTCAG-----ATGCCAAACAAATGAAACCCAGGTGAGGATCTGCATC 1841
Db 1761 TACCTCTATAGCTTACAAAGATTTGGAGTACAAATGAAACAGAGGACAGGAACTTA 1820
QY 1842 TAAACTTTTAAAGTTCAGATGCTATCAACATTAATTAATTTAGCAACAGATATGCT 1901
Db 1821 CGAATCAATTTGTCAAGTGTGCTTCTACTAATCAGAGCGATCTGCTTTTACATTTAC 1880
QY 1902 AGCATTTGAACATAATTTAGTGAAGACCCCTAATTCACATTAATCTGTTATAGTTTACGT 1961
Db 1881 ACAAGCTCAAGAAATTTTAACTAATCTTGCAGAAAGTGTGTAGCACCGGTAGTGAATTTT 1940
QY 1962 T---GACCGAATCGAATTCATCCAGTGTAGATGAGACATATGAAGCGGAAACAGATTTAGA 2018
Db 1941 TATAGATAGATTTGAATCATCTCTGTGAACCCGGCACGGAAGCAGAGGATTTAGA 2000
QY 2019 AGCAGCGAAGAGCAGTGAATCCCTTGTGTTTACGAATACAAAAGATGGCTTTAGCACGAG 2078

Db 2001 AGCAGCGAAGAAAGCGGTGGCGAACTTGTTTACACGTACAAGGACGGATTACAGGTAAA 2060
QY 2079 CGTAAACGGATTTATGAATGAATCAAGCGGCAAACTTTAGTGGAAATGCTATCGGATGATTT 2138
Db 2061 TGTGACAGATTTATCAAGTGGACCAAGCGCAAAATTTTAGTGTCTATGCTTTATCCGATGAACA 2120
QY 2139 GTATCCAAATGAAAACGATTTGTTATTTTCATGCAAGTGAAGAGGCAAAAACGCTCTCAGTGA 2198
Db 2121 ATATGGGCAATGACAAAAGATGTTATTTGAAGCGGTGAAGCGGCAAAAACGCTCTCAGCG 2180
QY 2199 GGCACGTAAATTTGCTTTCAAGATCCAGATTTCCAAAGAGATAAAT-----GGAGAAAATGG 2252
Db 2181 CGAAACCAACTTTACTTTCAAGATCCAGATTTTAAATACAATCAATAGTACAGAAGAGATGG 2240
QY 2253 CTGGACGGCAAGTACCGGAAATTTGAGGTTATAGAAGGGATGCTTTATTTCAAAGGGGCTTAA 2312
Db 2241 CTGGAAGGCAAGTAAACGGTGTACTATTAGCGAGGCGGTCCATTTCTTTAAAGGCTGTCG 2300
QY 2313 TCTACGCTTACCAGGTGCGAGAGAAATAGATACGGAACGTTATCCAAACGTTATCTGTATCA 2372
Db 2301 ACTTCAGTTAGCAAGCGCAAGA-----GAAAATTTATCCAAACATACATTTATCA 2348
QY 2373 AAAAGTAGAGGAGGTGTATTTAAACCATACACAGATATAGATTTGAGAGGGTTTCTCGG 2432
Db 2349 AAAAGTAGATGATCGTGTCTTAAAGCCTTATACACGCTATAGACTAGATGGATTTCTGAA 2408
QY 2433 AAGCAGTCAAGATTTGGAATTTTCAATTTCTGTCATCAAAACGAAACCGAATTTGTAATAAAA 2492
Db 2409 GAGTAGTCAAGATTTAGAAAATTTGATCTCATCCACCATCAATAAAGTCCATCTTTGTAATAAAA 2468
QY 2493 TGTACCGGATGATTTGCTGCCAGATGATCTCTCTGTTAACTCGGATGTTAGTATCAATCG 2552
Db 2469 TGTACCAAGATATTTAGTATCTGATACCTTACTCAGATGTTCTTGCAGCGGAATCAACCG 2528
QY 2553 ATGACGCGAACAAGATATGTGAATAGCGGTTTGAAGTAGAATAACCGT-----2601
Db 2529 TTGTGATGAACAGCATCAGTAGATATGATGATGATGCGAGCATCATCCAAATGATTTG 2588
QY 2602 -----TCTGGTGAAGCGCATGAGTTCTTATTTCTTATTTAGTACAGGTGAATTCGATTA 2654
Db 2589 CTGTGAAGCGGCTCAACACATGAGTTTCTTCTATATTAATACAGGGGATCTAAATGC 2648
QY 2655 CAATGAAATGACAGAAATATGTTGTTGTTTAAAGATTAACGACCCAGGAGGATATCAAC 2714
Db 2649 AAGTGTAGATCAGGGCATTTGGGTTGTATTTAAAGTTTGAACAAACAGATGGGTATCGGAC 2708
QY 2715 ACTCGGAAACCTAGAAATTTGTCGAAAGAGGACCTTTTATCAGGAGAGCGCATTAAGAACGTT 2774
Db 2709 GTTAGGAAATCTTGAATTTGGTAGAGTTGGGCCCATTTATCGGGTGAATCTCTAGAACGGGA 2768
QY 2775 GCAAGAGAGAAACAAACAGTGAAGATTTCAAATGACAGAAGAGCGTGAAGAAACAGATAG 2834
Db 2769 ACAAAGAGATAATGCGAAATGGAATGCGAGCTAGGAAGAAACCGTGCAGAAATAGATCG 2828
QY 2835 AAGGTATATGCGATCGAAACAGCGGTAGATGTTTATATGCGGATTTATCAGATCAGCA 2894
Db 2829 TGTGTATTTAGTGTGGAACCAAGCAATTAATCATCTGTTTGTAGACTCAAGATCAACA 2888
QY 2895 ACTGAATCTGTATGAGATTAACAGATCTTACTGCGGCCCAAGATCTGATACAGTCCAT 2954
Db 2889 ATTAAATCCAGAAATTTGGGCTAGCAGAAATTAATGAAGCTTCAAAATCTTTGTAGAGTCAAT 2948
QY 2955 TCGTTACGTATATACGAAATGTTTCCGAAATATACAGGGATGAACATACAGAAATTTTAC 3014
Db 2949 TTTCCGGTGTATATAGTGAATACATTTACAGATTTCTTGGGATTAACATCGAAATTTTACAC 3008
QY 3015 AGAATTTAACAGATCCGATCCCAACAGCGTGGAGTTTGTATGATCAGCGGAAATGCCATACC 3074
Db 3009 AGAGTTATCCGATCCGTTTACAAACAGATTCGTTATCTGTATACGTCTAGAAATTTGCGGTGA 3068
QY 3075 AAATGGTGAATTTTGAATTTGGGTTAAGTAAATTTGGAATGCAACGCTGGCGGTAGAAATGACA 3134
Db 3069 AAATGGAGACTTTAACAGTGGTCTAGATAGTTTGGAAATACAACTATGATGTCATCGGTTCA 3128

QY 3135 ACAAATCAATCATATCTGCTTGTGATTCCTCAAACTGGGATGAGCAAGTTTCGCAACA 3194
DB 3129 GCAAGATGCAATATGCAATTTCTTAGTTCTTTCGATTTGGGATGCAAGTTTCGCAACA 3188
QY 3195 GTTTACAGTTCAACCGAATCAAAAGATATGTGTTACGATTTACTGCGAGAAAGAGGGGT 3254
DB 3189 ATTGAGAGTAAATCCGAATTTGTAAGTATGTTTACGTTGTGACAGCAAGAAAGTAGGAGG 3248
QY 3255 AGGAATGGATGTAAAGTATCCGTTGATGCGGATGGAATCAACAGCAAGCGTTACTTTTAG 3314
DB 3249 CGGAGATGATACGTCACAAATCCGAGATGGCGCTCATCACCAGAAAGCTCTTACATTTAA 3308
QY 3315 TCGAAGCGATTATGATACAAATCGGAATGTATTAATACGCAAGTGTCCAATACAAATGGGATA 3374
DB 3309 TGCATGTGACTACGATGTAATGGTACGTATGCTCAATGACAAATTCGTATATACAGAGA 3368

RESULT 15

US-08-542-921-1
; Sequence 1, Application US/08542921
; Patent No. 5736514
; GENERAL INFORMATION:
; APPLICANT: IIZUKA, TOSHIHIKO
; APPLICANT: TAGAWA, MICHIO
; APPLICANT: ARAI, SATOSHI
; APPLICANT: NIIZEKI, MASATSUGU
; APPLICANT: MIYAKE, TOSHIRO
; TITLE OF INVENTION: NOVEL BACILLUS STRAIN AND HARMFUL
; TITLE OF INVENTION: ORGANISM CONTROLLING AGENTS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON SPIVAK, MCCLELLAND, MAIER & NEUSTADT
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/542,921
; FILING DATE: 13-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 276082/94
; FILING DATE: 14-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 49-209-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3759 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis var. japonensis
; STRAIN: N141
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 47..3556
US-08-542-921-1

Query Match 23.4%; Score 848.6; DB 1; Length 3759;
Best Local Similarity 56.2%; Pred. No. 5.4e-176;
Matches 1930; Conservative 0; Mismatches 1414; Indels 93; Gaps 14;
QY 1 ATGAGTCCAAATATCAAAATGAATATGAATATATAGATGGGACACCTTCTACTTCTGTGA 60
DB 47 ATGAATCGAAATATCAAAATGAATATGAATATATAGATGGGACACCTTCTACTTCTGTGA 106
QY 61 TCCAAATGATTCTTAACAGATACCTTTTGGCGAATGAGCGCAACAAATCGCTACAAATATG 120
DB 107 GCAGATGATGTTGTAATATATCCCTTTCACAGATGATCCGATGCTGGATGCAAAATATG 166
QY 121 GATTATAAAGATATATTAATAATATCTGCGGGAATCTAGTGAATACCCCTGGTTCACCT 180
DB 167 AACTATAAGGAATATTTACAAACGATATGCTGGAGACTATACAGATCCTCTTATTAACTCT 226
QY 181 GAAGTACTTGTAGCGGACAGATGCGAGCTAAGCGCGCAATGATGATATAGTAGGTAATAATTA 240
DB 227 AACTTATCTGTTAGTGGAAAGATGTAATACAACTTGGAAATTAATATTTAGGGAGATTA 286
QY 241 CTATCAGGTTTGGGCTCCCAATTTGTTGGGCGGATAGTGAATCTTTATATCTCAACTTATT 300
DB 287 CTAAGCTTTTGGATTCCTCTTCTAGTCAATGGGTTACTGTATATACCTATCTCTTTTA 346
QY 301 GATATTCTGTGGCCTTCAGGGGAAAAGAGTCAATGGGAAAATTTTATGGAAACAAGTAGAA 360
DB 347 AACAGCTTGTGGCGGATGACGAGAAATCTGTATGGGACGCTTTTATGGAGAGTAGAA 406
QY 361 GAATCTAATTAATCAAAATATAGCAGAAATATGCAAGGAATTAAGCGCTTTCGGAATTAAGAA 420
DB 407 GAACTTATGATCAAAATATCTCAGAAAGCAGTAAGGAGGATAGGCAATGGATGACCTAACT 466
QY 421 GGATAGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 480
DB 467 GGATTAACAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 526
QY 481 AATGGTTCAAGAGCCTTACGAGATGTCGGAATCGAATTTGAAATCCTGGATAGTTTATT 540
DB 527 AATGGCGCAAGGCAATCCTTAGTTTCTC---AGCGATTTAACTTTTAGATAGCTATT 583
QY 541 ACGCAATATATGCCATCTTTTA-----GAGTGAACAATTTTGAAGTACCATT 588
DB 584 ACACAATTTATGCCAAGCTTTGGCTCTGGTCTCGGAAAGTCAAAATTTATGCAACTATATTA 643
QY 589 CTTACTGTATATGCAATGGGACCAACCTTCATTTACTGTTATTATAAGGACGCTCAATT 648
DB 644 CTTCCAGTATATGCAACAGCAGCAAACTTCATTTGTTATTATTATAAAGATGCGACACT 703
QY 649 TTTGGAGAAAGATGGGATGGTCAACAACTACTATTAACTATTATATGATCGTCAAAATG 708
DB 704 TATGGAGCTAGATGGGCGCTGAATCAAACTCAATAGATCAATTCCTCTCGTCAACAA 763
QY 709 AAATTTACTGCAGAATATTTCTGATCACTGTGTAAAGTGGTATGAACTGGTTTATAGCAAAA 768
DB 764 AGCTTACTCAGACTTATACAAATCAATTTGTGTACTGCGTATATATGATGGATTAGCGGAA 823
QY 769 TTAAGAGCAGCAGCGCTTAACAATGGTGGTGACTATACCAATTCGCTAGAGAAATGACA 828
DB 824 TTAAGAGGCAACACCGCTGAGAGTTGGTTTAAATACAACTCAATATCGTAGAGAAATGACT 883
QY 829 CTGGCGGTTTTAGATGTTGTCATTTATCCCAATATATGACACACGACGCTACCCCAATG 888
DB 884 TTGACGGCAATGGATTTAGTGGCAATTTCCCATTTATATATTTACGCAATATCCAGAT 943
QY 889 GAAACGAAAGCAACAACTAAAGGAAAGTATATACA-----GATCCACTGT 933
DB 944 GGGACAAATCTCAACTTACACGCTGAGGCTTATACAGATCCGATTCGATTTGATCCACTGT 1003
QY 934 GCGCGGTTAAACGTGCTTCAATTTGGTTCCTGGTATGCAAGACACCTTCTTTGGAGTG 993
DB 1004 GAACAACCAACTACTCAATTTATGTCGATCATGGTACATTAACCCAGCTTTTCGAAATCAT 1063
QY 994 ATGAATCATCCGTTATTTCGACACCCCATGTTTGTGTTATATAACGGGACTCACAGTG 1053

Db	1064	TTGAATTTCTCTGTACTAGAAATTCATTGATTCGTCCTCCCGCACCTTTTGTGAAGGTGA	1123
Qy	1054	TATACACAATCAAGAAGCATTTCTTCGCTCGCTATATAAGACATTTGGGCTGGTCATCAA	1113
Db	1124	AGTAATTTGCCAAATTTTAGTTAATTAACCAACAAACGGTAGCGCTTGGCGTGGGTCAAGG	1183
Qy	1114	ATAAGCTACCATCGTCTCAGTAGGGGTAGTAATCTTCCAAACAATGTATGAACTAATCAA	1173
Db	1184	GTAAGATACCATTTATTTGCATAGTTCTCTATAATACAGGAAAAAAGTAGTACGSCCTCCTCAGT	1243
Qy	1174	AATCTACACAGCACTAGTACCTTTTGATTTTACGAAATTTATGATATTTTACAGACTCTATCA	1233
Db	1244	GATCCGTTGGAGCTAATA---TCAATGTTCAAAATAATGATATTTATCAGATTAATTCG	1300
Qy	1234	AAGGAT-GCAGTACTCCTTGTGATATGTTTACCCTCGTGTATACGTATATATTTTTCGAAT	1292
Db	1301	CAGGTTAGCAATTTTCTAGTCTCTGTGGCTCATCATATAGTGTGTTGGGACACTAATTTT	1360
Qy	1293	GCCAGAGTCGAGTTTTTCATGTGTAAACCAATTTGAATAATACAGAAAGACGTTAAAGTA	1352
Db	1361	TATTTGAGTTTCAGGACAAGTAAGTGGGATTTCCAGGATATACACAGCAAGGTATACCAGCA	1420
Qy	1353	TAATCCAGTTTCCAAAGATATATACGGAGTAC-AAGAGATTCCGGAATTAGAATTTACCTC	1411
Db	1421	GTTTGTCTTCAACACGAAATTCACCTGATGTTTCCAAAGCTTTAATCCGGAAGGAGAT	1480
Qy	1412	CAGAAACTTTCAGATCAACCAAAATTTATGAGTCATATAGCCATAGATTATGTATATACAA	1471
Db	1481	ATCATTAGAAATTAATAGTCAATAGGTTATCTCATATAACCCNAATCGTTTTCAAGCACT	1540
Qy	1472	GTATTCGCCGACGGGTAAAC-ACTACCGAATTAGTACCTGTATTTTCTTGGACACATCGA	1530
Db	1541	CAAAAGTGTAGTCCATCAACTGTTAGCGCAAAATTTTACCTACTTGTGTATGGAACGATCGA	1600
Qy	1531	AGTCAGAGTTTAAACAAATCAATATATTCAGATAAATCACTCAAAATTCGGCCGTTAAA	1590
Db	1601	GATGTGGACCTTGATTAATACCAATTTACTGCGAAATCAAAATTAACAACATCCATTTAGTAAAG	1660
Qy	1591	TGTTGGGATAAATTTTACCGTTTGTTCAGTGGTAAAAAGGACCGAGCATACAGCAGGGGAT	1650
Db	1661	GCATATGACTAAGTAGTGGTGTCTACTGTCTGGAAGTCCAGANTTCAAGGAGAGAT	1720
Qy	1651	TTATTAAGTATAATAGAAAGTACTCGTTCTGTAGGAACCTTATTTCTAGCTCGATATGGC	1710
Db	1721	GTAAATCCGAAGAAACAAATACTGGTGAATTCGGAGCAATRAAGGTGTCTGACCTGGACCG	1780
Qy	1711	CTAGCAATTAGAAAGCAGGGAATATCGTGTAAAGACTGAGATATGCTACTGATCGAGAT	1770
Db	1781	CTAACACACGATATCGCATAAAGTTCCGTTATGCTTTCGCAATAGATTTTGTGATTTCTTT	1840
Qy	1771	ATTGTATTGCATGTAAACGATG---CTCAGATTAGATGCCCCAAAAACAATGAACCCAGGT	1827
Db	1841	GTAAACCGTGGAGGAACACTATAAATATTTTAGATTTACGTCATATGAACAGGGGA	1900
Qy	1828	GAGGATCTGACATCTAAAACTTTTAAAGTTGACAGTGTCTATCAACAATTTAAATTTAGCA	1887
Db	1901	CAGGAATCAAGATATGAAATCTCTATCGTACTGTAGAGTTTACAACCTCTTTTAACCTTACA	1960
Qy	1888	ACAGATAGTTTCGTACGATTGAAACATAATTTTAGTGAAGACCCCTAATTCACAACTATCT	1947
Db	1961	CAAAGTCT--AAGATATAATTCGAACATCTATCCAGGA-----CTTAGTGGAAAT	2008
Qy	1948	GCTATATTTTACTGTTGACCGGAATTCGAATTCATCCGATAGTAGAGACATATGAAGCGGA	2007
Db	2009	GGGGAAGTATACTTGATAGAAATTTGAATTCATCCCTGTGNAACCCGCGACGGAAGCAGAA	2068
Qy	2008	CAAGATTTAGAAACGACGGAAGAAAGCAG---TGAATGCTCTTGTTTACGAATACAAAGAT	2064
Db	2069	GAGGATTTAGAGACGGAAGAAAGCGGTAGSCAGNACTTGTGTTTACAGCTACAGGGAC	2128
Qy	2065	GGCTTACGACCGGCGTAACGGATTTAGAGTGAATCAAGCGGCNAACCTTAGTGGAAATGC	2124

Db	2129	GGATTACAGGTAAATGTGACAGAGTTATCAAGTGGACCAAGCGGCAGAAATTTTAGTGTCTATGC	2188
QY	2125	CTATCCGATGATTTGTATCCAAATGAAAAACGATTTGTTATTTGATGCAGTGAGAGAGCA	2184
Db	2189	TTATCCGATGAAACATATGGCCATGACAAAAGATGTTATTGGAACGGTGAAGACGGCA	2248
QY	2185	AAACGCTCTAGTGAGGCACGTAAATTTGCTTCAAGATCCAGATTTCTCAAGAGATAAAT---	2241
Db	2249	AAACGCTCTAGCGCGGAAACCACTTACTTCAAGATCCAGATTTTAAATACAATCAATAGT	2308
QY	2242	---GGAGAAATGCTCGACGGCAGTACGGGAAATGAGGTTATAGAGGGGATGCTTTA	2298
Db	2309	ACAGAGAGAAATGCTCGAAGGCAAGTAAACGGTGTACTATTAGCGAGCGCGTCCATTC	2368
QY	2299	TTCAAGCGGCGTTATCTTACGCCCTACCAGGTGCGAGAGAAATAGATACGGAACCGTATCCA	2358
Db	2369	TTTAAAGGTCGTGCACCTTCAGTTAGCAAGCGCAAG-----GAAATTTATCCA	2416
QY	2359	ACGTATCTGATCAAAAAGGTAGAGGAGGTGATTAAAAACATACACAAGATATAGATTG	2418
Db	2417	ACATACATTTATCAAAAAGGTAGATGCATCGGTGTAAAGCCCTTATACACGCTATAGACTG	2476
QY	2419	AGAGGGTTTCTCGGAAGCAGTCAAGATTTGGAATTTTCCANATTCGTCTATCAACGAC	2478
Db	2477	GATGGGTTCTGGAAGAGTAGTCAAGATTTAGAAATTTGATCTCATTCACTATCATAAAGTC	2536
QY	2479	CGAATGTGAAAAATGTACCCGATGATTTGCTGCCAGATGTATCTCTGTTAACTCCGAT	2538
Db	2537	CATCTTGTGAAAAATTTAGTATCCGATACCTTACTCGATGGTCTTCTTGC	2596
QY	2539	GGTAGTATCAATCGATCCAGCGAACAAAGTATGTGAATAGCCGTTTAGAAGTAGAAGAAC	2598
Db	2597	AGTGGATGAATCGATGTGAGGAAACAAAGATGGTAAATGCCAACTGGAAAACAGAACAT	2656
QY	2599	CGT-----TCTGCTGAAGCGCATGAGTCTCTATTCCTTCTATTGAT	2637
Db	2657	CATCATCCGATGGATTCTGTGGAAGCGGCTCAACACATGAGTTTTCTTCCTATATTAAT	2716
QY	2638	ACAGTCAAAATCGATTACAATGAAATGCAGGAATATCGGTTGGATTTTAAGATTACGGAC	2697
Db	2717	ACAGGGATCTAAATGCAAGTGTAGATCAGGCAATTCGGTTGTATTAAAGTTTCGAACA	2776
QY	2698	CCAGAGGGATATGCACACTCGGAAACCTTAGAATTTGGTCGAAGAGGCACTTTATCAGGA	2757
Db	2777	ACAGATGGGTATCGACGTTTAGGAAATCTTGAATTTGGTAGAGGTTGGGCCATTATCGGT	2836
QY	2758	GACCCATTAGAAACGTTTGCMAAGAGAGAGAACAAAGTGCGAAGATTCAATGCAAGAAGA	2817
Db	2837	GAATCTCTAGAAACGGGAACAAAGAGATATGCGAAATGCGAATGCAGAGCTAGGAAGAAA	2896
QY	2818	CGTGAAGAAACAGATAGAAGGTATATGGCATCGAAACCAAGCGGTAGATCGTTTATATGCC	2877
Db	2897	CGTGCAGAAATAGATCGTGTGTTATTAGCTGCGAAACCAAGCAATTAATCATCTGTTGTA	2956
QY	2878	GATTATCAGGATCAGCAACTGAAATCCTGATGTAGAGATTACAGATCTTACTCGGCGCCAA	2937
Db	2957	GACTATCAAGATCAACAAATTAATCCAGAAATTCGGCTAGCAGAAATTAATGAAGCTTCA	3016
QY	2938	GATCTGATACAGTCCATTCCTCTAGTATATACGAATATGTTCCAGCAAAATACAGAGGATG	2997
Db	3017	AATCTCTAGAGTCAATTTCTGGGTGTATATAGTGTATACACTTAATACAGATTCCTCGGGAT	3076
QY	2998	AACATACGAAGTTTACGAATTTACAGATCGACTCCAAACAGCGGTGGAGTTCTATGAT	3057
Db	3077	AACATACGAATTTACACAGAGTTATCCGATCGCTTACAAACAGCATCGTATCTGTATACG	3136
QY	3058	CAGCGAAATGCCATACCAATGGTGATTTTCCAAATGGGTTAAGTAATTTGGAATGCAACG	3117
Db	3137	TCTCGAAATCGGTGCAAATGGAGACTTTAACAGTGGCTAGATAGTTGGAATACAAC	3196
QY	3118	CCTGGCTAGAAGTACAAACAAATCAATCATACATCTGCTTGTGATTCAAACTCGGAT	3177
Db	3197	ACGATGCATCGGTTCAGCAAGATGCAATATGCAATTTCTTAGTTCTTTCCGATTTGGAT	3256

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 7, 2003, 00:48:42 ; Search time 6104 Seconds
(without alignments)
17264.295 Million cell updates/sec

Title: US-10-032-717-1
Perfect score: 3621
Sequence: 1 atgagccaataatcaaaa.....tgattgtagagtagagtaa 3621

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.om.*
- 21: em.or.*
- 22: em.ov.*
- 23: em.pat.*
- 24: em.ph.*
- 25: em.pl.*
- 26: em.ro.*
- 27: em.sts.*
- 28: em.un.*
- 29: em.vi.*
- 30: em.htg_hum.*
- 31: em.htg_inv.*
- 32: em.htg_other.*
- 33: em.htg_mus.*
- 34: em.htg_pin.*
- 35: em.htg_rtd.*
- 36: em.htg_mam.*
- 37: em.htg_vrt.*
- 38: em.sv.*
- 39: em.htgo_hum.*
- 40: em.htgo_mus.*
- 41: em.htgo_other.*

Pred. No. is the number of results predicted by chance to have a

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2565.2	70.8	3507	1	BTU04365	U04365 Bacillus th
2	2565.2	70.8	3507	6	125972	125972 Sequence 3
3	1812.2	50.0	3471	1	BTU04364	U04364 Bacillus th
4	1812.2	50.0	3471	6	125971	125971 Sequence 1
5	1185.6	32.7	3435	1	AB089299	AB089299 Bacillus
6	1180	32.6	3483	1	BTU04366	U04366 Bacillus th
7	1180	32.6	3797	6	AR005118	AR005118 Sequence
8	1180	32.6	3797	6	AR050172	AR050172 Sequence
9	1180	32.6	3797	6	E06830	E06830 DNA sequence
10	900	24.9	3459	6	AX189653	AX189653 Sequence
11	883.4	24.4	3474	6	AX100532	AX100532 Sequence
12	883.4	24.4	4344	6	A73540	A73540 Sequence 4
13	883.4	24.4	4344	6	AR031103	AR031103 Sequence
14	883.4	24.4	5772	1	BTCRY9COP	BTCRY9COP
15	882.8	24.4	3471	6	AR205864	AR205864 Sequence
16	882.8	24.4	3471	6	AX098657	AX098657 Sequence
17	881.8	24.4	4344	6	A73785	A73785 Sequence 4
18	848.6	23.4	3759	6	BACN141	D85560 Bacillus th
19	848.6	23.4	3759	6	AR000568	AR000568 Sequence
20	848.6	23.4	3759	6	AR053979	AR053979 Sequence
21	848.6	23.4	3759	6	AR055735	AR055735 Sequence
22	848.6	23.4	3759	6	E11968	E11968 gDNA encodi
23	822.2	22.7	3453	6	AR205865	AR205865 Sequence
24	822.2	22.7	3867	1	AB011496	AB011496 Bacillus
25	740.4	20.4	4000	1	BTCRVIX	X75019 B.thuringie
26	740.4	20.4	12579	1	BTCRVIX	X58120 B.thuringie
27	734.2	20.3	3411	6	AR205866	AR205866 Sequence
28	733.6	20.3	3414	1	BTU04368	U04368 Bacillus th
29	731.4	20.2	3414	1	BTU04367	U04367 Bacillus th
30	726.6	20.1	4623	1	BTU28801	U28801 Bacillus th
31	726	20.0	3651	6	AX138576	AX138576 Sequence
32	726	20.0	3651	6	AX146768	AX146768 Sequence
33	721.4	19.9	3663	6	AX088010	AX088010 Sequence
34	721.4	19.9	3663	6	AX088012	AX088012 Sequence
35	718.2	19.8	3627	6	AX138580	AX138580 Sequence
36	718.2	19.8	3627	6	AX146772	AX146772 Sequence
37	712	19.7	4004	1	BACCRV11C	M64478 Bacillus th
38	712	19.7	4004	6	A07236	A07236 B.thuringie
39	706.8	19.5	3624	6	AX138578	AX138578 Sequence
40	706.8	19.5	3624	6	AX146770	AX146770 Sequence
41	681.6	18.8	3687	6	AX189649	AX189649 Sequence
42	681.6	18.8	4173	6	AX098667	AX098667 Sequence
43	678	18.7	3934	1	BACCRVIE	L32020 Bacillus th
44	678	18.7	3934	6	AR068828	AR068828 Sequence
45	678	18.7	3934	6	I38760	I38760 Sequence 3

ALIGNMENTS

RESULT 1
LOCUS BTU04365
DEFINITION Bacillus thuringiensis kumamotoensis PS50C(b) CryIII
ACCESSION U04365
VERSION U04365.1
KEYWORDS GI:436834
SOURCE Bacillus thuringiensis.
ORGANISM Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.
REFERENCE 1 (bases 1 to 3507)
AUTHORS Narva,K.E. and Fu,J.
TITLE Novel Coleopteran-Active Toxins from Bacillus thuringiensis

BTU04365 3507 bp DNA linear BCT 27-AUG-1994
Bacillus thuringiensis kumamotoensis PS50C(b) CryIII
delta-endotoxin gene, partial cds.

JOURNAL Unpublished (1994)
REFERENCE 2 (bases 1 to 3507)
AUTHORS Feitelson, J. S.
TITLE Direct Submission
JOURNAL Submitted (15-DEC-1993) Jerald S. Feitelson, Molecular Biology,
Mycogen Corporation, 4980 Carroll Canyon Road, San Diego, CA 92121,
USA

FEATURES
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ORIGIN

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RESULT 2

I25972

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

Sequence 3 from patent US 5554534.

I25972.1 GI:1605842

Unknown.

Unclassified.

1 (bases 1 to 3507)

Michaels, T.E., Narva, K.E. and Fonceerrada, L.

Bacillus thuringiensis toxins active against scarab pests

Patent: US 5554534-A 3 10-SEP-1996;

Location/Qualifiers

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PAT 07-OCT-1996


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RESULT 3
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ACCESSION
  U04364
VERSION
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KEYWORDS
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  Narva, K.E. and Fu, J.
  Novel Coleopteran-Active Toxins from Bacillus thuringiensis
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  Feitelson, J.S.
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ORIGIN

Query Match 50.0%; Score 1812.2; DB 1; Length 3471;

Best Local Similarity 72.2%; Pred. No. 0;

Matches 2504; Conservative 0; Mismatches 908; Indels 57; Gaps 9;

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Db 298 GGTCAATTTATGCGCTCAAAGAGCGTAGATATATGCGGAGAAATTTATGAAACGAGTGGAA 357
Qy 361 GAACCTAATTAATCAAAATATGAGAGATATGCAAGGAATTAAGCGCTTTTCGGAAATTAGA 420
Db 358 GAACCTCGTTGATCAAAATATGAGAAATATGTAAGAGATAGGCTCTTCTGCTGAATTTAAAA 417
Qy 421 GGATTAGGTAAATTTACCAATTTATATCTAACTGCGCTTTGAAGAAATGGGAAGAAATCCA 480
Db 418 GGGCTAGGAATGCTTTGGATGATATATCAGCAGTCACTTTGAAGATTTGGCTGGAAATCCG 477
Qy 481 AATGGTTTCAAGAGCTTTACGAGATGCGAAATTCGAATTTGAAATCTGGATAGTTTATTT 540
Db 478 AATGATGCAAGAACTAGAGAGTGTGTTTCTAATCAATTTATAGCTTTAGATCTTAACTTT 537
Qy 541 ACGCAATATATGCCATCTTTTATAGATGACAAATTTTGAAGTACCATTCTTCTACTGTATAT 600
Db 538 GTTAGTTCAATTTCCATCTTTTTCAGTATCCGACACAGAAAGTACTATTTATAGCAGTATAT 597
Qy 601 GCAATGGCAGCCAACTTCAATTTACTGTTTATTAAGAGCGCGTCAATTTTGGAGAGAA 660
Db 598 GCACAGGCTGTGAACTTCAATTTATTTATTAAGAGATGCTTCTATTTTGGAGAGAGAG 657
Qy 661 TGGGATGCTCAACAACTACTATTAATACTATTATGATCGTCAAAATGAAACTTACTGCA 720
Db 658 TGGGATTTACACCAAGGTGAAATTTCTAGATTTTATAATCGTCAAGTGCAACTTACCGCT 717
Qy 721 GAATATTTCTGATCACTGTGTAAGTGGTATGAACTGGTTTAGCAAAATTTAAAGGCAG 780
Db 718 GAATATTTCTAGACTATTTGTGTAAGTGGTATAAATCGGCTTTAGATAAATTTGAAGGTACC 777
Qy 781 AGCGCTTAAACAAATGGGTGACTATTAACCAATTTCCGTPAGAGAAATGACACTGGCGGTTT 840
Db 778 ACTTCTTAAAGTTGGCTGAAATTTATCATCAGTTCCGTPAGAGATGACATTTACTGGTATTA 837
Qy 841 GATGTTGTTGCAATTTATCCCAATTAATGACACAGCAGCTACCCAAATGAAACGAAAGCA 900
Db 838 GATTTGGTGGCGTATTTCCAAACTATGACACACATATGATTCCAATCCAAATCCAAACAGCT 897
Qy 901 CAACTAACAGGAGATATATACAGATTCACCTGGGCGCGGTAAACGTCGTTCTCAATGGT 960
Db 898 CAACTTACCGGAGTGTATACAGATCCGATGACATTTTAAACATAGTGAACAAGTACTGGA 957
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Qy 961 TCCTGGTATG-----ACAAAGCACCTTCTTTCCGAGTGATAGAAATCATCCGTT 1008
Db 958 TTTGCAACCCCTTGGTCAACCCACAGTGGTATCTTTTATGAAGTTGAAACCAAGCTA 1017
Qy 1009 ATTGCAACACCCCTGATTTTGGATTTATTAAGGGACTCACAGTGTATACACATCAAGA 1068
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Qy 1069 AGCATTTCTTCGGCTCGCTATATA-AGACATTTGGCTGCTCATCAAAATGAAGTCCATCG 1127
Db 1078 GGTATTTAGCTTAAATATATGATGATATATAAACTACTGCTGAGGACATACCTAAATAT 1137
Qy 1128 TGTCAGTAGGGGTAGTAACTTTCAAATAATGATGAACTAAATCAAAATCTACACAGCAC 1187
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Qy 1188 TAGTA--CCTTTGATTTACGAAATATATGATTTTCAAGACTCTATCAAGAGTGCAGTA 1245
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Qy 1954 GTTTTACGTTGACCGAATCGAATTTCAATCCAGTGTAGATGAGACATATGAAGCGGAAACAGAT 2013
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Db 2071 CCAGGTGTAAACGGAATTAAGATGAATCAAGCGGCAAACTTAGTGAATCCCTATCGGAT 2130
Qy 2134 GATTTGTATCCAAATCAAAACGATTTGTTATTTGATGTCAGTGAAGGCAAAACGCTC 2193
Db 2131 GATTTATATCCAAATCAAAACGATTTGTTATTTGATGTCAGTGAAGGCAAAACGCTC 2190
Qy 2194 AGTGAGGCACTGAATTTGCTTCAAGATCCAGATTTCCAGAGATATAATGGAGAAATGGC 2253
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Db 2731 GTCCGAGAGGACCTTTTGTCCAGAGAGCGGATTTAGAACGTTTCAAGAGAGAGAACACAG 2790
Qy 2794 TGGAGATTTCAAATGACAAAGAGACGTTGAAGAAACAGATAGAGAGTATATGGCATCGAA 2853
Db 2791 TGGAGATTTCAAATGACAAAGAGACGTTGAAGAAACAGATAGAGAGTATATGGCATCGAA 2850
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Db 2851 CAAAGCGGTAGATGCTTTATATGCGGATTTATCAGGATCAGCAACTGAAATCTGTATGAG 2910
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Db 2911 ATTAAGATCTTATCTGCGGCGCAAGATCTGATACAGTCCAAATCTTACGATATAACGAA 2970
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Db 3031 CAAAGCGGTGAGTTTGTATGATCAGCGAAATGCGCATCAAAATGGTGTATTTTCCAAAT 3090
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RESULT 4
125971
LOCUS 125971
DEFINITION Sequence 1 from patent US 5554534.
ACCESSION 125971
VERSION 125971.1 GI:1605841
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassefied.
REFERENCE 1 (bases 1 to 3471)
AUTHORS Michaels,T.E., Narva,K.E. and Foncerrada,L.
TITLE Bacillus thuringiensis toxins active against scarab pests
JOURNAL Patent: US 5554534-A 1 10-SEP-1996;
FEATURES
Location/Qualifiers
1..3471
source
BASE COUNT 1200 a 567 c 751 g 953 t
ORIGIN

Query Match 50.0%; Score 1812.2; DB 6; Length 3471;
Best Local Similarity 72.2%; Pred. No. 0;
Matches 2504; Conservative 0; Mismatches 908; Indels 57; Gaps 9;

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Qy 2614 CATGAGTCTCTATTCCTATTCATGATACAGGTGAATCGATTACCAATGAAATGACGCAATA 2673
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Qy 2674 TGGGTTGGATTAAAGATTACGACCCAGAGGGATATGCAACATCTCGGAACCTAGAAATG 2733
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Db 3391 ACAGATCAATGTTGATTAAGTGAACAGAGGTTAGTTCTTATA 3439

RESULT 5
LOCUS AB089299
DEFINITION Bacillus thuringiensis serovar galleriae cry8 gene, complete cds.
ACCESSION AB089299
VERSION AB089299.1 GI:22122187
KEYWORDS Bacillus thuringiensis serovar galleriae (strain:SDS-502) DNA.
SOURCE Bacillus thuringiensis serovar galleriae
ORGANISM Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
cereus group.
REFERENCE 1

AUTHORS Asano,S. and Yamamoto,T.
TITLE a novel cry8 gene highly toxic to Anomala cuprea
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3435)
AUTHORS Asano,S. and Yamamoto,T.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-2002) Shin-ichiro Asano, Hokkaido University,
Graduate school of Agriculture; N9W9, Sapporo, Hokkaido 060-8589,
Japan (E-mail:sangaku@abs.agr.hokudai.ac.jp. Tel:81-11-706-2423,
Fax:81-11-706-2423)

FEATURES
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BASE COUNT 1179 a 576 c 706 g 974 t

Query Match 32.7%; Score 1185.6; DB 1; Length 3435;
Best Local Similarity 62.7%; Pred. No. 8.3e-228;
Matches 2152; Conservative 0; Mismatches 1104; Indels 174; Gaps 13;

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Qy 301 GATATTCTGTGGCTTCAGGGGAAAAGAGTCAATGGGAAATTTTTATGGAAACAGTAGAA 360

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Graduate school of Agriculture; N9W9, Sapporo, Hokkaido 060-8589,
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Db 1 ATGAGTCCAAATTAATCAAAATGAATGAATGAATATAGATGCGTTCATCATCTCTCTGTA 60
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RESULT 6

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 DEFINITION gene, complete cds.
 ACCESSION U04366
 VERSION U04366.1 GI:532523
 KEYWORDS

SOURCE Bacillus thuringiensis.
 ORGANISM Bacillus thuringiensis
 Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus; Bacillus cereus group.
 REFERENCE 1 (bases 1 to 3483)
 AUTHORS Sato, R., Takeuchi, K., Ogiwara, K., Minami, M., Kaji, Y., Suzuki, N., Hori, H., Asano, S., Ohba, M. and Iwahana, H.
 TITLE Cloning, heterologous expression, and localization of a novel crystal protein gene from Bacillus thuringiensis serovar japonensis strain buihui toxic to scarabaeid insects
 JOURNAL Curr. Microbiol. 28 (1), 15-19 (1994)
 MEDLINE 94100786
 PUBMED 7764305
 REFERENCE 2 (bases 1 to 3483)
 AUTHORS Feitelson, J. S.
 TITLE Direct Submission
 JOURNAL Submitted (15-DEC-1993) Jerald S. Feitelson, Molecular Biology, Mycogen Corporation, 4980 Carroll Canyon Road, San Diego, CA 92121, USA
 COMMENT On Aug 27, 1994 this sequence version replaced gi:436836.

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BASE COUNT 1217 a 577 c 712 g 977 t
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Matches 2094; Conservative 0; Mismatches 1230; Indels 86; Gaps 9;

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Qy 2493 TGTACCGGATGATTTCTGCGCAGATGATCTCTGTTTAACTCGATCGGATGATGATCAATCG 2552
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RESULT 7

AR005118
LOCUS AR005118 3797 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 1 from patent US 5747450.
ACCESSION AR005118
VERSION AR005118.1 GI:3965997
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3797)
AUTHORS Ohba,M., Iwahana,H., Sato,R., Suzuki,N., Ogiwara,K., Sakanaka,K.,
Hori,H., Asano,S. and Kawasugi,T.
TITLE Microorganism and insecticide
JOURNAL Patent: US 5747450-A 1 05-MAY-1998;
FEATURES
source 1..3797
BASE COUNT 1345 a 606 c 776 g 1070 t
ORIGIN
Query Match 32.6%; Score 1180; DB 6; Length 3797;
Best Local Similarity 61.4%; Pred. No. 1.1e-226;
Matches 2094; Conservative 0; Mismatches 1230; Indels 86; Gaps 9;
Qy 1 ATGAGTCCAAATAATCAAAATGAATATGAATATAGATGCGACACCTTCTACTTCTGTA 60
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RESULT 9

E06830

LOCUS

DEFINITION DNA sequence encoding insecticidal protein against coleopteran

3797 bp

DNA

linear

PAT 29-SEP-1997

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larvae.
ACCESSION E06830
VERSION GI:2175012
KEYWORDS JP 1994065292-A/1.
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE artificial sequences.
AUTHORS 1 (bases 1 to 3797)
Ogiwara, K., Minami, M., Suzuki, N., Hori, H., Asano, M., Kawaabagi, T.,
Sato, R., Oba, M. and Iwabana, S.
TITLE INSECTICIDAL PROTEIN AGAINST LARVA OF COLEOPTERAN INSECT AND NEW
JOURNAL DNA ENCODING THE SAME
PATENT: JP 1994065292-A 1 08-MAR-1994;
KUBOTA CORP
COMMENT
OS Artificial gene
OC Artificial sequence; Genes.
OS Bacillus thuringiensis serovar japonensis
PN JP 1994065292-A/1
PD 08-MAR-1994
PF 11-AUG-1992 JP 1992213886
PI OGIIWARA KATSUTOSHI, MINAMI MASAYOSHI, SUZUKI NOBUKAZU, PI
HORI HIDEAKA,
ASANO MASASHI, KAWASUGI TADAAKI, SATO REIICHI, OBA MICHIO, PI
IWABANA SHIYUUSUKE
PC C07K13/00, A01H5/00, A01N63/02, C12N1/21, C12N5/10, C12N15/32, PC
C12N15/70,
C12N15/75, C12N15/78//C12P21/02, (C12N1/21, C12R1:19), (C12N1/21,
C12R1:38),
PC (C12N1/21, C12R1:07), (C12P21/02, C12R1:19), (C12P21/02, C12R1:38);
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CC topology: Linear;
CC *source: strain=Buibui;
CC *source: clones=E.C. JM109 strain transformed with a plasmid;
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FT CDS 187..3636
FT /product='insecticidal protein against FT
FEATURES
source Location/Qualifiers
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/organism='synthetic construct'
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BASE COUNT 1345 a 606 c 776 g 1070 t
ORIGIN
Query Match 32.6%; Score 1180; DB 6; Length 3797;
Best local Similarity 61.4%; Pred. No. 1.1e-226;
Matches 2094; Conservative 0; Mismatches 1230; Indels 86; Gaps 9;
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RESULT 10

AX189653

LOCUS

Sequence 5 from Patent WO0147952.

AX189653

ACCESSION

AX189653.1

VERSION

GI:15143042

KEYWORDS

SOURCE

ORGANISM

Bacillus thuringiensis.

Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus

cereus group.

REFERENCE

AUTHORS

1 (bases 1 to 3459)

Arnaut, G., Boets, A., Damme, N., Mathieu, B., Vanneste, S. and van

Rie, J.

AX189653

Sequence 5 from Patent WO0147952.

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GI:15143042

Bacillus thuringiensis.

Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus

cereus group.

REFERENCE

1 (bases 1 to 3459)

Arnaut, G., Boets, A., Damme, N., Mathieu, B., Vanneste, S. and van

Rie, J.

TITLE Insecticidal proteins from *Bacillus thuringiensis*
JOURNAL Patent: WO 0147952-A 5 05-JUL-2001;
Aventis CropScience N.V. (BE)

FEATURES
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Location/Qualifiers

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RESULT 11

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DEFINITION Sequence 1 from Patent WO0121821.
ACCESSION AX100532
VERSION AX100532.1 GI:13619536
KEYWORDS
SOURCE Bacillus thuringiensis.
ORGANISM Bacillus thuringiensis
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          cereus group.
REFERENCE 1 (bases 1 to 3474)
AUTHORS Michiels,F., Jansens,S., Kumar,H., Lobo,D. and Samson,J.
TITLE Insect-resistant rice plants
JOURNAL Patent: WO 0121821-A 1 29-MAR-2001;
        Aventis CropScience N.V. (BE)
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PAT 15-OCT-1999
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1436 a 713 c 936 g 1259 t

BASE COUNT
ORIGIN

BASE COUNT	1436 a	713 c	936 g	1259 t
ORIGIN				

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Matches 1936;	Conservative	0;	Mismatches 1386;	Indels 101;
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LOCUS AR031103 4344 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 4 from patent US 5861543.
ACCESSION AR031103
VERSION AR031103.1 GI:5944317
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 4344)
AUTHORS Lambert, B., Jansens, S., Van Audenhove, K., Referoen, M., Van Rie, J.
and Van Aarseen, R.
TITLE Bacillus thuringiensis strains and their insecticidal proteins
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VERSION	AR205864.1		
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ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 3471)		
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JOURNAL	and Muller-Cohn,J.		
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 7, 2003, 00:39:12 ; Search time 479 Seconds
(without alignments)
17023.979 Million cell updates/sec

Title: US-10-032-717-1

Perfect score: 3621

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Scoring table: IDENTIFY NUC

Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq 101002:**

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3621	100.0	3621	24	Bacillus thuringie
2	3621	100.0	4874	24	Bacillus thuringie
3	3151.8	87.0	3633	24	Bacillus thuringie
4	3151.8	87.0	6613	24	Bacillus thuringie
5	2565.2	70.8	3507	17	Antiscarab pest to
6	2008.4	55.5	2010	24	Bacillus thuringie
7	2003	55.3	2003	24	Bacillus thuringie
8	1987.4	54.9	2013	24	Bacillus thuringie
9	1986.4	54.9	2022	24	Bacillus thuringie

10	1986.4	54.9	2022	24	ABK87244	Bacillus thuringie
11	1986.4	54.9	2022	24	ABK87256	Bacillus thuringie
12	1985.8	54.8	2013	24	ABK87258	Bacillus thuringie
13	1848.4	51.0	1860	24	ABK87243	Bacillus thuringie
14	1827.4	50.5	1854	24	ABK87249	Bacillus thuringie
15	1826.4	50.4	1863	24	ABK87251	Bacillus thuringie
16	1825.8	50.4	1854	24	ABK87259	Bacillus thuringie
17	1824.8	50.4	1863	24	ABK87250	Bacillus thuringie
18	1821.6	50.3	1863	24	ABK87257	Bacillus thuringie
19	1813.8	50.1	3471	13	AAQ30821	Toxin 50C. Bacill
20	1812.2	50.0	3471	13	AAQ27167	Delta-endotoxin ge
21	1812.2	50.0	3471	13	AAQ28940	B.thuringiensis PS
22	1812.2	50.0	3471	14	AAQ38653	Bt isolate P850C c
23	1812.2	50.0	3471	17	AAQ43222	Antiscarab pest to
24	1807.4	49.9	3471	14	AAQ51704	Bacillus thuringie
25	1539.2	42.5	2022	24	ABK87242	Bacillus thuringie
26	1521.8	42.0	2003	24	ABK87237	Bacillus thuringie
27	1317.6	36.4	3690	24	ABK51132	cDNA encoding Baci
28	1180	32.6	3797	14	AAQ38666	Coeloptera toxin f
29	983.6	27.2	3797	15	AAQ58975	B.thuringiensis se
30	983.6	27.2	2010	24	ABK87238	Maize optimised B.
31	900	24.9	3459	22	AAH28242	Nucleotide sequenc
32	883.4	24.4	3474	22	AAH19323	Cry9C coding sequenc
33	883.4	24.4	4344	20	AAV99986	Nucleotide sequenc
34	882.8	24.4	3471	19	AAV16516	DNA encoding a Bac
35	882.8	24.4	3471	20	AAH83877	Bacillus thuringie
36	882.8	24.4	3471	22	AAQ502477	B. thuringiensis D
37	881.8	24.4	4344	15	AAQ56782	Insecticidal toxin
38	848.6	23.4	3759	17	AAAT27148	Bacillus thuringie
39	822.2	22.7	3453	19	AAV16517	DNA encoding a Bac
40	822.2	22.7	3453	20	AAH83878	Bacillus thuringie
41	822.2	22.7	3667	19	AAV38466	DNA encoding a Bac
42	734.2	20.3	3411	19	AAV16518	DNA encoding a Bac
43	734.2	20.3	3411	20	AAH83879	Bacillus thuringie
44	732	20.2	3414	14	AAQ41745	DNA encoding B.t.
45	732	20.2	3414	15	AAQ56922	Bacillus thuringie

ALIGNMENTS

RESULT 1

ABK87234

ID ABK87234 standard; DNA; 3621 BP.

XX AC ABK87234;

XX DT 07-OCT-2002 (first entry)

XX DE Bacillus thuringiensis Cry1218-1 gene sequence.

XX KW Pesticidal; spraying; dusting; broadcasting; seed coating; insect pest;

XX KW Colorado potato beetle; western corn rootworm; southern corn rootworm;

XX KW insect target range; endotoxin; Cry1218; gene; ds.

XX OS Bacillus thuringiensis.

XX FN WO200234774-A2.

XX PD 02-MAY-2002.

XX PF 24-OCT-2001; 2001WO-US45468.

XX PR 24-OCT-2000; 2000US-242838P.

XX PR 23-OCT-2001; 2001US-0032717.

XX PA (DUPO) DU PONT DE NEMOURS & CO E I.

XX PI Abad AR, Duck NB, Feng X, Flannagan RD, Kahn TW, Sims LE;

XX DR WPI; 2002-519178/55.

XX DR P-PSDB; AAU99255.

PT New isolated pesticidal polypeptide useful for impacting insect pest
XX e.g. Colorado potato beetle -

PS Claim 1; Page 91-96; 176pp; English.

XX The present invention relates to a new pesticidal polypeptide. The
CC invention is useful for impacting an insect pest by applying the
CC the molecules of the invention to the environment of the insect pest by
CC spraying, dusting, broadcasting, or seed coating, where the insect pest
CC is selected from Colorado potato beetle, western corn rootworm or
CC southern corn rootworm. The invention is also useful for increasing
CC insect target range and for producing transgenic microorganisms and
CC plants that express the pesticidal polypeptide. The invention is also
CC useful for producing transformed plants and in transforming any organism
CC to produce the pesticidal polypeptide of the invention. The present
CC nucleic acid sequence encodes a *Bacillus thuringiensis* wild-type
CC Cry12i8 endotoxin protein.

XX Sequence 3621 BP; 1277 A; 608 C; 771 G; 965 T; 0 other;

Query Match 100.0%; Score 3621; DB 24; Length 3621;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGAGTCCAAATAATCAAAATGAATATGAATATATAGATGCGACACCTTCTACTTCTGTA	60
Db	1	ATGAGTCCAAATAATCAAAATGAATATGAATATATAGATGCGACACCTTCTACTTCTGTA	60
Qy	61	TCCAATGATTCACAGATACCCCTTTGGGAATGAGCCAAAGTGGCTACAAATATG	120
Db	61	TCCAATGATTCACAGATACCCCTTTGGGAATGAGCCAAAGTGGCTACAAATATG	120
Qy	121	GATTATAAGATTATTTAAAGATGTCGGGAAATGCTAGTGAATACCTCGTTCACCT	180
Db	121	GATTATAAGATTATTTAAAGATGTCGGGAAATGCTAGTGAATACCTCGTTCACCT	180
Qy	181	GAACTACTTGTAGCGGCAAGATGACGCTAAGCGCGCAATTTGATATAGTAAATTA	240
Db	181	GAACTACTTGTAGCGGCAAGATGACGCTAAGCGCGCAATTTGATATAGTAAATTA	240
Qy	241	CTATCAGTTTGGGGTCCCATTTGTTGGCCGATAGTGAAGTCTTATCTCACTTAT	300
Db	241	CTATCAGTTTGGGGTCCCATTTGTTGGCCGATAGTGAAGTCTTATCTCACTTAT	300
Qy	301	GATATCTGTGGCTTCAGGGGAAAAGAGTCAATGGGAAATTTTATGAAACAAGTAGAA	360
Db	301	GATATCTGTGGCTTCAGGGGAAAAGAGTCAATGGGAAATTTTATGAAACAAGTAGAA	360
Qy	361	GAACTCATTAATCAAAAAATAGCAGATATGCAAGGAATAAAGCGCTTTCGGAATTAGAA	420
Db	361	GAACTCATTAATCAAAAAATAGCAGATATGCAAGGAATAAAGCGCTTTCGGAATTAGAA	420
Qy	421	GGATTAGTAAATTAACCAATATATCTCACTGGCTTGAAGATGGGAAGAAATCCA	480
Db	421	GGATTAGTAAATTAACCAATATATCTCACTGGCTTGAAGATGGGAAGAAATCCA	480
Qy	481	AATGGTTCAAGAGCCCTTACGAGATGCGAAATTCGATTTGAAATCCTCGATAGTTTAT	540
Db	481	AATGGTTCAAGAGCCCTTACGAGATGCGAAATTCGATTTGAAATCCTCGATAGTTTAT	540
Qy	541	ACGCAATATATGCCATCTTTTATAGTGAACAAATTTTGAAGTACCATTCCTACTGTATAT	600
Db	541	ACGCAATATATGCCATCTTTTATAGTGAACAAATTTTGAAGTACCATTCCTACTGTATAT	600
Qy	601	GCAATGGGAGCCAACTTCATTTACTGTATTAAGGACGCGTCAATTTTGGAGAGAA	660
Db	601	GCAATGGGAGCCAACTTCATTTACTGTATTAAGGACGCGTCAATTTTGGAGAGAA	660
Qy	661	TGGGATGTCACCAACTACTATTAATACTATTTATGATCGTCAAAATGAACTTACTGCA	720
Db	661	TGGGATGTCACCAACTACTATTAATACTATTTATGATCGTCAAAATGAACTTACTGCA	720
Qy	721	GAATATTCATGATCACTGTGTAAAGTGTATGAACTGGTTTATGCAAAATTTAAAGGCACG	780

Db	721	GAATATTCATGATCACTGTGTAAAGTGTATGAACTGGTTTATGCAAAATTTAAAGGCACG	780
Qy	781	AGCGCTAAACAATGGGTTGACTATAACAATTCGCTAGAGAAATGACACTGCGCGTTT	840
Db	781	AGCGCTAAACAATGGGTTGACTATAACAATTCGCTAGAGAAATGACACTGCGCGTTT	840
Qy	841	GATGTGTGTCATTAATCCCAATTTATGACACACGACGTAACCAATGGAACGAAAGCA	900
Db	841	GATGTGTGTCATTAATCCCAATTTATGACACACGACGTAACCAATGGAACGAAAGCA	900
Qy	901	CAACTAACAGGGAAGTATATACAGATCCACTGGGCGGTAAGCTGTCTTCAATTTGGT	960
Db	901	CAACTAACAGGGAAGTATATACAGATCCACTGGGCGGTAAGCTGTCTTCAATTTGGT	960
Qy	961	TCCTGGTATGACAAAGCACCTTCTTTCGGAGTGTAGAAATCATCCGTTTATTCGACACCC	1020
Db	961	TCCTGGTATGACAAAGCACCTTCTTTCGGAGTGTAGAAATCATCCGTTTATTCGACACCC	1020
Qy	1021	CATGTATTTGATTAATAACGGGACTCAACAGTGTATACAAATCAAGAAAGCAATTTCTTCC	1080
Db	1021	CATGTATTTGATTAATAACGGGACTCAACAGTGTATACAAATCAAGAAAGCAATTTCTTCC	1080
Qy	1081	GCTCGCTATATAAGACATTTGGGCTGGTCAATCAATTAAGCTACCATCGTGTCAATAGGGGT	1140
Db	1081	GCTCGCTATATAAGACATTTGGGCTGGTCAATCAATTAAGCTACCATCGTGTCAATAGGGGT	1140
Qy	1141	AGTAATCTTCAACAAATGATGGAACCTAATCAAAATCTACACAGCAGTACCTTTTCT	1200
Db	1141	AGTAATCTTCAACAAATGATGGAACCTAATCAAAATCTACACAGCAGTACCTTTTCT	1200
Qy	1201	TTTACGAATTAATGATTAATTAACAAGACTCTAACAAGGATGCACTCTCTTGTGATTTGT	1260
Db	1201	TTTACGAATTAATGATTAATTAACAAGACTCTAACAAGGATGCACTCTCTTGTGATTTGT	1260
Qy	1261	TACCTCGTTATACGTATATATTTTGGAAATGCGAAGTTCGAGTTCATGTTGTAATAC	1320
Db	1261	TACCTCGTTATACGTATATATTTTGGAAATGCGAAGTTCGAGTTCATGTTGTAATAC	1320
Qy	1321	CAATTTGAATATACCAAGAAAGCTTAAAGTATATCCAGTTTCCAAAGATATATAGCG	1380
Db	1321	CAATTTGAATATACCAAGAAAGCTTAAAGTATATCCAGTTTCCAAAGATATATAGCG	1380
Qy	1381	AGTACAAGAGATTCGGAATTAAGAAATTTACCTCCAGAACTTCAGATCAACCAAAATATGAG	1440
Db	1381	AGTACAAGAGATTCGGAATTAAGAAATTTACCTCCAGAACTTCAGATCAACCAAAATATGAG	1440
Qy	1441	TCATATAGCCATAGATTAATGATCATCAAGTATTTCCCGGACGCGGTAAACCTACCGGA	1500
Db	1441	TCATATAGCCATAGATTAATGATCATCAAGTATTTCCCGGACGCGGTAAACCTACCGGA	1500
Qy	1501	TTAGTACCTGTATTTTCTTGGACACATCGAAGTGCAGATTTAAACAATACATATATTC	1560
Db	1501	TTAGTACCTGTATTTTCTTGGACACATCGAAGTGCAGATTTAAACAATACATATATTC	1560
Qy	1561	GATAAATCACTCAAAATCCGCGCGTTAAATTTGGGTAATTTTACCGTTTGTTCAGTG	1620
Db	1561	GATAAATCACTCAAAATCCGCGCGTTAAATTTGGGTAATTTTACCGTTTGTTCAGTG	1620
Qy	1621	GTAAAGGACCAAGGACATACAGAGGGGATTTATACAGTATATAGAAATCTCGTTCT	1680
Db	1621	GTAAAGGACCAAGGACATACAGAGGGGATTTATACAGTATATAGAAATCTCGTTCT	1680
Qy	1681	GTAGGAACCTTATTTCTAGCTCGATATGCGCTAGCATTTAGAAAAAGAGGGAATATCGT	1740
Db	1681	GTAGGAACCTTATTTCTAGCTCGATATGCGCTAGCATTTAGAAAAAGAGGGAATATCGT	1740
Qy	1741	GTAAAGGACCAAGGACATACAGAGGGGATTTATACAGTATATAGAAATCTCGTTCT	1800
Db	1741	GTAAAGGACCAAGGACATACAGAGGGGATTTATACAGTATATAGAAATCTCGTTCT	1800
Qy	1801	CAGATGCCAAAAACAATGAACCCAGGTGAGATCTGAATCTTAAACCTTTTAAAGTTGCA	1860

Db 1801 CAGATGCCAAAAAACAATGAACCCAGGTGAGGATCTGACATCTTAAACTTTTAAAGTTGCA 1860
Qy 1861 GATGCTATCAACAATTAATTTAGCAACAGATAGTTCGCTAGCATTTGAAACATATTTA 1920
Db 1861 GATGCTATCAACAATTAATTTAGCAACAGATAGTTCGCTAGCATTTGAAACATATTTA 1920
Qy 1921 GGTGAAGACCTTAATCAACATTAATCTGTATAGTTTACGTTGACCGAATCGAATTCATC 1980
Db 1921 GGTGAAGACCTTAATCAACATTAATCTGTATAGTTTACGTTGACCGAATCGAATTCATC 1980
Qy 1981 CCAGTAGATGAGACATATCAAGCGGAACAAGATTATTAGAAGCAGCGAAGAAACAGTGAAT 2040
Db 1981 CCAGTAGATGAGACATATCAAGCGGAACAAGATTATTAGAAGCAGCGAAGAAACAGTGAAT 2040
Qy 2041 GCCTTTGTTTACGAATACAAAAGATGCTTTACGACACGAGGCGTAACGGAATTAAGAGTAAT 2100
Db 2041 GCCTTTGTTTACGAATACAAAAGATGCTTTACGACACGAGGCGTAACGGAATTAAGAGTAAT 2100
Qy 2101 CAAGCGGCAAACTTAGTGAATGCCCTATCGGATGATTGTATCCAAATGAAGAAACGATTTG 2160
Db 2101 CAAGCGGCAAACTTAGTGAATGCCCTATCGGATGATTGTATCCAAATGAAGAAACGATTTG 2160
Qy 2161 TTATTTGATGCAAGTGAAGAGGCAAAACGCTCAGTGAGGCAAGTAAATTTGCTTCAAGAT 2220
Db 2161 TTATTTGATGCAAGTGAAGAGGCAAAACGCTCAGTGAGGCAAGTAAATTTGCTTCAAGAT 2220
Qy 2221 CCAGATTTTCCAAAGAGATAAATGGAGAAATATGGCTGACGCGCAAGTACGGGAATTTGAGTT 2280
Db 2221 CCAGATTTTCCAAAGAGATAAATGGAGAAATATGGCTGACGCGCAAGTACGGGAATTTGAGTT 2280
Qy 2281 ATAGAAGGGGATGCTTTATTTCAAAGGGGCTTATCTACGGCTTACCGGTCGCGAGAGAAATA 2340
Db 2281 ATAGAAGGGGATGCTTTATTTCAAAGGGGCTTATCTACGGCTTACCGGTCGCGAGAGAAATA 2340
Qy 2341 GATACGGAACGTAATCCACGATCTGTATCAAAAGTAGAGGAAGGTGTATTAAGAACCA 2400
Db 2341 GATACGGAACGTAATCCACGATCTGTATCAAAAGTAGAGGAAGGTGTATTAAGAACCA 2400
Qy 2401 TACACAAGATATAGATTGAGAGGGTTTGTCCGAAGCAGTCAAGGATTTGAAATTTTCA 2460
Db 2401 TACACAAGATATAGATTGAGAGGGTTTGTCCGAAGCAGTCAAGGATTTGAAATTTTCA 2460
Qy 2461 ATTGCTCATCAACGAAACCGAATTTGAAAGAAATGTAACGGATGATTGTCGCGAGATGA 2520
Db 2461 ATTGCTCATCAACGAAACCGAATTTGAAAGAAATGTAACGGATGATTGTCGCGAGATGA 2520
Qy 2521 TCTCTGTTTAACTCGGATGGTAGTATCAATCGATGAGCGAACAAGATGTGGAATAGC 2580
Db 2521 TCTCTGTTTAACTCGGATGGTAGTATCAATCGATGAGCGAACAAGATGTGGAATAGC 2580
Qy 2581 CGTTTAGAAGTAGAAGAACCGTTCTGGTGAAGCGCATGAGTTCTTATTTCTATTGATACA 2640
Db 2581 CGTTTAGAAGTAGAAGAACCGTTCTGGTGAAGCGCATGAGTTCTTATTTCTATTGATACA 2640
Qy 2641 GGTGAATCGATTACAAATGAAATCAGGAATATGCGTTTGAATTTAAGATTACGGAACCA 2700
Db 2641 GGTGAATCGATTACAAATGAAATCAGGAATATGCGTTTGAATTTAAGATTACGGAACCA 2700
Qy 2701 GAGGGATATGCAACACTCGGAAACCTTAGAATTTGGTTCGAAGAGGACCTTTATCAGGAGAC 2760
Db 2701 GAGGGATATGCAACACTCGGAAACCTTAGAATTTGGTTCGAAGAGGACCTTTATCAGGAGAC 2760
Qy 2761 GCATTAGAAGCGTTGCAAGAGAGAGAACCAACAGTGAAGATTCAAAATGACAGAGACCT 2820
Db 2761 GCATTAGAAGCGTTGCAAGAGAGAGAACCAACAGTGAAGATTCAAAATGACAGAGACCT 2820
Qy 2821 GAAGAAACAGATAGAGGTATATGGCATCGAAACAGCGGTAGATCGTTTATATGCCGAT 2880
Db 2821 GAAGAAACAGATAGAGGTATATGGCATCGAAACAGCGGTAGATCGTTTATATGCCGAT 2880
Qy 2881 TATCAGGATCAGCAACTGAATCTGTATGTAGAGATTACAGATCTTATCTCGGCGCCCAAGAT 2940
Db 2881 TATCAGGATCAGCAACTGAATCTGTATGTAGAGATTACAGATCTTATCTCGGCGCCCAAGAT 2940

Qy 2941 CTGATACAGTCCATTCCTTACGTATATAACGAAATGTTCCAGAAATACCGGGATGAAC 3000
Db 2941 CTGATACAGTCCATTCCTTACGTATATAACGAAATGTTCCAGAAATACCGGGATGAAC 3000
Qy 3001 TATACGAAGTTTACAGAAATTAACAGATCGATCCCAACAGCGTGGAGTTTGTATGATCAG 3060
Db 3001 TATACGAAGTTTACAGAAATTAACAGATCGATCCCAACAGCGTGGAGTTTGTATGATCAG 3060
Qy 3061 CGAAATGCCATACCAATGGTGAATTTTCGAAATGGTTTAAAGTAATTTGGAATGCAACGCT 3120
Db 3061 CGAAATGCCATACCAATGGTGAATTTTCGAAATGGTTTAAAGTAATTTGGAATGCAACGCT 3120
Qy 3121 GCGGTAGAGTAACCAACAAATCAATCATCATCTGTCTTGTGATTCCTTGTGATTCGAGTGGATGAG 3180
Db 3121 GCGGTAGAGTAACCAACAAATCAATCATCATCTGTCTTGTGATTCCTTGTGATTCGAGTGGATGAG 3180
Qy 3181 CAGTTTTCGCAACAGTTTACAGTTTCAACCGAATCAAGATATGTTAGGATTTACTGGC 3240
Db 3181 CAGTTTTCGCAACAGTTTACAGTTTCAACCGAATCAAGATATGTTAGGATTTACTGGC 3240
Qy 3241 AGAAAGAGGCGGTAGGAAATGGATATGTAATGGAATGTTTAAATGGAATCAGAAACAGAA 3300
Db 3241 AGAAAGAGGCGGTAGGAAATGGATATGTAATGGAATGTTTAAATGGAATCAGAAACAGAA 3300
Qy 3301 AGCTTTACTTTTGTGTCAGGCGATTATGATACAAATGGAATGTTTAAATGGAATGTTTCC 3360
Db 3301 AGCTTTACTTTTGTGTCAGGCGATTATGATACAAATGGAATGTTTAAATGGAATGTTTCC 3360
Qy 3361 AATACAAATGGAATTAACACAAATTAATGCGTATATAACAAAGCATCGAGTACAAACGGA 3420
Db 3361 AATACAAATGGAATTAACACAAATTAATGCGTATATAACAAAGCATCGAGTACAAACGGA 3420
Qy 3421 TATACGCAAAATTAATGTAATACGCAAGCATCGAATACAAACGCGATATAACACAAAT 3480
Db 3421 TATACGCAAAATTAATGTAATACGCAAGCATCGAATACAAACGCGATATAACACAAAT 3480
Qy 3481 AGTGTGTACAATGATCAAAACCGGCTTATATCAAAACAGTGACATTCATCCGTTATACA 3540
Db 3481 AGTGTGTACAATGATCAAAACCGGCTTATATCAAAACAGTGACATTCATCCGTTATACA 3540
Qy 3541 GATCAAAATGCGATTGAGATGAGTGAAGAGACAGAGGTACATTTCTATATAGAAAGTGTAGAA 3600
Db 3541 GATCAAAATGCGATTGAGATGAGTGAAGAGACAGAGGTACATTTCTATATAGAAAGTGTAGAA 3600
Qy 3601 TTGATTGTAGACGTAGACTAA 3621
Db 3601 TTGATTGTAGACGTAGACTAA 3621

RESULT 2

ABK87247

ID ABK87247 standard; DNA; 4874 BP.

XX AC ABK87247;

XX DT 07-OCT-2002 (first entry)

XX DE Bacillus thuringiensis genomic Cry1218-1 DNA sequence.
XX KW Pesticidal; spraying; dusting; broadcasing; seed coating; insect pest;
XX KW Colorado potato beetle; western corn rootworm; southern corn rootworm;
XX KW insect target range; endotoxin; Cry1218; gene; ds.
XX OS Bacillus thuringiensis.

XX PN WO200234774-A2.

XX PD 02-MAY-2002.

XX PF 24-OCT-2001; 2001WO-US45468.

XX PR 24-OCT-2000; 2000US-242838P.


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PR 23-OCT-2001; 2001US-0032717.
XX (DUPO ) DU PONT DE NEMOURS & CO E I.
PA Abad AR, Duck NB, Feng X, Flannagan RD, Kahn TW, Sims LB;
PI WPI; 2002-519178/55.
XX New isolated pesticidal polypeptide useful for impacting insect pest
XX e.g. Colorado potato beetle -
XX Claim 13; Page 144-145; 176pp; English.
XX The present invention relates to a new pesticidal polypeptide. The
XX invention is useful for impacting an insect pest by applying the
XX the molecules of the invention to the environment of the insect pest by
XX spraying, dusting, broadcasting, or seed coating, where the insect pest
XX is selected from Colorado potato beetle, western corn rootworm or
XX southern corn rootworm. The invention is also useful for increasing
XX insect target range and for producing transgenic microorganisms and
XX plants that express the pesticidal polypeptide. The invention is also
XX useful for producing transformed plants and in transforming any organism
XX to produce the pesticidal polypeptide of the invention. The present
XX nucleic acid sequence encodes a Bacillus thuringiensis wild-type
XX Cry1218 endotoxin protein.
XX
XX Sequence 4874 BP; 1707 A; 787 C; 1003 G; 1377 T; 0 other;
XX
XX Query Match 100.0%; Score 3621; DB 24; Length 4874;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 3621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 ATGAGTCCAAATCAATCAAAATGAATGAATGAATATATAGTCGACACCTTCTACTCTGTA 60
XX DB 731 ATGAGTCCAAATCAATCAAAATGAATGAATGAATATATAGTCGACACCTTCTACTCTGTA 790
XX
XX 61 TCCAAATGATTTAAACAGATACCTTTTGGCAATCAGCCAAACAAATGCGCTACAAAATATG 120
XX DB 791 TCCAAATGATTTAAACAGATACCTTTTGGCAATGAGCCAAACAAATGCGCTACAAAATATG 850
XX
XX 121 GATTATAAGATTATTTAAATATGTCGCGGAAATGCTAGTGAATACCTCGTTACCT 180
XX DB 851 GATTATAAGATTATTTAAATATGTCGCGGAAATGCTAGTGAATACCTCGTTACCT 910
XX
XX 181 GAAGTACTTGTAGCGGACAAAGATGAGCTAAGCCGCAATTCATATAGTAGTAAATTA 240
XX DB 911 GAAGTACTTGTAGCGGACAAAGATGAGCTAAGCCGCAATTCATATAGTAGTAAATTA 970
XX
XX 241 CTATCAGGTTTAGGGTCCCAATTTGTTGGCCGATAGTGAAGTCTTTATCTCAACTTAT 300
XX DB 971 CTATCAGGTTTAGGGTCCCAATTTGTTGGCCGATAGTGAAGTCTTTATCTCAACTTAT 1030
XX
XX 301 GATATCTGTGGCTTCAGGGGAAAGAGTCAATGCGAAATTTTATGGAACAAAGTAGAA 360
XX DB 1031 GATATCTGTGGCTTCAGGGGAAAGAGTCAATGCGAAATTTTATGGAACAAAGTAGAA 1090
XX
XX 361 GAACTCATTAATCAAAAATAGCAGATATGCAAGGATTAAGCGCTTTCCGGAATAGAA 420
XX DB 1091 GAACTCATTAATCAAAAATAGCAGATATGCAAGGATTAAGCGCTTTCCGGAATAGAA 1150
XX
XX 421 GGATTAGGTAATTAATACCAATATATCTAACTGCGCTTGAAGAAATGGGAAGAAATCCA 480
XX DB 1151 GGATTAGGTAATTAATACCAATATATCTAACTGCGCTTGAAGAAATGGGAAGAAATCCA 1210
XX
XX 481 AATGGTTCAAGAGCCTTACGAGATGCGAAATCGAATTTGAAATCCTGGATAGTTATTT 540
XX DB 1211 AATGGTTCAAGAGCCTTACGAGATGCGAAATCGAATTTGAAATCCTGGATAGTTATTT 1270
XX
XX 541 AGCAATATATGCAATCTTTTAGAGTACAAAATTTTGAAGTACCAATTCCTTACTGTATAT 600
XX DB 1271 AGCAATATATGCAATCTTTTAGAGTACAAAATTTTGAAGTACCAATTCCTTACTGTATAT 1330
XX
XX 601 GCAATGGCAGCCCACTTCACTTACTTCTTATTAAGGACGCGTCAATTTTGGGAGAGAA 660
XX
XX Db 1331 GCAATGGCAGCCCACTTCACTTACTTCTTATTAAGGACGCGTCAATTTTGGGAGAGAA 1390
XX
XX Qy 661 TGGGATGCTCAACAACTACTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 720
XX
XX Db 1391 TGGGATGCTCAACAACTACTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1450
XX
XX Qy 721 GAATATTTCTGATCACTGTGTAAGTGGTATGAAACTGGTTTAGCAAAATTTAAAGGCACG 780
XX
XX Db 1451 GAATATTTCTGATCACTGTGTAAGTGGTATGAAACTGGTTTAGCAAAATTTAAAGGCACG 1510
XX
XX Qy 781 AGCGTAAACAAATGGGTGACTATTAACCAATTCCTGAGAAATGACACTGGCGGTTTAA 840
XX
XX Db 1511 AGCGTAAACAAATGGGTGACTATTAACCAATTCCTGAGAAATGACACTGGCGGTTTAA 1570
XX
XX Qy 841 GATGTTGTTGCAATTAATCCCAATTAATGACACACGCTACCCCAATGGAAACGAAAGCA 900
XX
XX Db 1571 GATGTTGTTGCAATTAATCCCAATTAATGACACACGCTACCCCAATGGAAACGAAAGCA 1630
XX
XX Qy 901 CAACTAAACAAAGGAAAGTATATACAGATCCACTGGGCGGGTAAAGCTGCTTCAATTTGT 960
XX
XX Db 1631 CAACTAAACAAAGGAAAGTATATACAGATCCACTGGGCGGGTAAAGCTGCTTCAATTTGT 1690
XX
XX Qy 961 TCCTGATGACAAAGCACCTTCTTTCGAGGTGATAGAAATCAATCCGTTATTCGACACCC 1020
XX
XX Db 1691 TCCTGATGACAAAGCACCTTCTTTCGAGGTGATAGAAATCAATCCGTTATTCGACACCC 1750
XX
XX Qy 1021 CATGTTATTTGATTAATTAACGGGACTCAGGTGTATACAAATCAAGAAAGCAATTTCTTCC 1080
XX
XX Db 1751 CATGTTATTTGATTAATTAACGGGACTCAGGTGTATACAAATCAAGAAAGCAATTTCTTCC 1810
XX
XX Qy 1081 GCTCGCTATATAAGACATTTGGGCTGCTCATCAATAAGCTACCATCGTCTAGTAGGGGT 1140
XX
XX Db 1811 GCTCGCTATATAAGACATTTGGGCTGCTCATCAATAAGCTACCATCGTCTAGTAGGGGT 1870
XX
XX Qy 1141 AGTAATCTTCAAACAAATGATGAACTAATCAAAATCTACACAGCACTAGTACCTTTGTAT 1200
XX
XX Db 1871 AGTAATCTTCAAACAAATGATGAACTAATCAAAATCTACACAGCACTAGTACCTTTGTAT 1930
XX
XX Qy 1201 TTTACGATTAATGATTTTACAAGACTCTATCAAAAGGATGAGTACTCTCTGATATTGTT 1260
XX
XX Db 1931 TTTACGATTAATGATTTTACAAGACTCTATCAAAAGGATGAGTACTCTCTGATATTGTT 1990
XX
XX Qy 1261 TACCTCGTTATACGTATATATTTTGGAAATGCGAAGTCCAGTCTTTCATGGTAAAC 1320
XX
XX Db 1991 TACCTCGTTATACGTATATATTTTGGAAATGCGAAGTCCAGTCTTTCATGGTAAAC 2050
XX
XX Qy 1321 CAATTAATTAATTAACAGAAAGACGTTAAAGTATAATCCAGTTTCCAAAGATATTATAGCG 1380
XX
XX Db 2051 CAATTAATTAATTAACAGAAAGACGTTAAAGTATAATCCAGTTTCCAAAGATATTATAGCG 2110
XX
XX Qy 1381 AGTACAAAGATTCGGAATTAGAATTTACTCCAGAAACTTCAGATCAACCAATATTATAG 1440
XX
XX Db 2111 AGTACAAAGATTCGGAATTAGAATTTACTCCAGAAACTTCAGATCAACCAATATTATAG 2170
XX
XX Qy 1441 TCATATAGCCATAGATTTATGTCATATCAAACTATTTCCCGCAGCGGTAACTACCGGA 1500
XX
XX Db 2171 TCATATAGCCATAGATTTATGTCATATCAAACTATTTCCCGCAGCGGTAACTACCGGA 2230
XX
XX Qy 1501 TTAGTACCTGTTATTTCTTGGGACACATCGAAGTGCAGATTTTAAACAAATATATTATCA 1560
XX
XX Db 2231 TTAGTACCTGTTATTTCTTGGGACACATCGAAGTGCAGATTTTAAACAAATATATTATCA 2290
XX
XX Qy 1561 GATTAATAATCACTCAAAATTCGGGCGGTAAATGTTGGGATAAATTTACCGTTTGTTCAGTG 1620
XX
XX Db 2291 GATTAATAATCACTCAAAATTCGGGCGGTAAATGTTGGGATAAATTTACCGTTTGTTCAGTG 2350
XX
XX Qy 1621 GTAAAGGACAGGACATACAGGGGATTTTATTAAGTAAATAGAGTACTGTTCT 1680
XX
XX Db 2351 GTAAAGGACAGGACATACAGGGGATTTTATTAAGTAAATAGAGTACTGTTCT 2410
XX
XX Qy 1681 GTAGGAACCTTATTTCTAGCTCGATATGCGCTAGCAATTAGAAAAAGACGGGAAATATCGT 1740
XX
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Db 2411 GTAGGAACCTTATTTCTAGCTCGATATGGCTAGCATTAGAAAAAGCAGGAAATATCGT 2470
Qy 1741 GTAAGACTGAGATATGCTACTGATGACAGATATGTATGTCATGTAAACGATGCTCAGATT 1800
Db 2471 GTPAAGACTGAGATATGCTACTGATGACAGATATGTATGTCATGTAAACGATGCTCAGATT 2530
Qy 1801 CAGATGCCAAAAAACAATGAACCCAGGTGAGGATCTGACATCTTAAAGTTGCA 1860
Db 2531 CAGATGCCAAAAAACAATGAACCCAGGTGAGGATCTGACATCTTAAAGTTGCA 2590
Qy 1861 GATGCTATCACAACATTAATTTAGCAACAGATAGTTGCTAGCATGTAAACATTAATTTA 1920
Db 2591 GATGCTATCACAACATTAATTTAGCAACAGATAGTTGCTAGCATGTAAACATTAATTTA 2650
Qy 1921 GGTGAAGACCCCTAATTTCAACATTTATCTGGTATAGTTTACGCTGACCGAATCGAATTCATC 1980
Db 2651 GGTGAAGACCCCTAATTTCAACATTTATCTGGTATAGTTTACGCTGACCGAATCGAATTCATC 2710
Qy 1981 CCAAGTATGAGACATATGAAGCGGAACAAGNTTTAGAAGCAGCGAAGAACGAGTGAAT 2040
Db 2711 CCAAGTATGAGACATATGAAGCGGAACAAGNTTTAGAAGCAGCGAAGAACGAGTGAAT 2770
Qy 2041 GCCTTGTTTACGATACAAAGATGGCTTACGACCGAGGCTAACGATTTATGAAGTGAAT 2100
Db 2771 GCCTTGTTTACGATACAAAGATGGCTTACGACCGAGGCTAACGATTTATGAAGTGAAT 2830
Qy 2101 CAAGCGGCAAACTTAGTGGAAATGCCCTATCGGATGATTTGTATCCAAATGAAGAACGATTG 2160
Db 2831 CAAGCGGCAAACTTAGTGGAAATGCCCTATCGGATGATTTGTATCCAAATGAAGAACGATTG 2890
Qy 2161 TTAATTTGATGCAATGAGAGAGGCAAAACCGCTTCAAGTGAAGCAGTAAATTTGCTTCAAGAT 2220
Db 2891 TTAATTTGATGCAATGAGAGAGGCAAAACCGCTTCAAGTGAAGCAGTAAATTTGCTTCAAGAT 2950
Qy 2221 CCAGATTTCCAGAGATAAATGAGAAAAATGGCTGAGCGCAAGTACGGGAATTTAGGTT 2280
Db 2951 CCAGATTTCCAGAGATAAATGAGAAAAATGGCTGAGCGCAAGTACGGGAATTTAGGTT 3010
Qy 2281 ATAGAAGGGGATGCTTTATTTCAAGGCGTTATCTACGCTTACCGCTACCGTGCAGAGAAATA 2340
Db 3011 ATAGAAGGGGATGCTTTATTTCAAGGCGTTATCTACGCTTACCGCTACCGTGCAGAGAAATA 3070
Qy 2341 GATACGGAAACGTPATCAACGATATCTGTATCAAAAAGTAGAGGAAGGTGTATTTAAACCA 2400
Db 3071 GATACGGAAACGTPATCAACGATATCTGTATCAAAAAGTAGAGGAAGGTGTATTTAAACCA 3130
Qy 2401 TACACAAGATATAGATGAGAGGTTTGTGCGAAGCAGTCAAGGATTTGGAATTTTCACA 2460
Db 3131 TACACAAGATATAGATGAGAGGTTTGTGCGAAGCAGTCAAGGATTTGGAATTTTCACA 3190
Qy 2461 ATTCTGTCATCAACGAAACCGAATTTGTAATAAATGTAACCGGATGATTTGCTGCCAGATGTA 2520
Db 3191 ATTCTGTCATCAACGAAACCGAATTTGTAATAAATGTAACCGGATGATTTGCTGCCAGATGTA 3250
Qy 2521 TCTCTCTGTTAACTCGGATGATGATCAATTCGATGCGAAGCAAAAGATGTGCAATAGC 2580
Db 3251 TCTCTCTGTTAACTCGGATGATGATCAATTCGATGCGAAGCAAAAGATGTGCAATAGC 3310
Qy 2581 CGTTTGAAGTAGAAAAACCGTTCTGGTGAAGCGGATGATTTGCTATTCCTATTGTATACA 2640
Db 3311 CGTTTGAAGTAGAAAAACCGTTCTGGTGAAGCGGATGATTTGCTATTCCTATTGTATACA 3370
Qy 2641 GGTGAATCGATTACAAATGAAGATGCAAGGAATATGGTTGGAATTTAAGATTACGGACCA 2700
Db 3371 GGTGAATCGATTACAAATGAAGATGCAAGGAATATGGTTGGAATTTAAGATTACGGACCA 3430
Qy 2701 GAGGGATATGCAACACTCGGAAACCTAGAAATTTGCTGAAGAGGACCTTTTATCAGGAGAC 2760
Db 3431 GAGGGATATGCAACACTCGGAAACCTAGAAATTTGCTGAAGAGGACCTTTTATCAGGAGAC 3490
Qy 2761 GCATTTAGACGCTTTCGAAGAGAGAACCAACAGTGGGAAGATTCAAATGCAAGAACGAT 2820
Db 3491 GCATTTAGACGCTTTCGAAGAGAGAACCAACAGTGGGAAGATTCAAATGCAAGAACGAT 3550

Qy 2821 GAAGAAAACAGATAGAGAGTATATGGCATCCAAAACGACGCTAGATCGTTTATATGCCGAT 2880
Db 3551 GAAGAAAACAGATAGAGAGTATATGGCATCCAAAACGACGCTAGATCGTTTATATGCCGAT 3610
Qy 2881 TATCAGGATCAGCAACTGAATCCTGATGATGAGATTTACAGATCTTACTCGGCGCCCAAGAT 2940
Db 3611 TATCAGGATCAGCAACTGAATCCTGATGATGAGATTTACAGATCTTACTCGGCGCCCAAGAT 3670
Qy 2941 CTGATACAGTCCATTCCTTACGTTATATACGAAATGTTTCCAGAAATACACGGGATGAAC 3000
Db 3671 CTGATACAGTCCATTCCTTACGTTATATACGAAATGTTTCCAGAAATACACGGGATGAAC 3730
Qy 3001 TATACGAAAGTTTACAGAAATTAACAGATCGACTCCAAACGCGTGGAGTTTGTATGATCAG 3060
Db 3731 TATACGAAAGTTTACAGAAATTAACAGATCGACTCCAAACGCGTGGAGTTTGTATGATCAG 3790
Qy 3061 CGAAATGCCATACCAAATGGTGAATTTTCCAAATGGGTTAAAGTAAATGGAAATGCAACGCCT 3120
Db 3791 CGAAATGCCATACCAAATGGTGAATTTTCCAAATGGGTTAAAGTAAATGGAAATGCAACGCCT 3850
Qy 3121 GCGTAGAAGTACAAACAAATCAATCATCATCTGCTCTTGTGATTCCAAACCTGGGATGAG 3180
Db 3851 GCGTAGAAGTACAAACAAATCAATCATCATCTGCTCTTGTGATTCCAAACCTGGGATGAG 3910
Qy 3181 CAAAGTTTCCAAACAGTTTACAGTTCAAACGAAATCAAGATATGTGTTACGAGTTACTGCG 3240
Db 3911 CAAAGTTTCCAAACAGTTTACAGTTCAAACGAAATCAAGATATGTGTTACGAGTTACTGCG 3970
Qy 3241 AGAAAGAAAGGGTAGGAAATCGATATGATTAAGTATCCGTTGATGGTGGAAATCAAAACAGAA 3300
Db 3971 AGAAAGAAAGGGTAGGAAATCGATATGATTAAGTATCCGTTGATGGTGGAAATCAAAACAGAA 4030
Qy 3301 AGCTTTACTTTTGTAGTCCAGCGATTTATGATACAAATGGGATCTATATACGCAAGTGTCC 3360
Db 4031 AGCTTTACTTTTGTAGTCCAGCGATTTATGATACAAATGGGATCTATATACGCAAGTGTCC 4090
Qy 3361 AATACAAATGGATATACAAACAAATATGCTATATACAAAGCATCGAGTACAAACGGA 3420
Db 4091 AATACAAATGGATATACAAACAAATATGCTATATACAAAGCATCGAGTACAAACGGA 4150
Qy 3421 TATAACGCAAAATTAATATGATTAATACGCAAGCATCGAATACAAACGGAATTAACACAAAT 3480
Db 4151 TATAACGCAAAATTAATATGATTAATACGCAAGCATCGAATACAAACGGAATTAACACAAAT 4210
Qy 3481 AGTGTGTACAAATGATCAAAACCGCTATATACAAACAAAGCATCGATTCATCCGTTATACA 3540
Db 4211 AGTGTGTACAAATGATCAAAACCGCTATATACAAACAAAGCATCGATTCATCCGTTATACA 4270
Qy 3541 GATCAAAATGCTGATTTGAGATGAGTGAAGAGGATCAATTCTATATAGAAAGTGTAGAA 3600
Db 4271 GATCAAAATGCTGATTTGAGATGAGTGAAGAGGATCAATTCTATATAGAAAGTGTAGAA 4330
Qy 3601 TTGATTTGATAGCTAGAGTAA 3621
Db 4331 TTGATTTGATAGCTAGAGTAA 4351

RESULT 3
ABK87235

ID ABK87235 standard; DNA; 3633 BP.

XX AC ABK87235;

XX XX

DT 07-OCT-2002 (first entry)

XX Bacillus thuringiensis Cry1218-2 gene sequence.

DE Pesticidal; spraying; dusting; broadcasing; seed coating; insect pest;
KW Colorado potato beetle; western corn rootworm; southern corn rootworm;
KW insect target range; endotoxin; Cry1218; gene; ds.

OS Bacillus thuringiensis.

XX WO200234774-A2.
XX PD 02-MAY-2002.
XX PF 24-OCT-2001; 2001WO-US45468.
XX PR 24-OCT-2000; 2000US-242838P.
XX PR 23-OCT-2001; 2001US-0032717.
XX PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX PI Abad AR, Duck NB, Feng X, Flannagan RD, Kahn TW, Sims LE;
XX DR WPI; 2002-519178/55.
XX DR P-PSDB; RAU99256.
XX PT New isolated pesticidal polypeptide useful for impacting insect pest
XX PT e.g. Colorado potato beetle -
XX PS Claim 1; Page 98-103; 176pp; English.
XX CC The present invention relates to a new pesticidal polypeptide. The
XX CC invention is useful for impacting an insect pest by applying the
XX CC the molecules of the invention to the environment of the insect pest by
XX CC spraying, dusting, broadcasting, or seed coating, where the insect pest
XX CC is selected from Colorado potato beetle, western corn rootworm or
XX CC southern corn rootworm. The invention is also useful for increasing
XX CC insect target range and for producing transgenic microorganisms and
XX CC plants that express the pesticidal polypeptide. The invention is also
XX CC useful for producing transformed plants and in transforming any organism
XX CC to produce the pesticidal polypeptide of the invention. The present
XX CC nucleic acid sequence encodes a *Bacillus thuringiensis* wild-type
XX CC Cry1218 endotoxin protein.
XX SQ Sequence 3633 BP; 1277 A; 609 C; 767 G; 980 T; 0 other;

Query Match 87.0%; Score 3151.8; DB 24; Length 3633;
Best Local Similarity 92.1%; Pred. No. 0;
Matches 3353; Conservative 0; Mismatches 262; Indels 24; Gaps 2;

Qy 1 ATGAGTCAAAATCAAAATGAATATGAAATATAGATGCGACACCTTCTACTCTGTA 60
Db 1 ATGAGTCAAAATCAAAATGAATATGAAATATAGATGCGACACCTTCTACTCTGTA 60
Qy 61 TCCATGATCTCAACAGATACCTTTTCGATGAGCCAAACAAATGCGCTACAAATATG 120
Db 61 TCCATGATCTCAACAGATACCTTTTCGATGAGCCAAACAAATGCGCTACAAATATG 120
Qy 121 GATTATAAGATTATTATAAATGCTCGGGAAATGCTAGTGAATACCTGGTTCACT 180
Db 121 GATTATAAGATTATTATAAATGCTCGGGAAATGCTAGTGAATACCTGGTTCACT 180
Qy 181 GAAGTACTTTAGCGGCAAGATGAGTAAAGCGGCAATGATATAGTAAATTA 240
Db 181 GAAGTACTTTAGCGGCAAGATGAGTAAAGCGGCAATGATATAGTAAATTA 240
Qy 241 CTATCAGTTTAGGGTCCCATTTGTTGGCCGATAGTAGCTTTTATCTCACTTAT 300
Db 241 CTATCAGTTTAGGGTCCCATTTGTTGGCCGATAGTAGCTTTTATCTCACTTAT 300
Qy 301 GATATTCTGTGGCTTCAGGGGAAAGAGTCAATGGGAAATTTTATGGAAACAAGTAGAA 360
Db 301 GATATTCTGTGGCTTCAGGGGAAAGAGTCAATGGGAAATTTTATGGAAACAAGTAGAA 360
Qy 361 GAACCTCATTAATCAAAAAATAGCAGAAATGCAAGAAATTAAGCGCTTTTGGAAATAGAA 420
Db 361 GAACCTCATTAATCAAAAAATAGCAGAAATGCAAGAAATTAAGCGCTTTTGGAAATAGAA 420
Qy 421 GGATTAGGTAATTAATCAAAATATATCTAATCTGAGCTTGAAGATGGGAAAGAAATCA 480
Db 421 GGATTAGGTAATTAATCAAAATATATCTAATCTGAGCTTGAAGATGGGAAAGAAATCA 480

Qy 481 AATGGTTCAAGAGCCTTACGAGATGTCGAAATCGAATTTGAAATCCTGGATAGTTATTT 540
Db 481 AATGGTTCAAGAGCCTTACGAGATGTCGAAATCGAATTTGAAATCCTGGATAGTTATTT 540
Qy 541 ACGCAATATATGCCATCTTTTAGAGTGACAAATTTTGAAGTACCATTCCTTACTGTATAT 600
Db 541 ACGCAATATATGCCATCTTTTAGAGTGACAAATTTTGAAGTACCATTCCTTACTGTATAT 600
Qy 601 GCAATGCGAGCCAACTTCATTTACTGTATTAAGAGCGCTCAATTTTGGAGAGAA 660
Db 601 ACACAGGCGCCAACTTCATTTACTGTATTAAGAGCGCTCAATTTTGGAGAGAA 660
Qy 661 TGGGGATGGTCAACAACTATCTATTAATACTATATGATCGTCAAAATGAACTTACTGCA 720
Db 661 TGGGGATGGTCAACAACTATCTATTAATACTATATGATCGTCAAAATGAACTTACTGCA 720
Qy 721 GAATATTTCTGATCACTGTGTAAGTGTATGAACCTGGTTTAGCAAAATTAAGGCGACG 780
Db 721 GAATATTTCTGATCACTGTGTAAGTGTATGAACCTGGTTTAGCAAAATTAAGGCGACG 780
Qy 781 AGCGCTAAACAATGGGTTGACTATAACAATTCGTAGAGAAATGACACTGCGCGTTT 840
Db 781 AGCGCTAAACAATGGGTTGACTATAACAATTCGTAGAGAAATGACACTGCGCGTTT 840
Qy 841 GATGTTGTTGCAATTTATCCCAATTTATGACACACGACGTACCCAAATGGAACGAAAGCA 900
Db 841 GATGTTGTTGCAATTTATCCCAATTTATGACACACGACGTACCCAAATGGAACGAAAGCA 900
Qy 901 CAACTAACAGGGAAGTATATACAGATCCACTGGGCGGTAAACGTGCTCTTCAATTGGT 960
Db 901 CAACTAACAGGGAAGTATATACAGATCCACTGGGCGGTAAACGTGCTCTTCAATTGGT 960
Qy 961 TCCTGGTATGACAAAGCACCTTCTTTCGAGTGATAGAATCATCCGTTTATTCGACACCC 1020
Db 961 TCCTGGTATGACAAAGCACCTTCTTTCGAGTGATAGAATCATCCGTTTATTCGACACCC 1020
Qy 1021 CATGTATTTGATTATATAACGGGACTCACAGTGTATACAAATCAAGAAGCAATTTCTTCC 1080
Db 1021 CATGTATTTGATTATATAACGGGACTCACAGTGTATACAAATCAAGAAGCAATTTCTTCC 1080
Qy 1081 GCTCGCTATATAAGACATTTGGGCTGGTCAATCAATAGCTACCATCGTTCAGTAGGGT 1140
Db 1081 GCTCGCTATATAAGACATTTGGGCTGGTCAATCAATAGCTACCATCGTTCAGTAGGGT 1140
Qy 1141 AGTAATCTTCAACAAATGATGGAATCAATCATAATCTACACAGCACTAGTACCTTTGAT 1200
Db 1141 AATATTAATAAACAAGATGATGGAATCAATCATAATCTACACAGCACTAGTACCTTTGAT 1200
Qy 1201 TTTACGAATTAATGATATTTTACAGACTCTATCAAGAGTGCAGTACTCTCTTGATTTGTT 1260
Db 1201 TTTACGAATTAATGATATTTTACAGAGCTTATCAAGAGTGCAGTACTCTCTTGATTTGTT 1260
Qy 1261 TACCTCGTTATACGTATATATTTTGGAAATGCGAAGTFCGAGTTTTTCAATGGTAAAC 1320
Db 1261 TTTCTCGTTATACGTATATATTTTGGAAATGCGAAGTFCGAGTTTTTCAATGGTAAAC 1320
Qy 1321 CAATTTGAATATACGAAAGACCTTAAAGTATATCCAGTTTCCCAAGATATATATAGCG 1380
Db 1321 CAATTTGAATATACGAAAGACCTTAAAGTATATCCAGTTTCCCAAGATATATATAGCG 1380
Qy 1381 AGTACAGAGATTCGGAAATTAGAATTTACCTCAGAAACCTTCAGATCAACCAAAATATAG 1440
Db 1381 GGGACAGAGATTCGGAAATTAGAATTTACCTCAGAAACCTTCAGATCAACCAAAATATAG 1440
Qy 1441 TCATATAGCCATAGATTTATGTCATATCAAGATATTCGCGCAAGGGTAACTACCGGA 1500
Db 1441 TCATATAGCCATAGATTTATGTCATATCAAGATATTCGCGCAAGGGTAACTACCGGA 1500
Qy 1501 TTAGTACCTGTATTTCTTGGACACATCGAAGTCAATTTAACAATATATATATCA 1560
Db 1501 TTAGTACCTGTATTTCTTGGACACATCGAAGTCAATTTAACAATATATATATCA 1560
Qy 1561 GATAAAATCACTCAAAATTCGCGCGGTTAAATGTTGGGATATTTTACCCTTTGT ----- 1613

||||| 1561 GATAAAATTAAGTTCAGATTCGGTTCGTAAGGTTTCTGATTTGGCTCCCTCTATAACAGGA 1620
QY 1614 -----TCCAGTGTAAAGACGACAGGACATACAGAGGGGNTTTATTACAGTAT 1662
Db 1621 GGGCCAAATAATACCGTTGATTCGGGTCTCGGATTTACAGGGGGGGGATAAATAAAGTA 1680.
QY 1663 AATAGAAAGTACGTGTTCTGTAGGAACCTTATTTCTAGCTCGATATGGCCTTAGCATTAGAA 1722
Db 1681 AATAAGAAATGGAGTAATATACATATCGCGTGTAAATAATTTACAGACATTTACAAAGAA 1740
QY 1723 AAAGCAGGGAATATCGTGTAGACGTGAGATATGCTATGATGAGATATATGTTATGTCAT 1782
Db 1741 TATAGTATGAGGATTCGGTATGCTTCGGCTAATAATACTGAAATTTATATAAAATCCCTTCT 1800
QY 1783 GTAACGATGCTCAGATTCAGATGCGCAAAACAACTGAACCCAGCTGAGGATCTGACATCT 1842
Db 1801 GAAGAAACGTTAAATCTCAGCTCAAAAACCTATGATGATAGAGTGAGCTTTTAACATAT 1860
QY 1843 AAAAATTTTAAAGTTGACATGCTATCACAAACATTAATAATTTAGCAACAGATAGTTGCTTA 1902
Db 1861 AATAAAATTTAATGTCGACTTTGCCCCCTTATTAATTTTACGACAAACCGAACCTTTCAAT 1920
QY 1903 GCATTTGAACATTAATTTAGTGAAGACCTTAATTTCAACATTTATCTGGTATAGTTTACGTT 1962
Db 1921 ACTTAGGGGCTATATTTGAAGCGGAAGACTTTCTTGGAAAT-----TGAAGCTTATATA 1974
QY 1963 GACCGAATCGAATTCATCCAGTAGATGACATATGAACGGGAAACAGATTTTAGAGCA 2022
Db 1975 GACCGAATCGAATTTATCCAGTAGATGACATATGAACGGGAAACAGATTTTAGAGCA 2034
QY 2023 GCGAAGAAAGCAGTGAATGCTTTGTTTACCAATACAAAGATGCTTACGACACAGGGCTA 2082
Db 2035 GCGAAGAAAGCAGTGAATGCTTTGTTTACCAATACAAAGATGCTTACGACACAGGGCTA 2094
QY 2083 ACGGATTTGAAGTGAATCAAGCGGCAAACTTATAGTGAATGCTTATCGGATGATTTGTAT 2142
Db 2095 ACGGATTTGAAGTGAATCAAGCGGCAAACTTATAGTGAATGCTTATCGGATGATTTGTAT 2154
QY 2143 CCATATGAAGAAACGATGTTTATTTGATGACAGTGAAGAGGCAAAACGCTCAGTGAGGCA 2202
Db 2155 CCAATGAAGAAACGATGTTTATTTGATGACAGTGAAGAGGCAAAACGCTCAGTGAGGCA 2214
QY 2203 CGTAATTTGCTTCAAGATCCAGATTTCCAAAGAGATAAATGGAGAAATGCTGACGCGCA 2262
Db 2215 CGTAATTTGCTTCAAGATCCAGATTTCCAAAGAGATAAATGGAGAAATGCTGACGCGCA 2274
QY 2263 AGTACGGGAATTCAGGTTATAGAAAGGGGATGCTTTATTTCAAAGGGCGTTATCTACGCCTA 2322
Db 2275 AGTACGGGAATTCAGGTTATAGAAAGGGGATGCTTTATTTCAAAGGGCGTTATCTACGCCTA 2334
QY 2323 CCAGGTGCGAGAGAAATAGATACGGAACCGTATCCACGATCTGTTATCAAAAAGTAGAG 2382
Db 2335 CCAGGTGCGAGAGAAATAGATACGGAACCGTATCCACGATCTGTTATCAAAAAGTAGAG 2394
QY 2383 GAAGTGTATTAATAACATACAGATATAGATTGAGAGGGTTTGTCCGAAGCAGTCAA 2442
Db 2395 GAAGTGTATTAATAACATACAGATATAGATTGAGAGGGTTTGTCCGAAGCAGTCAA 2454
QY 2443 GGATTCGAAATTTTCAATTCGTTCATCAAACCGAATTTGTAATAAATGTAACCGGAT 2502
Db 2455 GGATTCGAAATTTTCAATTCGTTCATCAAACCGAATTTGTAATAAATGTAACCGGAT 2514
QY 2503 GATTTGCTGCCAGATGATCTCTGTTAACTCGGATGGTAGTATCAATCGATGAGCGAA 2562
Db 2515 GATTTGCTGCCAGATGATCTCTGTTAACTCGGATGGTAGTATCAATCGATGAGCGAA 2574
QY 2563 CAAAAGTATGTAATAGCCGTTTAGAAGTAGTGAAGAACCGTTCTGCTGAAGCGCATGATTC 2622
Db 2575 CAAAAGTATGTAATAGCCGTTTAGAAGTAGTGAAGAACCGTTCTGCTGAAGCGCATGATTC 2634
QY 2623 TCTATTCTTATGATACAGGTGAAATCGATTACAATGAAATTCAGGAATATGGGTTGGA 2682
|||||

Db 2635 TCTATTCTCTATTGATACAGGTGAAATCGATTACAATGAAATTCAGGAATATGGGTTGGA 2694
QY 2683 TTTAAAGATTTACGACCCAGAGGGATATGCAACACTCGGAAACCTAGAAATTTGGTTCGAAGAG 2742
Db 2695 TTTAAGATTTACGACCCAGAGGGATATGCAACACTCGGAAACCTAGAAATTTGGTTCGAAGAG 2754
QY 2743 GGAACCTTTATCAGGAGACGCTTTAGAACCTTTGCAAGAGAGAAACAACAGTTCGAAGATT 2802
Db 2755 GGAACCTTTATCAGGAGACGCTTTAGAACCTTTGCAAGAGAGAAACAACAGTTCGAAGATT 2814
QY 2803 CAAATGCAAGAGAGACGCTGAGAAACAGATAGAGGTATATGCTGCAAGCAAGCGGTA 2862
Db 2815 CAAATGCAAGAGAGACGCTGAGAAACAGATAGAGGTATATGCTGCAAGCAAGCGGTA 2874
QY 2863 GATCGGTTTATATGCCGATTTATCAGGATCAGCAACTCAATCTCTGATGTAGAGATTACAGAT 2922
Db 2875 GATCGGTTTATATGCCGATTTATCAGGATCAGCAACTCAATCTCTGATGTAGAGATTACAGAT 2934
QY 2923 CTTTACCTGCGGCCCAAGATCTGATACAGTCCATTCCTTACGATATATAACGAAATGTTCCCA 2982
Db 2935 CTTTACCTGCGGCCCAAGATCTGATACAGTCCATTCCTTACGATATATAACGAAATGTTCCCA 2994
QY 2983 GAAATACCAAGGATGAACTTATACGAAATTTACAGATTAACAGATCGACTCCCAACAGCG 3042
Db 2995 GAAATACCAAGGATGAACTTATACGAAATTTACAGATTAACAGATCGACTCCCAACAGCG 3054
QY 3043 TGGAGTTTGTATGATCATCGGAAATGCCATACCAAAATGGTGATTTTCGAAATGGTTAAAGT 3102
Db 3055 TGGAGTTTGTATGATCATCGGAAATGCCATACCAAAATGGTGATTTTCGAAATGGTTAAAGT 3114
QY 3103 AATTGGAATGCAACGCTGCGGTAGAGTAACAACAAATCAATCATCATCTGTCCTTTGTG 3162
Db 3115 AATTGGAATGCAACGCTGCGGTAGAGTAACAACAAATCAATCATCATCTGTCCTTTGTG 3174
QY 3163 ATTCCAAAATCTGGATGAGCAAGTTTCGCAACAGTTTACAGTTCAACGGAATCAAGATAT 3222
Db 3175 ATTCCAAAATCTGGATGAGCAAGTTTCGCAACAGTTTACAGTTTCAACGGAATCAAGATAT 3234
QY 3223 GTGTTACGAGTTTACTCGGAGAAAGAGGGTAGGAAATGGAATATGTAAGTATCCGTTGAT 3282
Db 3235 GTGTTACGAGTTTACTCGGAGAAAGAGGGTAGGAAATGGAATATGTAAGTATCCGTTGAT 3294
QY 3283 GGTGGAATCAAAACAGAAACGCTTACTTTTAGTGCAAGCGATTATGATACAAATGGAATG 3342
Db 3295 GGTGGAATCAAAACAGAAACGCTTACTTTTAGTGCAAGCGATTATGATACAAATGGAATG 3354
QY 3343 TATAATACGCAAGTGTCCAAATCAAAATGGAATTAACAACAAATTAATGCGTATATACAA 3402
Db 3355 TATAATACGCAAGTGTCCAAATCAAAATGGAATTAACAACAAATTAATGCGTATATACAA 3414
QY 3403 GCATCGAGTACAAACGATATAACGAAATAATATGTAATATACGCAAGCATCGAATACA 3462
Db 3415 GCATCGAGTACAAACGATATAACGAAATAATATGTAATATACGCAAGCATCGAATACA 3474
QY 3463 AACGGATATACAAATAGTGTGTAACAAATGATCAAAACGGCTATATACAAAAACAGTG 3522
Db 3475 AACGGATATACAAATAGTGTGTAACAAATGATCAAAACGGCTATATACAAAAACAGTG 3534
QY 3523 ACATTCATCCCGTATACAGATCAAAATGTTGAGATGAGTGAAGAGAGGTTACATTC 3582
Db 3535 ACATTCATCCCGTATACAGATCAAAATGTTGAGATGAGTGAAGAGAGGTTACATTC 3594
QY 3583 TATATGAAGTGTAGAAATTTGTTAGACGTAGGTAA 3621
Db 3595 TATATGAAGTGTAGAAATTTGTTAGACGTAGGTAA 3633

RESULT 4

ABK87248

ID ABK87248 standard; DNA; 6613 BP.

XX

AC ABK87248;

XX

DT 07-OCT-2002 (first entry)
 XX Bacillus thuringiensis genomic Cry1218-2 DNA sequence.
 XX
 KW Pesticidal; spraying; dusting; broadcasting; seed coating; insect pest;
 KW Colorado potato beetle; western corn rootworm; southern corn rootworm;
 KW insect target range; endotoxin; Cry1218; ds.
 XX
 XX Bacillus thuringiensis.
 XX
 XX WO200234774-A2.
 XX
 XX 02-MAY-2002.
 XX
 XX 24-OCT-2001; 2001WO-US45468.
 XX
 XX 24-OCT-2000; 2000US-242838P.
 PR 23-OCT-2001; 2001US-0032717.
 XX
 XX (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 XX Abad AR, Duck NB, Feng X, Flannagan RD, Kahn TW, Sims LE;
 XX
 XX WPI; 2002-519178/55.
 XX
 XX New isolated pesticidal polypeptide useful for impacting insect pest
 XX e.g. Colorado potato beetle -
 XX
 XX Claim 13; Page 145-147; 176pp; English.
 XX
 XX The present invention relates to a new pesticidal polypeptide. The
 CC invention is useful for impacting an insect pest by applying the
 CC the molecules of the invention to the environment of the insect pest by
 CC spraying, dusting, broadcasting, or seed coating, where the insect pest
 CC is selected from Colorado potato beetle, western corn rootworm or
 CC southern corn rootworm. The invention is also useful for increasing
 CC insect target range and for producing transgenic microorganisms and
 CC plants that express the pesticidal polypeptide. The invention is also
 CC useful for producing transformed plants and in transformation any organism
 CC to produce the pesticidal polypeptide of the invention. The present
 CC nucleic acid sequence represents the *Bacillus thuringiensis* Cry1218-2
 CC endotoxin genomic DNA sequence.
 XX
 XX Sequence 6613 BP; 2289 A; 1049 C; 1306 G; 1969 T; 0 other;
 SQ

Query Match 87.0%; Score 3151.8; DB 24; Length 6613;
 Best Local Similarity 92.1%; Pred. No. 0;
 Matches 3353; Conservative 0; Mismatches 262; Indels 24; Gaps 2;

QY 1 ATGAGTCCAAATAAATCAAAATGAATATGAATTTATAGATGCGACACCTTCTACTCTGTA 60
 DB 1254 ATGAGTCCAAATAAATCAAAATGAATATGAATTTATAGATGCGACACCTTCTACTCTGTA 1313

QY 61 TCCAAATGATTTCAACAGATACCCCTTTTGGGAATGAGCCAAACAAATCGCTACAAAATATG 120
 DB 1314 TCCAAATGATTTCAACAGATACCCCTTTTGGGAATGAGCCAAACAAATCGCTACAAAATATG 1373

QY 121 GATTATAAAGATATTTTAAATATGCTGGGGAAATGCTAGTGAATACCCCTGGTTCACT 180
 DB 1374 GATTATAAAGATATTTTAAATATGCTGGGGAAATGCTAGTGAATACCCCTGGTTCACT 1433

QY 181 GAAGTACTTTGTTAGCGGACAAAGATGAGCTAAGCGCGCAATTGATATAGTAGTAATTA 240
 DB 1434 GAAGTACTTTGTTAGCGGACAAAGATGAGCTAAGCGCGCAATTGATATAGTAGTAATTA 1493

QY 241 CTATCAGGTTTAGGGTCCCATTTGTTGGCCGATAGTGAGTCTTTATACTCAACTTAT 300
 DB 1494 CTATCAGGTTTAGGGTCCCATTTGTTGGCCGATAGTGAGTCTTTATACTCAACTTAT 1553

QY 301 GATATTTCTGGCTTCAGGGGAAAGAGTCAATGGGAAATTTTATGGAAACAAAGTAGAA 360
 DB 1554 GATATTTCTGGCTTCAGGGGAAAGAGTCAATGGGAGATTTTATGGAAACAAAGTAGAA 1613

QY 361 GAACTCATTAATCAAAAATAGCAGAAATATGCAAGGAATAAAGCGCTTTTCGGAATTAGAA 420
 DB 1614 GAACTCATTAATCAAAAATAGCAGAAATATGCAAGGAATAAAGCGCTTTTCGGAATTAGAA 1673

QY 421 GGATTAGTAATTAATTAATCAAAATATATCTAATGCGCTTGAAGAAATGGGAAGAAATCCA 480
 DB 1674 GGATTAGTAATTAATTAATCAAAATATATCTAATGCGCTTGAAGAAATGGGAAGAAATCCA 1733

QY 481 AATGGTTCAAGAGCCCTTACGAGATGTCGGAATCGATTTGAAATCCTCGATAGTTTATTT 540
 DB 1734 AATGGTTCAAGAGCCCTTACGAGATGTCGGAATCGATTTGAAATCCTCGATAGTTTATTT 1793

QY 541 ACGCAATATATGCCATCTTTTAGAGTGACAAATTTTGAAGTACCAATTCCTTACTGTATAT 600
 DB 1794 ACGCAATATATGCCATCTTTTAGAGTGACAAATTTTGAAGTACCAATTCCTTACTGTATAT 1853

QY 601 GCAATGGGAGCCCAACCTTCACTTACTGTATTAAGAGACGGCTCAATTTTTCGGAGAGAA 660
 DB 1854 ACACAGGAGCCCAACCTTCACTTACTGTATTAAGAGACGGCTTCAATTTTTCGGAGAGAA 1913

QY 661 TGGGATGCTCAACCAACTACTTAAATAACTATTAATGATCGTCAATGAAACTTACTGCA 720
 DB 1914 TGGGATGCTCAACCAACTACTTAAATAACTATTAATGATCGTCAATGAAACTTACTGCA 1973

QY 721 GAATATTCCTGATCACTGTGTAAAGTGTATGAAACTGGTTTAGCAAAATTTAAAGGCACG 780
 DB 1974 GAATATTCCTGATCACTGTGTAAAGTGTATGAAACTGGTTTAGCAAAATTTAAAGGCACG 2033

QY 781 AGCGCTAAACCAATGGGTGACATTAACCAATTCCTGAGAGAAATGACACTGACGGTTTAA 840
 DB 2034 AGCGCTAAACCAATGGGTGACATTAACCAATTCCTGAGAGAAATGACACTGACGGTTTAA 2093

QY 841 GATGTTGTTGCAATTTATCCCAATTTATGACACACCGCTACCCCAATGGGAACGAAAGCA 900
 DB 2094 GATGTTGTTGCAATTTATCCCAATTTATGACACACCGCTACCCCAATGGGAACGAAAGCA 2153

QY 901 CAACTAAACAGGAAGTATATACAGATCACTGGGCGGGTAAACGCTGCTTCAATTTGT 960
 DB 2154 CAACTAAACAGGAAGTATATACAGATCACTGGGCGGGTAAACGCTGCTTCAATTTGT 2213

QY 961 TCCTGGTATGACAAAGCACCTTCTTTCGAGTGATAGAAATCATCCGTTATTCGACACCC 1020
 DB 2214 TCCTGGTATGACAAAGCACCTTCTTTCGAGTGATAGAAATCATCCGTTATTCGACACCC 2273

QY 1021 CATGTTATTTGATATATAACGGGACTCAAGTGATATACATCAAGAGCAATTTCTTCC 1080
 DB 2274 CATGTTATTTGATATATAACGGGACTCAAGTGATATACATCAAGAGCAATTTCTTCC 2333

QY 1081 GCTCGCTATATAAGACATTTGGGCTGTCATCAATAAGCTACCATCGTGTCAAGTAGGGGT 1140
 DB 2334 GCTCGCTATATAAGACATTTGGGCTGTCATCAATAAGCTACCATCGGATTTTGTAGTAT 2393

QY 1141 AGTAATCTTCAACAAATGTATGGAATCAATCAAAATCTACACAGCACTAGTACCTTTGAT 1200
 DB 2394 AATAATATAAAGACGATGTATGGAATCAATCAAAATCTACACAGCACTAGTACCTTTGAT 2453

QY 1201 TTTAGCAATATGATTTTACAGACTCTTCAAGAGGATGAGTACTCTTCAATTTGTT 1260
 DB 2454 TTTAGCAATATGATTTTACAGACTCTTCAAGAGGATGAGTACTCTTCAATTTGTT 2513

QY 1261 TACCTCGTTATACGTTATATTTTTTGGAAATGCCAGAAAGTCCAGTTTTCATGGTAAAC 1320
 DB 2514 TTTCTCGTTATACGTTATATTTTTTGGAAATGCCAGAAAGTCCAGTTTTCATGGTAAAC 2573

QY 1321 CAAATTAATAATACAGAAAGCGTTAAAGTATAATTCAGTTTCCAAAGATATTATAGCG 1380
 DB 2574 CAAATTAATAATACAGAAAGCGTTAAAGTATAATTCAGTTTCCAAAGATATTATAGCG 2633

QY 1381 AGTACAAGAGATTCGGAATTAGAATTAATCTCCAGAACTTCAGATCAACCAATTTATG 1440
 DB 2634 GGGACAAGAGATTCGGAATTAGAATTAATCTCCAGAACTTCAGATCAACCAATTTATG 2693

QY 1441 TCATATAGCCATAGATTATGTCTATATCAAGTATTTCCGCGACGGGTAACTACCGGA 1500

Db 2694 TCATATAGCCATAGATATATGTCTATATCACAAGTATTTCCGCGACGGTTCACATCCCGA 2753
Qy |||||
Db 1501 TTAGTACCTGTATTTCTTGGACACATCGAAGTGCAGATTTAAACAATACATATATTTCA 1560
Qy |||||
Db 2754 TTAGTACCTGTATTTCTTGGACACATCGAAGTGCAGATTTAAACAATAGCAGTTCATTTCA 2813
Qy |||||
Db 1561 GATAAATACATCAAAATCCGCGCGTTAAATGTGGGATAAATTTACCGTTTGT----- 1613
Qy |||||
Db 2814 GATAAATTTACTCAGATTCGGTCTGTAAGGTTTCTGATTTGGCTCCCTCTATAACAGGA 2873
Qy |||||
Qy 1614 -----TCCAGTGTAAAGGACACAGACATACAGGAGGGATTTTATACAGTAT 1662
Db 2874 GGGCCAAATTAATACCGTTGTATCGGCTCTCGGATTTACAGGGGGGGGATAATANAAGTA 2933
Qy |||||
Db 1663 AATAGAGTACTGGTCTCTAGGACCTTTATTTCTAGCTCGATATGCGCTAGCATTTAGAA 1722
Qy |||||
Db 2934 ATAAGAAATGGAGTAATTAATATACATATCGCGTGTAAATTTTACAGACATTTAAACAAAGAA 2993
Qy |||||
Qy 1723 AAAGCAGGGAATATCGTGTAAAGCTGAGATATGCTACTGATGCGATATTTGTATTGCAT 1782
Db 2994 TATAGTATGAGGATTCGGTATGCTTCGCGTAATTAATCTGAAATTTTATATAAATCCTTCT 3053
Qy |||||
Qy 1793 GTAACGATGCTCAGATTCAGATGCCAAAAAATGAAACCCAGGTGAGGATCTGACATCT 1842
Db 3054 GAAAGAAAACGTTAAATCTCAGCTCAAAAAAATCTATGAATAGAGGTGAAGCTTTAAACATAT 3113
Qy |||||
Qy 1843 AAAAATTTTAAAGTTGCAGATGCTATCAACAATTAATTTAGCAACAGATAGTTCGCTA 1902
Db 3114 AATAAATTTTAAATTTGCGACTTTGCCCCCTATTAATTTTACGACAAACCGAACCCTTTTCA 3173
Qy |||||
Qy 1903 GCATTTGAAACATAATTTAGGTGAAGACCTTAATTTCAACATTAATCTGGTATAGTTTACGTT 1962
Db 3174 ACTCTAGGGGCTATATTTGAAGCGGAAGACTTTCTTGGAT-----TGAAGCTTATATA 3227
Qy |||||
Qy 1963 GACCAATCGAATTTCTCCAGTAGATGAGACATATGAAGCGGAAACAAGATTTGAAGCA 2022
Db 3228 GACCAATCGAATTTATCCAGTAGATGAGACATATGAAGCGGAAACAAGATTTGAAGCA 3287
Qy |||||
Qy 2023 GCGAAGAAAGCAGTGAATGCTTTGTTTTCGAAATACAAAAGATGGCTTACGCCAGCGCTA 2082
Db 3288 GCGAAGAAAGCAGTGAATGCTTTGTTTTCGAAATACAAAAGATGGCTTACGCCAGCGCTA 3347
Qy |||||
Qy 2083 ACGGATTTAGAAAGTGAATCAAGCGGCAAACTTAGTGGAAATGCTATCGGAATGATTTGTAT 2142
Db 3348 ACGGATTTAGAAAGTGAATCAAGCGGCAAACTTAGTGGAAATGCTATCGGAATGATTTGTAT 3407
Qy |||||
Qy 2143 CCAATGAAAAACGATTTGTTTATGTCAGTGAGAGAGCAAAACGCTCTCAGTGAGGCA 2202
Db 3408 CCAATGAAAAACGATTTGTTTATGTCAGTGAGAGAGCAAAACGCTCTCAGTGAGGCA 3467
Qy |||||
Qy 2203 CGTAATTTGCTTCAGATCCAGATTTCCAGAGATTAATGGAGAAATGGCTGCGACGCA 2262
Db 3468 CGTAATTTGCTTCAGATCCAGATTTCCAGAGATTAATGGAGAAATGGCTGCGACGCA 3527
Qy |||||
Qy 2263 AGTACGGGAATTTGAGTTATAGAGGGGATGCTTTTATCAAGGGGCTTATCTACGCCCTA 2322
Db 3528 AGTACGGGAATTTGAGTTATAGAGGGGATGCTTTTATCAAGGGGCTTATCTACGCCCTA 3587
Qy |||||
Qy 2323 CCAAGTGCAGAGAAATAGATACGGAACCGTATCCAAACGATCTGATCAAAAAGTAGAG 2382
Db 3588 CCAAGTGCAGAGAAATAGATACGGAACCGTATCCAAACGATCTGATCAAAAAGTAGAG 3647
Qy |||||
Qy 2383 GAAGGTGTTTAAACCATACACAGATATAGATTGAGAGGGTTTGTCCGAGCAGTCAA 2442
Db 3648 GAAGGTGTTTAAACCATACACAGATATAGATTGAGAGGGTTTGTCCGAGCAGTCAA 3707
Qy |||||
Qy 2443 GGAATGGAATTTTCAAAATTCGTATCAAAACGAAATGTAATAAATGTACCGGAT 2502
Db 3708 GGAATGGAATTTTCAAAATTCGTATCAAAACGAAATGTAATAAATGTACCGGAT 3767
Qy |||||
Qy 2503 GAATTTGCTGCCAGATGATCTCTGTTAACTCGGATGGTAGTATCAATCGATGCGAGCA 2562
Db |||||

Db 3768 GAATTTGCTGCCAGATGATCTCTGTTAACTCGGATGGTAGTATCAATCGATGCGAGCA 3827
Qy |||||
Qy 2563 CAAAAGTATGCAATAGCCGTTTAGAAAGTACGAAACCGTTCTGCTGAAAGCGCATGAGTTC 2622
Db 3828 CAAAAGTATGCAATAGCCGTTTAGAAAGTACGAAACCGTTCTGCTGAAAGCGCATGAGTTC 3887
Qy |||||
Qy 2623 TCTATTTCTTATTGATACAGGTGAAATCGAATTAACAATGAAAAATGCAAGGATATGGGTTGA 2682
Db 3888 TCTATTTCTTATTGATACAGGTGAAATCGAATTAACAATGAAAAATGCAAGGATATGGGTTGA 3947
Qy |||||
Qy 2683 TTTAAGATTTACGAGCCGACAGAGGATATGCAACACCTCGGAAACCTAGAAATGGTTCGAAGAG 2742
Db 3948 TTTAAGATTTACGAGCCGACAGAGGATATGCAACACCTCGGAAACCTAGAAATGGTTCGAAGAG 4007
Qy |||||
Qy 2743 GGACCTTTTATCAGGAGAGCGCATTTAGAAACCTTTGCAAGAGAGAAACAACAAGTGGAGATT 2802
Db 4008 GGACCTTTTATCAGGAGAGCGCATTTAGAAACCTTTGCAAGAGAGAAACAACAAGTGGAGATT 4067
Qy |||||
Qy 2803 CAAATGCAAGAGAGCGTGAAGAAAAACAGATAGAGGTATATGGCATCGAAAAACAAGCGGTA 2862
Db 4068 CAAATGCAAGAGAGCGTGAAGAAAAACAGATAGAGGTATATGGCATCGAAAAACAAGCGGTA 4127
Qy |||||
Qy 2863 GATCGTTTATATGCGCGATTTATCAGGATCAGCAACTGAAATCCTGATGTAGAGATTACAGAT 2922
Db 4128 GATCGTTTATATGCGCGATTTATCAGGATCAGCAACTGAAATCCTGATGTAGAGATTACAGAT 4187
Qy |||||
Qy 2923 CTTTACTGCGGCCCAAGATCTGATACAGTCCATTTCTTCTAGTATATAACGAAATGTTCCCA 2982
Db 4188 CTTTACTGCGGCCCAAGATCTGATACAGTCCATTTCTTCTAGTATATAACGAAATGTTCCCA 4247
Qy |||||
Qy 2983 GAAATACCAAGGATGAACTATACGAAGTTTACAGAAATTAACAGAGTCGACTCCAAACAAGCG 3042
Db 4248 GAAATACCAAGGATGAACTATACGAAGTTTACAGAAATTAACAGAGTCGACTCCAAACAAGCG 4307
Qy |||||
Qy 3043 TGGAGTTTGTATGATCAGCGAAATGCCATACCAAAATGCTGATTTTCGAAATGGGTTAAGT 3102
Db 4308 TGGAGTTTGTATGATCAGCGAAATGCCATACCAAAATGCTGATTTTCGAAATGGGTTAAGT 4367
Qy |||||
Qy 3103 AATTGGAATGCAACCCCTGGCGTAGAAGTACAAACAAATCAATCATACATCTCTGCTTGTG 3162
Db 4368 AATTGGAATGCAACCCCTGGCGTAGAAGTACAAACAAATCAATCATACATCTCTGCTTGTG 4427
Qy |||||
Qy 3163 AYTCCAAATCGGATGAGCAAGTTTCGCAACAGTTTACAGTTTCAACCGGAATCAAAAGATAT 3222
Db 4428 AYTCCAAATCGGATGAGCAAGTTTCGCAACAGTTTACAGTTTCAACCGGAATCAAAAGATAT 4487
Qy |||||
Qy 3223 GTGTTACGAGTTATCTGCGAGAAAAAGAGGGTAGGAAATGGATATGTAAGTATCCGTGAT 3282
Db 4488 GTGTTACGAGTTATCTGCGAGAAAAAGAGGGTAGGAAATGGATATGTAAGTATCCGTGAT 4547
Qy |||||
Qy 3283 GGTGGAATTCAAACAGAAACGCTTACTTTTACTGTCGAGCGATTTAGTACAAATGGAATG 3342
Db 4548 GGTGGAATTCAAACAGAAACGCTTACTTTTACTGTCGAGCGATTTAGTACAAATGGAATG 4607
Qy |||||
Qy 3343 TATAATAGCAAGTGTCCAAATCAAAATGATATAACAATAATGCGGATTAATAACACAA 3402
Db 4608 TATAATAGCAAGTGTCCAAATCAAAATGATATAACAATAATGCGGATTAATAACACAA 4667
Qy |||||
Qy 3403 GCATCGAGTACAAACGAGATATAACGCAATAATATGTAATAACGCAAGTATCGGAATACA 3462
Db 4668 GCATCGAGTACAAACGAGATATAACGCAATAATATGTAATAACGCAAGTATCGGAATACA 4727
Qy |||||
Qy 3463 AACGATATAACAATAAGTGTGATCAATGATCAACCGGCTATATACAAAAACAGTG 3522
Db 4728 AACGATATAACAATAAGTGTGATCAATGATCAACCGGCTATATACAAAAACAGTG 4787
Qy |||||
Qy 3523 ACATTCATCCCGTATACAGATCAAAATGCTGATGAGTGGAGTGGAGACAGAGGTACATTC 3582
Db 4788 ACATTCATCCCGTATACAGATCAAAATGCTGATGAGTGGAGTGGAGACAGAGGTACATTC 4847
Qy |||||
Qy 3583 TATATAGAAAGTGTAGAAATTTGATTTAGACGTAGAGTAA 3621
Db 4848 TATATAGAAAGTGTAGAAATTTGATTTAGACGTAGAGTAA 4886

RESULT 5

AAT43221
ID AAT43221 standard; DNA; 3507 BP.

XX AC AAT43221;

XX DT 28-JAN-1997 (first entry)

XX DE Antiscarab pest toxin 50C(b) coding sequence.

XX KW Toxin 50C(b); scarab pest; toxin; insect; scarabaeidae; pest control;
XX KW larval stage insect; grain; tuberous crop; white grub; chafer grub;
XX KW cyclocephala; popillia; ds.

XX OS Bacillus thuringiensis strain kumamotoensis.

XX PN US554534-A.

XX PD 10-SEP-1996.

XX PF 30-SEP-1994; 94US-0315468.

XX PR 01-FEB-1993; 93US-0014941.

XX PR 16-DEC-1991; 91US-0808316.

XX PR 30-JAN-1992; 92US-0828430.

XX PR 30-SEP-1994; 94US-0315468.

XX PA (MYCO) MYCOGEN CORP.

XX PI Foncerrada L, Michaels TE, Narva KE;

XX DR WPI; 1996-424659/42.

XX DR P-PSDB; AA06417.

XX PT New nucleic acid encoding B.thuringiensis toxin active against
XX PT scarab(s) - also related toxin and transformed microbes, effective
XX PT against adult pests and their larvae

XX PS Claim 2; Column 27-30; 24pp; English.

XX CC AAT43221-T43223 represent the coding sequences for toxins that are
XX CC active against scarab pests. This sequence was isolated from the
XX CC Bacillus thuringiensis strain kumamotoensis. Insects in the family
XX CC Scarabaeidae constitute a serious pest control problem, especially when
XX CC destructive larval stage insects infest high value turf found in golf
XX CC courses, playing fields and lawns. The larvae of many species also
XX CC attack grains, tuberous crops, and ornamentals. The larvae are known as
XX CC white grubs, or chafer grubs, and can be found in decaying organic
XX CC matter, or in the soil where they consume plant roots. In Europe and the
XX CC U.S. populations of these larvae and adults have developed resistance to
XX CC chemical insecticides such as the organochlorines and DDT. The toxins
XX CC encoded by these sequences, and intact cells that are capable of
XX CC expressing the proteins, can be used to control many pests of the family
XX CC scarabaeidae, such as species of Cyclocephala, and Popillia. The toxins
XX CC are active against larvae (present in soil) and against adults.

XX SQ Sequence 3507 BP; 1256 A; 576 C; 732 G; 943 T; 0 other;

Query Match 70.8%; Score 2565.2; DB 17; Length 3507;
Best Local Similarity 85.1%; Pred. No. 0;
Matches 2906; Conservative 0; Mismatches 493; Indels 15; Gaps 3;

Qy 1 ATGAGTCCAAATTAATCAAAATGAATATGAATATATAGATCGCACACCTTCTACTCTGTA 60

Db 1 ATGAGTCCAAATTAATCAAAATGAATATGAATATATAGATCGCACACCTTCTACTCTGTA 60

Qy 61 TCCAAATGATCTTAACAGATACCCCTTTTGGGAATGAGCCAAATATGCGCTACAAATATG 120

Db 61 TCCAAATGATCTTAACAGATACCCCTTTTGGGAATGAGCCAAATATGCGCTACAAATATG 120

Qy 121 GATTATAGATTAATTTAAATATGTCGCGGGAATGCTAGTGAATACCCCTGGTTCACT 180

Db 121 GATTATAGATTAATTTAAATATGTCGCGGGAATGCTAGTGAATACCCCTGGTTCACT 180

Qy 181 GAAGTACTTTGTAGCGGACAAGATGACAGTAAGCGCGCAATTGATATAGTAGTAAATTA 240

Db 181 GAGGTATTTCTAAGCGACGAAGTGCAGTTAAGCGCGCAATTGATATAGTAGTAAATTA 240

Qy 241 CTATCAGGTTTGGGGTCCCAATTTGTTGGGCGATAGTAGTGTCTTTATACCTCACTATT 300

Db 241 CTAACAGGTTTGGGGTCCCAATTTGTTGGGCGATAGTAGTGTCTTTATACCTCACTATT 300

Qy 301 GATATTTGTGCGCTTACGGGGAAGAGTCAATGGGAAATTTTATGGAACAAGTAGAA 360

Db 301 GATATTTGTGCGCTTCAAAACAAAAGAGTCAATGGGAAATTTTATGGAACAAGTAGAA 360

Qy 361 GAACTCATTATCAAAATATGACAGATATGCAAGGATTAAGCGCTTTCCGAATTAGAA 420

Db 361 GAACTCATTATCAAAATATGACAGATATGCAAGGATTAAGCGCTTTCCGAATTAGAA 420

Qy 421 GGATTAGGTAATTAATTACCAATTTATCTAACTGCGCTTGAAGAAATGGAAGAAATCCA 480

Db 421 GGGTAGGGAATTAATTACCAATTTATCTAACTGCGCTTGAAGAGTGGAGAAATCCA 480

Qy 481 AATGGTTCAAGAGCCTTACGAGATGTCGAAATCGAATTCGAAATCCTGGATAGTTATT 540

Db 481 AATGGTTCAAGAGCCTTACGAGATGTCGAAATCGAATTCGAAATCCTGGATAGTTATT 540

Qy 541 AGCAATATATGCCATCTTTTAGAGTGACAAATTTGAAGTACCAATTCCTACTGTATAT 600

Db 541 AGCAATATATGCCATCTTTTAGAGTGACAAATTTGAAGTACCAATTCCTACTGTATAT 600

Qy 601 GCAATGGCAGCCCAACCTTCATTACTGTATTATAAGGACGGCTCAATTTTGGAGAAGAA 660

Db 601 ACAATGGCAGCAAAACCTTACTTTTATAAGGAGCGCATCAATTTTGGAGAAGAA 660

Qy 661 TGGGATGCTCAACAACTACTTAATAACTATTATGATCGTCAATGAAATCTTACTGCA 720

Db 661 TGGGATGCTCAACAACTACTTAATAACTATTATGATCGTCAATGAAATCTTACTGCA 720

Qy 721 GAATATCTGATCACTGTGTAAAGTGTATGAACTGGTTAGCAAAATTAAGAGCAGG 780

Db 721 GAATATCTGACCACTGTGTAAAGTGTATGAACTGGTTAGCAAAATTAAGAGCAGG 780

Qy 781 AGCGCTAAACAATGGTTGACTATATAACCAATTCGCTAGAGAAATGACACTGCGGTTTA 840

Db 781 AGCGCTAAACAATGGTTGACTATATAACCAATTCGCTAGAGAAATGACACTGCGGTTTA 840

Qy 841 GATGTTGTTGCAATTAATCCCAATTTATGACACACGACGATACCCCAATGGAACGAAAGCA 900

Db 841 GACGTTGTTGCAATTAATTTCAAACTATGATAGCGGTACGTATCCACTGGCAACACAGCT 900

Qy 901 CAACTAACAGGGAAGTATATACAGATCCACTGGCGCGGTAAACGTGCTCTCAATTTGT 960

Db 901 CAGCTTACAAGGGAAGTATATACAGATCCACTGGCGCGGTAGATGTCCTTAATTTTGGC 960

Qy 961 TCCTGATGACAAAGACCTTCTTTTCGAGTGTAGATCATCCGTTATTCGACACCCC 1020

Db 961 TCCTGATGACAAAGACCTTCTTTTCGAGTGTAGATCATCCGTTATTCGACACCCC 1020

Qy 1021 CATGTATTTGATTAATAACGGGACTCAAGTGTATATACAAATCAAGAAGCAATTTCTTCC 1080

Db 1021 CATGTATTTGATTAATAACGGGACTCAAGTGTATATACAAATAAGTAGTCTTCACTTCT 1080

Qy 1081 GCTCGCTATATAAGACATTTGGGCTGGTCAATCAATTAAGTACCATCGTGTAGTAGGGGT 1140

Db 1081 GATCGTATATGAGATATTTGGGCTGGTCAATCAATTAAGTATATAAGCATATCGTACGAGT 1140

Qy 1141 AGTATCTTCAACAAATGATGGAATCAATCAAAATCTACACAGCACTAGTACCTTTGAT 1200

Db 1141 AGTACCTTTACACAGATGATGGAACCAATCAAAATTTACAAAGTACTAGCAATTTTGT 1200

Qy 1201 TTTTACGAATTAATGATTTTACAAAGCTTATCAAAAGGATGACAGTACTCTCTGATATTGTT 1260

Db 1201 TTACGAATTAACGATATTTTCAAGACTTTATCAAAATGGTGCAGTACTCCTTGATATAGTT 1260
Qy 1261 TACCTCTGGTTATACGTATATATTTTTTGGAAATGCCAGAAAGTCAGATTTTTCATGGTAAAC 1320
Db 1261 TACCTCTGGTTATACGTATATATTTTTTGGAAATGCCAGAAAGTCAGATTTTTCATGGTAAAC 1320
Qy 1321 CAATTTGAATTAATACCAAGAAAGCGTTTAAAGTATTAATCCAGTTTCCAAAGATATTTATAGCG 1380
Db 1321 CAATTTGAATTAATACCAAGAAAGCGTTTAAAGTATTAATCCAGTTTCCAAAGATATTTATAGAG 1380
Qy 1381 AGTACAGAGATTCGGAATTTAGATTTTACCTTCGAAACCTTCAGATCAACCAAAATTTATAGAG 1440
Db 1381 CGACAGAGATTCGGAATTTAGATTTTACCTTCGAAACCTTCAGATCAACCAAAATTTATAGAG 1440
Qy 1441 TCATATAGCATATAGTATTTATCATATCAAGTATTTCCGCGAGCGGTAACATCCCGGA 1500
Db 1441 TCATATAGCATATAGTATTTATCATATCAATTTATTTTACTCCA---GTTCAATAGCAGCG 1497
Qy 1501 TTAGTACCTGTATTTTCTTGGACACATCGAAGTGCAGATTTTAAACAAATCAATATATTTCA 1560
Db 1498 TATGTACCTGTATTTTCTTGGACACATCGGAGTGCAGATCTAACAAATACAGTTTAAAGT 1557
Qy 1561 GATAAATACATCAAAATTCGCGCGGTTAAATGTTGGGATTAATTTACCGTTTGTTCAGTG 1620
Db 1558 GCGGAATCACCCNAATACAGGGGCAAGTCTAGCACCATAGGCGAGAAATACTTATATA 1617
Qy 1621 GTAAAGGACACAGGACATACAGAGGGGATTTATACAGTATATAGAGTACTGTTCT 1680
Db 1618 ATAAAGGGCGTGTATACAGGGGAGACTTAGTGCGTTTAAAGGACCGCATCGGAAT 1677
Qy 1681 GPAGGAACCTTATTTCTAGCTCGATATGCGCTAGCAATAGAAAGAACGAGGAAATATCGT 1740
Db 1678 TGTGAGTTTCAGATGATCTTTCCAGAGTCTCAACGATTCGATTCGATTCGTTACGCT 1737
Qy 1741 GTAAGCTGAGATATGCTACTGATGACAGATTTGTAATGATGTAAGTAAACGATTCAGAT 1800
Db 1738 TCTAATGAACTAGTTATATATAGTTTATACGCACTTAAACCAAGCGGAACCTTTAAATTC 1797
Qy 1801 CAGATGCCAAACCAATGAACCCAGGTGAGGATCTGACATCTAAAACCTTTTAAAGTTGCA 1860
Db 1798 AACGACAGATATCTTAATAAAATGAAGATTTAACAATATATGATTTCAATATATA 1857
Qy 1861 GATGCTATCAACACATTAATTAATTTAGCAACAGATAGTTTCGCTAGCATTTGAAACATATTTA 1920
Db 1858 GAATATC---CAAGATCTATTCAGTAATGCTTCTTCAACATACAGAGTTATCTATA 1914
Qy 1921 GGTGAAGCCCTTAATCAACATTAATCTGATATAGTTTACGTTGACCGAATTCGAATTCATC 1980
Db 1915 GGTATACAAACGAATACAAATTTATTTATTTA-----GACCGAATCGAATTCATC 1965
Qy 1981 CCAGTAGATGACATATCAAGCGGAACAAGATTTTAAAGCAGCGAAGAACGAGTGAAT 2040
Db 1966 CCAGTAGATGACATATCAAGCGGAACAAGATTTTAAAGCAGCGAAGAACGAGTGAAT 2025
Qy 2041 GCCTTGTTTACGAATACAAAGATGCTTTACGACCAAGGCGTAAACGATTTATGAAGTGAAT 2100
Db 2026 GCCTTGTTTACGAATACAAAGATGCTTTACGACCAAGGCGTAAACGATTTATGAAGTGAAT 2085
Qy 2101 CAAGCGGCAAACTTAGTGAATGCCTTATCGGATGATTTGATCCAAATGAAACCAATGG 2160
Db 2086 CAAGCGGCAAACTTAGTGAATGCCTTATCGGATGATTTGATCCAAATGAAACCAATGG 2145
Qy 2161 TTATTTGATGAGTGAAGGACCAAAACCGCTCAGTGCAGCGATTAATTTGCTTCAAGT 2220
Db 2146 TTATTTGATGAGTGAAGGACCAAAACCGCTTACGAGCGATTAATTTGCTTCAAGT 2205
Qy 2221 CCAGATTTCCAGAGATTAATGGAGAAATGGCTGACGCGAGTACGGGAATTTGAGGTT 2280
Db 2206 CCAGATTTCCAGAGATTAATGGAGAAATGGCTGACGCGAGTACGGGAATTTGAGGTT 2265
Qy 2281 ATAGAAGGGGATGCTTTATTTCAAGGGCGTTATCTACGCTACCGATCGCAGAGAAATA 2340
Db 2266 ATAGAAGGGGATGCTTTATTTCAAGGGCGTTATCTACGCTACCGATCGCAGAGAAATA 2325

Qy 2341 GATACGGAACCGTATCTCAACGATCTGTATCAAAAGTAGAGAAAGGTGTATTTAAACCA 2400
Db 2326 GATACGGAACCGTATCTCAACGATCTGTATCAAAAGTAGAGAAAGGTGTATTTAAACCA 2385
Qy 2401 TACACAAGATATAGATTCAGAGGGTTTGTGGAAGCAGTCAAGGATTTGGAATTTTCA 2460
Db 2386 TACACAAGATATAGATTCAGAGGGTTTGTGGAAGCAGTCAAGGATTTGGAATTTTATAG 2445
Qy 2461 ATTCTGTATCAACCAACCGAATTCGAAATGTAATGATTCGCGATGATTTGCTGCCAGATGA 2520
Db 2446 ATTCTGTATCAACCAACCGAATTCGAAATGTAATGATTCGCGATGATTTGCTGCCAGATGA 2505
Qy 2521 TCTCTCTGTTAACTCTCGATGTTAGTATCAATCGATGCGCGAACAAGATGTAATAGC 2580
Db 2506 CTTCTCTGTAACAATGATGTTAGATCAATCGATGCGCGAACAAGATGTAATAGT 2565
Qy 2581 CTTTATAGATTAAGAAAACCGTTCTGGTGAAGCGCATGTTCTTATTCCTATTTATACA 2640
Db 2566 CTTTATAGATTAAGAAAACCGTTCTGGTGAAGCGCATGTTCTTATTCCTATTCGATACA 2625
Qy 2641 GGTGAATTCGATTAACAATGAAATCGAAGATATCGGTTGGATTTTAAAGATTAACGACCCA 2700
Db 2626 GGAGAGCTGGATTAACAATGAAATCGAAGATATCGGTTGGATTTTAAAGATTAACGACCCA 2685
Qy 2701 GAGGATATGCAACACTCGGAAACCTAGAAATTTGGTTCGAAGAGGACCTTTTATCAGGAGAC 2760
Db 2686 GAGGATATGCAACACTCGGAAATTTGGAAATCTTGAATTTGGTTCGAAGAGGACCTTTTGCAGGAGAC 2745
Qy 2761 GCATTTAGAACCGTTCCAAAGAGAGAAACAACAGTGGAGATTTCAAATGACAGAGACGT 2820
Db 2746 GCATTTAGAACCGTTCCAAAGAGAGAAACAACAGTGGAGATTTCAAATGACAGAGACGT 2805
Qy 2821 GAAGAAACAGATAGAGATATATGTCATCGAACAAGCGGTAGATCGTTTATATCCGAT 2880
Db 2806 GAAGAAACAGATAGAGATATATGTCATCGAACAAGCGGTAGATCGTTTATATCCGAT 2865
Qy 2881 TATCAGGATTCAGCAACTGAACTCTGATCTAGATGATTAACAGATCTTACTCGCGCCCAAGAT 2940
Db 2866 TATCAGGATTCAGCAACTGAACTCTGATCTAGATGATTAACAGATCTTACTCGCGCTCAAGAT 2925
Qy 2941 CTGATACAGTCCATCTCTTACGTATATAACGAAATGTTCCAGAAATACACGAGATGAAC 3000
Db 2926 CTAAATACAGTCCATCTCTTACGTATATAACGAAATGTTCCAGAAATACACGAGATGAAC 2985
Qy 3001 TATACAGAGTTTACAGAAATTAACAGATCGACTCCAAACGCGTGGAGTTTGTATGATCAG 3060
Db 2986 TATACAGAGTTTACAGAGTTTAAACAGATCGACTCCAAACGCGTGGAGTTTGTATGATCAA 3045
Qy 3061 CGAAATGCGCATACCAAAATGTTGATTTTCGAAATGTTTAAAGTAAATTTGGAATTCGAACGCT 3120
Db 3046 CGAAATGCGCATACCAAAATGTTGATTTACGAAATGTTTAAAGTAAATTTGGAATTCGAACATCT 3105
Qy 3121 GCGGTAGAGTACAAACAAATCAATCATCATCTGCTCTTGTGATTCGAAATTCGAAATGAG 3180
Db 3106 GGTGTGAATGTACAAACAAATCAATCATCATCTGCTCTTGTGATTCGAAATTCGAAATGAA 3165
Qy 3181 CAAAGTTTCGCAACAGTTTACAGTTCAAACGATCAAGATATGTTTACGAGTTACTGCG 3240
Db 3166 CAAAGTTTCGCAACAGTTTACAGTTCAAACGATCAAGATATGTTTACGAGTTACTGCA 3225
Qy 3241 AGAAAGAGGCGGTAGGAAATGGATATGTAAGTATTCGCGTGGTGGAAATCAAACAGAA 3300
Db 3226 AGAAAGAGGCGGTAGGAAATGGATATGTAAGTATTCGCGTGGTGGAAATCAAACAGAA 3285
Qy 3301 ACGCTTACTTTTATGTCAGAGGATTTATGATACAAATGGAATGTTATTAATACGCAAGTGTCC 3360
Db 3286 ACGCTTACTTTTATGTCAGAGGATTTATGATACAAATGGAATGTTATTAATACGCAAGTGTCC 3345
Qy 3361 AATACAAATGGATTAACCAAAATGCGGTATTAATACCAAGCATCGAGTACA 3414
Db 3346 AATACAAAGCGGATTAACCAAAATGCGGTATTAATACCAAGCATCGAGTACA 3399

RESULT 6

ABK87241
 ID ABK87241 standard; DNA; 2010 BP.
 XX AC ABK87241;
 XX DT 07-OCT-2002 (first entry)
 XX DE Bacillus thuringiensis Cry1218-1A truncated gene sequence.
 XX KW Pesticidal; spraying; dusting; broadcasting; seed coating; insect pest;
 XX KW Colorado potato beetle; western corn rootworm; southern corn rootworm;
 XX KW insect target range; endotoxin; Cry1218; gene; ds.
 XX OS Bacillus thuringiensis.
 XX PN W0200234774-A2.
 XX PD 02-MAY-2002.
 XX PF 24-OCT-2001; 2001WO-US45468.
 XX PR 24-OCT-2000; 2000US-242838P.
 XX PR 23-OCT-2001; 2001US-0032717.
 XX PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX PI Abad AR, Duck NB, Feng X, Flannagan RD, Kahn TW, Sims LE;
 XX DR WPI; 2002-519178/55.
 XX DR P-PSDB; AAU99262.
 XX PT New isolated pesticidal polypeptide useful for impacting insect pest
 XX PT e.g. Colorado potato beetle -
 XX PS Claim 1; Page 123-125; 176pp; English.
 XX CC The present invention relates to a new pesticidal polypeptide. The
 CC invention is useful for impacting an insect pest by applying the
 CC the molecules of the invention to the environment of the insect pest by
 CC spraying, dusting, broadcasting, or seed coating, where the insect pest
 CC is selected from Colorado potato beetle, western corn rootworm or
 CC southern corn rootworm. The invention is also useful for increasing
 CC insect target range and for producing transgenic microorganisms and
 CC plants that express the pesticidal polypeptide. The invention is also
 CC useful for producing transformed plants and in transforming any organism
 CC to produce the pesticidal polypeptide of the invention. The present
 CC nucleic acid sequence encodes a Bacillus thuringiensis wild-type
 CC Cry1218 endotoxin protein.
 XX SQ Sequence 2010 BP; 690 A; 348 C; 394 G; 578 T; 0 other;

Query Match 55.5%; Score 2008.4; DB 24; Length 2010;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2009; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	241	CTATCAGGTTT	AGGGTCCCA	TTTGGTGGCCG	ATAGT	CTTTAT	TACTCA	CTTATT	300
DB	241	CTATCAGGTTT	AGGGTCCCA	TTTGGTGGCCG	ATAGT	CTTTAT	TACTCA	CTTATT	300
QY	301	GATATCTCTG	TGGCTTCAG	GGGAAAGAG	TCATG	GGAAATTT	TATGGA	CAAGTAGAA	360
DB	301	GATATCTCTG	TGGCTTCAG	GGGAAAGAG	TCATG	GGAAATTT	TATGGA	CAAGTAGAA	360
QY	361	GAACTCAATTA	TCAAAAAAT	AGCAGAAAT	ATGCAAG	GAATAAAG	CGCTTCG	GAATAGAA	420
DB	361	GAACTCAATTA	TCAAAAAAT	AGCAGAAAT	ATGCAAG	GAATAAAG	CGCTTCG	GAATAGAA	420
QY	421	GGATTAGGTA	ATAATTAACA	ATTATATCT	AACTGCG	TTGAAGAA	TGGGAAGAA	AAATCCA	480
DB	421	GGATTAGGTA	ATAATTAACA	ATTATATCT	AACTGCG	TTGAAGAA	TGGGAAGAA	AAATCCA	480
QY	481	AATGGTTCAAG	AGCCTTACG	AGATGTCG	GAATCGA	ATTTGAAAT	CCCTGGAT	TTTATT	540
DB	481	AATGGTTCAAG	AGCCTTACG	AGATGTCG	GAATCGA	ATTTGAAAT	CCCTGGAT	TTTATT	540
QY	541	ACGCAATATAT	TGCCATCTTT	TAGAGTGACA	CAAAATTT	TGAAATGTA	CTCTTCT	TACTGTATAT	600
DB	541	ACGCAATATAT	TGCCATCTTT	TAGAGTGACA	CAAAATTT	TGAAATGTA	CTCTTCT	TACTGTATAT	600
QY	601	GCAATGGCAG	CCCAACCTTCA	TTTACTGTTAT	TAAAGGAC	CGCTCAAT	TTTTGGGA	AGAA	660
DB	601	GCAATGGCAG	CCCAACCTTCA	TTTACTGTTAT	TAAAGGAC	CGCTCAAT	TTTTGGGA	AGAA	660
QY	661	TGGGATGGTCA	CAACTACTAT	TATTAATTA	CTATTA	TATGATCGT	CAAAATTA	GAATCTTACTGCA	720
DB	661	TGGGATGGTCA	CAACTACTAT	TATTAATTA	CTATTA	TATGATCGT	CAAAATTA	GAATCTTACTGCA	720
QY	721	GAATATCTGAT	CACTGCTGTA	AGTGTATG	AAATCTGTT	TAGCAAAAT	TAAAAAGG	CAAG	780
DB	721	GAATATCTGAT	CACTGCTGTA	AGTGTATG	AAATCTGTT	TAGCAAAAT	TAAAAAGG	CAAG	780
QY	781	AGCGCTAAACA	ATGGTGTGACT	ATAACCAAT	TCCGTAG	AGAAATGACA	TCGCGCGG	TTTTA	840
DB	781	AGCGCTAAACA	ATGGTGTGACT	ATAACCAAT	TCCGTAG	AGAAATGACA	TCGCGCGG	TTTTA	840
QY	841	GATGTTGTTG	CAATTTATCC	CAAAATTTATG	ACACAGC	AGTACCAAT	TGGAACGAA	AGCA	900
DB	841	GATGTTGTTG	CAATTTATCC	CAAAATTTATG	ACACAGC	AGTACCAAT	TGGAACGAA	AGCA	900
QY	901	CAACTAAACA	GGGAAGTATAT	TACAGATCC	ACTGGCG	CGGTAAAC	GTCTTCAAT	TGGT	960
DB	901	CAACTAAACA	GGGAAGTATAT	TACAGATCC	ACTGGCG	CGGTAAAC	GTCTTCAAT	TGGT	960
QY	961	TCCTGGTATGA	CAAGCACCTT	CTTTCCG	AGTGTAG	AATCATCCG	TTATTCG	ACCACCC	1020
DB	961	TCCTGGTATGA	CAAGCACCTT	CTTTCCG	AGTGTAG	AATCATCCG	TTATTCG	ACCACCC	1020
QY	1021	CATGTTATTTG	ATTATATAA	CGGGAATCA	AGTGTATAC	CAATCAAG	AAAGATTTCTTCC	1080	
DB	1021	CATGTTATTTG	ATTATATAA	CGGGAATCA	AGTGTATAC	CAATCAAG	AAAGATTTCTTCC	1080	
QY	1081	GCTCGCTATAT	AGACATTTGG	CGTGTCTCAT	CAATAGCT	ACCATCGT	GTCTCAGT	AGGGGT	1140
DB	1081	GCTCGCTATAT	AGACATTTGG	CGTGTCTCAT	CAATAGCT	ACCATCGT	GTCTCAGT	AGGGGT	1140
QY	1141	AGTAATCTTCA	CAAAATGATG	GAATCAAT	CAAAATCT	TACACAG	CATAGTACCTTTTGT	1200	
DB	1141	AGTAATCTTCA	CAAAATGATG	GAATCAAT	CAAAATCT	TACACAG	CATAGTACCTTTTGT	1200	
QY	1201	TTTACGAATTA	TGATTTTACA	GAATCTAT	CAAGGAAT	GAGTACTCT	CTTTGAT	TATTTT	1260
DB	1201	TTTACGAATTA	TGATTTTACA	GAATCTAT	CAAGGAAT	GAGTACTCT	CTTTGAT	TATTTT	1260
QY	1261	TACCTCGTTAT	ACGTATATAT	TTTTGG	AAATGCCA	AGTCGAGT	TTTTTCAT	GTAAAC	1320
DB	1261	TACCTCGTTAT	ACGTATATAT	TTTTGG	AAATGCCA	AGTCGAGT	TTTTTCAT	GTAAAC	1320
QY	1321	CAATTTGAATA	TACAGAAAG	CGTTAAAG	TATAAT	TCCAGT	TTTCCAA	GATATTATAGCG	1380

Db 1321 CAATTGAATTAATACCAAGAGCGTTAAAGTATAATCCAGTTTCCAAAGATATTATAGCG 1380
Qy 1381 AGTACAAGAGATTTCGGAATTAGAAATTACCTCCAGAACTTCAGATCAACCAATATTATAG 1440
Db 1381 AGTACAAGAGATTTCGGAATTAGAAATTACCTCCAGAACTTCAGATCAACCAATATTATAG 1440
Qy 1441 TCATATAGCATAGATATTATGTCATATCACAAAGTATTCCGCGACGGGTAACTACCGGA 1500
Db 1441 TCATATAGCATAGATATTATGTCATATCACAAAGTATTCCGCGACGGGTAACTACCGGA 1500
Qy 1501 TTAGTACCTGTATTTCCTGGGACACATCGAAGTGCAGATTAAACCAATATATATCA 1560
Db 1501 TTAGTACCTGTATTTCCTGGGACACATCGAAGTGCAGATTAAACCAATATATATCA 1560
Qy 1561 GATAAAATCACTCAAAATCCGCGCGTTAAATGTTGGGATAATTACCGTTTGTCCAGTG 1620
Db 1561 GATAAAATCACTCAAAATCCGCGCGTTAAATGTTGGGATAATTACCGTTTGTCCAGTG 1620
Qy 1621 GTAAAGGACCGAGGACATACAGAGGGGATTTATTACAGTATAATAGAAAGTACTGTTCT 1680
Db 1621 GTAAAGGACCGAGGACATACAGAGGGGATTTATTACAGTATAATAGAAAGTACTGTTCT 1680
Qy 1681 GTAGGAACCTTATTTCTAGCTGATATGCGCTAGCATTTAGAAAGGAGGAAATATCGT 1740
Db 1681 GTAGGAACCTTATTTCTAGCTGATATGCGCTAGCATTTAGAAAGGAGGAAATATCGT 1740
Qy 1741 GTAAGCTGAGATATGCTACTGATGCGAGATATTGTTATTCATGTAACGATGCTCAGATT 1800
Db 1741 GTAAGCTGAGATATGCTACTGATGCGAGATATTGTTATTCATGTAACGATGCTCAGATT 1800
Qy 1801 CAGATGCCAAAACCAATGAACCCAGGTGAGGATCTGACATCTAAACTTTTAAAGTTGCA 1860
Db 1801 CAGATGCCAAAACCAATGAACCCAGGTGAGGATCTGACATCTAAACTTTTAAAGTTGCA 1860
Qy 1861 GATGCTATCAACAATTAATTTAGCAACAGATAGTTTCGCTAGCATTTGAAACATATTTA 1920
Db 1861 GATGCTATCAACAATTAATTTAGCAACAGATAGTTTCGCTAGCATTTGAAACATATTTA 1920
Qy 1921 GGTGAAGCCCTTAATTCACATATCTGATATGTTTACGTTGACCGATCGAATTCATC 1980
Db 1921 GGTGAAGCCCTTAATTCACATATCTGATATGTTTACGTTGACCGAATCGAATTCATC 1980
Qy 1981 CCAGTATGATGACATATATGAAGCGGAACAA 2010
Db 1981 CCAGTATGATGACATATGAGCGGAATAA 2010

RESULT 7

ABK87236

ID ABK87236 standard; DNA; 2003 BP.

XX AC ABK87236;

XX DT 07-OCT-2002 (first entry)

XX DE Bacillus thuringiensis Cry1218-1 truncated gene sequence.

XX KW Pesticidal; spraying; dusting; broadcasting; seed coating; insect pest;

XX KW Colorado potato beetle; western corn rootworm; southern corn rootworm;

XX KW insect target range; endotoxin; Cry1218; gene; ds.

XX OS Bacillus thuringiensis.

XX FN WO200234774-A2.

XX PD 02-MAY-2002.

XX PF 24-OCT-2001; 2001WO-US45468.

XX PR 24-OCT-2000; 2000US-242838P.

XX PR 23-OCT-2001; 2001US-0032717.

XX XX

PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX Abad AR, Duck NB, Feng X, Flannagan RD, Kahn TW, Sims LE;
XX WPI; 2002-519178/55.
DR P-PSDB; AAU99257.
XX New isolated pesticidal polypeptide useful for impacting insect pest
e.g. Colorado potato beetle -
PT Claim 1; Page 106-108; 176pp; English.
PS The present invention relates to a new pesticidal polypeptide. The
invention is useful for impacting an insect pest by applying the
molecules of the invention to the environment of the insect pest by
spraying, dusting, broadcasting, or seed coating, where the insect pest
is selected from Colorado potato beetle, western corn rootworm or
southern corn rootworm. The invention is also useful for increasing
insect target range and for producing transgenic microorganisms and
plants that express the pesticidal polypeptide. The invention is also
useful for producing transformed plants and in transforming any organism
to produce the pesticidal polypeptide of the invention. The present
nucleic acid sequence encodes a Bacillus thuringiensis wild-type
Cry1218 endotoxin protein.
XX Sequence 2003 BP; 686 A; 348 C; 392 G; 577 T; 0 other;

Query Match 55.3%; Score 2003; DB 24; Length 2003;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2003; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGAGTCCAAATTAATCAAAATGAAATATGAAATATAGATGCGACACCTTCTACTTCTGTA 60
Db 1 ATGAGTCCAAATTAATCAAAATGAAATATGAAATATAGATGCGACACCTTCTACTTCTGTA 60
Qy 61 TCCAAATGATTTCAACAGATACCTTTTTCGGAATGAGCCAAACAAATGCGCTACAAATATG 120
Db 61 TCCAAATGATTTCAACAGATACCTTTTTCGGAATGAGCCAAACAAATGCGCTACAAATATG 120
Qy 121 GATTATAAGATTTTAAATATGTCGGGAAATGCTAGTGAATACCTCGTTCACCT 180
Db 121 GATTATAAGATTTTAAATATGTCGGGAAATGCTAGTGAATACCTCGTTCACCT 180
Qy 181 GAAGTACTTTGTTAGCGGACAGATGAGTAAAGCGCAATGATATAGTAAATTA 240
Db 181 GAAGTACTTTGTTAGCGGACAGATGAGTAAAGCGCAATGATATAGTAAATTA 240
Qy 241 CTATCAGGTTTAGGGGTCCCAATTTTTCGGCGGATAGTGAAGTCTTTTATCACTTAT 300
Db 241 CTATCAGGTTTAGGGGTCCCAATTTTTCGGCGGATAGTGAAGTCTTTTATCACTTAT 300
Qy 301 GATATCTGTGCGCTTCAGGGGAAAGAGTCAATGGGAAATTTTATGGAAACAGTAGAA 360
Db 301 GATATCTGTGCGCTTCAGGGGAAAGAGTCAATGGGAAATTTTATGGAAACAGTAGAA 360
Qy 361 GAACTCATTAAATCAAAATATGACAGATATGCAAGATATAAGCGCTTTCGGAAATAGAA 420
Db 361 GAACTCATTAAATCAAAATATGACAGATATGCAAGATATAAGCGCTTTCGGAAATAGAA 420
Qy 421 GGATTAGGTAATTAATACCAATTTATCTAATCTGCGCTTGAAGAATGGGAAGAAATCCA 480
Db 421 GGATTAGGTAATTAATACCAATTTATCTAATCTGCGCTTGAAGAATGGGAAGAAATCCA 480
Qy 481 AATGTTCAAGAGCTTACGAGATGCGAAATCGAATTTGAAATCTGATAGTTTATTT 540
Db 481 AATGTTCAAGAGCTTACGAGATGCGAAATCGAATTTGAAATCTGATAGTTTATTT 540
Qy 541 ACGCAATATGCGCATCTTTTAGAGTGCAATTTTGAAGTACCATTCTCTACTGTATAT 600
Db 541 ACGCAATATGCGCATCTTTTAGAGTGCAATTTTGAAGTACCATTCTCTACTGTATAT 600
Qy 601 GCAATGGCAGCCAACTTCAATTTTCTGTTTAAAGGACCGCTCAATTTTTCGAGAGAA 660
Db 601 GCAATGGCAGCCAACTTCAATTTTCTGTTTAAAGGACCGCTCAATTTTTCGAGAGAA 660

Db 601 GCAATGGCAGCAACCTTCATTCTTATTAAGAGCAGCGCTCAATTTTGGAGAAGAA 660
Qy 661 TGGGATGTCACAACTACTATTAATACTATTATGATCGTCAAAATGAACCTTACTGCA 720
Db 661 TGGGATGTCACAACTACTATTAATACTATTATGATCGTCAAAATGAACCTTACTGCA 720
Qy 721 GAATATTTCTGATCACTGTGTAAAGTGTATGAACCTGGTTTGAACAAATTAAGAGCAGC 780
Db 721 GAATATTTCTGATCACTGTGTAAAGTGTATGAACCTGGTTTGAACAAATTAAGAGCAGC 780
Qy 781 AGCGTAAACAATGGTGTGACTATACCAATTCCTGGTAGAGAAATGACCTGGCGGTTTTA 840
Db 781 AGCGTAAACAATGGTGTGACTATACCAATTCCTGGTAGAGAAATGACCTGGCGGTTTTA 840
Qy 841 GATGTTGTTGCAATATTCCTCAAAATATGACACAGCAGCTACCCCAATGAAACGAAAGCA 900
Db 841 GATGTTGTTGCAATATTCCTCAAAATATGACACAGCAGCTACCCCAATGAAACGAAAGCA 900
Qy 901 CAACTAACAGGGAAGTATATACAGATCCACTGGGCGCGGTAAACCGTCTTCAATTTGGT 960
Db 901 CAACTAACAGGGAAGTATATACAGATCCACTGGGCGCGGTAAACCGTCTTCAATTTGGT 960
Qy 961 TCCTGGTATGACAAAGCACCCTTCTTTCGGAGTGATAGAAATCATCCGTTATTGACACACC 1020
Db 961 TCCTGGTATGACAAAGCACCCTTCTTTCGGAGTGATAGAAATCATCCGTTATTGACACACC 1020
Qy 1021 CATGTTATTTGATTATATAACGGGACTCACAGTGTATACAAATCAAGAAGCATTTCTTCC 1080
Db 1021 CATGTTATTTGATTATATAACGGGACTCACAGTGTATACAAATCAAGAAGCATTTCTTCC 1080
Qy 1081 GCTCGCTATATAAGACATTTGGGCTGTCTATCAAAATAGCTTACCATCGTGTAGAGGGT 1140
Db 1081 GCTCGCTATATAAGACATTTGGGCTGTCTATCAAAATAGCTTACCATCGTGTAGAGGGT 1140
Qy 1141 AGTAATCTTCAACAAATGATGGAACCTATCAAAATCTACAGACTAGTACCTTTGAT 1200
Db 1141 AGTAATCTTCAACAAATGATGGAACCTATCAAAATCTACAGACTAGTACCTTTGAT 1200
Qy 1201 TTTACGAATATGATATTTACAGACTCTATCAAGAGTGCAGTACTCCTTGTATTTGTT 1260
Db 1201 TTTACGAATATGATATTTACAGACTCTATCAAGAGTGCAGTACTCCTTGTATTTGTT 1260
Qy 1261 TACCTCGTTATACGATATATTTTGGAAATCCAGAAAGTCAGTGTTCATGGTAAAC 1320
Db 1261 TACCTCGTTATACGATATATTTTGGAAATCCAGAAAGTCAGTGTTCATGGTAAAC 1320
Qy 1321 CAATTAATTAATACAGAAAGCGTTAAAGTATAAATCCAGTTTCCAAAGATATATAGCG 1380
Db 1321 CAATTAATTAATACAGAAAGCGTTAAAGTATAAATCCAGTTTCCAAAGATATATAGCG 1380
Qy 1381 AGTACAGAGATTCGGAATTTAGAAATTTACCTCCAGAAACTTCAGATCAACCAAAATATAG 1440
Db 1381 AGTACAGAGATTCGGAATTTAGAAATTTACCTCCAGAAACTTCAGATCAACCAAAATATAG 1440
Qy 1441 TCATATAGCATTAGATTTATGTCATATACAAAGTATTCCTCCGAGCGGTAACTACCGGA 1500
Db 1441 TCATATAGCATTAGATTTATGTCATATACAAAGTATTCCTCCGAGCGGTAACTACCGGA 1500
Qy 1501 TTAGTACCTGTTATTTCTGGACACATCGAAGTGCAGATTTAAACAAATATATTTCA 1560
Db 1501 TTAGTACCTGTTATTTCTGGACACATCGAAGTGCAGATTTAAACAAATATATTTCA 1560
Qy 1561 GATAAATCACTCAAAATCCGCGGTTAAATGTTGGATTAATTTACGTTTGTTCAGTG 1620
Db 1561 GATAAATCACTCAAAATCCGCGGTTAAATGTTGGATTAATTTACGTTTGTTCAGTG 1620
Qy 1621 GTAAAGGACCCAGGACATACAGAGGGGATTTATACGATATATAGAGTACTGGTTCT 1680
Db 1621 GTAAAGGACCCAGGACATACAGAGGGGATTTATACGATATATAGAGTACTGGTTCT 1680
Qy 1681 GTAGGAACCTTATTTCTAGCTCGATGCGCTAGCAATTAGAAAAGCAGGAAATATCGT 1740
Db 1681 GTAGGAACCTTATTTCTAGCTCGATGCGCTAGCAATTAGAAAAGCAGGAAATATCGT 1740

Qy 1741 GTAAGACTCAGATATGCTACTGATGCAGATATTTGTTATGCTGTAAGAGTCTCAGATT 1800
Db 1741 GTAAGACTCAGATATGCTACTGATGCAGATATTTGTTATGCTGTAAGAGTCTCAGATT 1800
Qy 1801 CAGATGCCAAAACAAATGAACCCAGGTGAGGATCTGACATCTAAACCTTTTAAAGTTGCA 1860
Db 1801 CAGATGCCAAAACAAATGAACCCAGGTGAGGATCTGACATCTAAACCTTTTAAAGTTGCA 1860
Qy 1861 GATGCTATCACAAACATTAATTTAGCAACAGATAGTTTCGTTAGCAATCGAATTAATT 1920
Db 1861 GATGCTATCACAAACATTAATTTAGCAACAGATAGTTTCGTTAGCAATCGAATTAATT 1920
Qy 1921 GGTGAAGACCCCTTAATTTCAACATTTCTGTTATGTTTACGTTGACCGAATCGAATTCATC 1980
Db 1921 GGTGAAGACCCCTTAATTTCAACATTTCTGTTATGTTTACGTTGACCGAATCGAATTCATC 1980
Qy 1981 CCAGTAGATGAGACATATGAAGC 2003
Db 1981 CCAGTAGATGAGACATATGAAGC 2003

RESULT 8

ABK87245

ID ABK87245 standard; DNA; 2013 BP.

XX AC ABK87245;

XX AC

DT 07-OCT-2002 (first entry)

XX XX

DE *Bacillus thuringiensis* LKMS.R1218-1 mutant gene sequence.

XX KW Pesticidal; spraying; dusting; broadcasting; seed coating; insect pest;

XX KW Colorado potato beetle; western corn rootworm; southern corn rootworm;

XX KW insect target range; endotoxin; Cry1218; gene; mutant; ds.

XX OS *Bacillus thuringiensis*.

XX XX

XX PN WO200234774-A2.

XX XX

XX PD 02-MAY-2002.

XX XX

XX PF 24-OCT-2001; 2001WO-US45468.

XX XX

XX PR 23-OCT-2000; 2000US-242838P.

XX PR 23-OCT-2001; 2001US-0032717.

XX XX

XX PA (DUPO) DU PONT DE NEMOURS & CO E I.

XX XX

XX PI Abad AR, Duck NB, Feng X, Flannagan RD, Kahn TW, Sims LB;

XX DR WPI; 2002-519178/55.

XX DR P-PSDB; AAU99266.

XX XX

XX PT New isolated pesticidal polypeptide useful for impacting insect pest

XX PT e.g. Colorado potato beetle -

XX XX

XX PS Claim 23; Page 139-142; 176pp; English.

XX XX

The present invention relates to a new pesticidal polypeptide. The invention is useful for impacting an insect pest by applying the molecules of the invention to the environment of the insect pest by spraying, dusting, broadcasting, or seed coating, where the insect pest is selected from Colorado potato beetle, western corn rootworm or southern corn rootworm. The invention is also useful for increasing insect target range and for producing transgenic microorganisms and plants that express the pesticidal polypeptide. The invention is also useful for producing transformed plants and in transforming any organism to produce the pesticidal polypeptide of the invention. The present nucleic acid sequence encodes a *Bacillus thuringiensis* mutant Cry1218 endotoxin protein.

XX SQ Sequence 2013 BP; 692 A; 348 C; 393 G; 580 T; 0 other;

Query Match 54.9%; Score 1987.4; DB 24; Length 2013;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2004; Conservative 0; Mismatches 6; Indels 3; Gaps 1;

Qy 1 ATGAGTCCAAATTAATCAAAATGAATGAAATGAAATTAATAGATGCGACACCTTCTACTTCTGTA 60
Db 1 ATGAGTCCAAATTAATCAAAATGAATGAAATTAATAGATGCGACACCTTCTACTTCTGTA 60

Qy 61 TCCATGATTTCTAAACAGATACCTTTTGGCAATGAGCCAAACAAATGCGCTACAAAATAG 120
Db 61 TCCATGATTTCTAAACAGATACCTTTTGGCAATGAGCCAAACAAATGCGCTACAAAATAG 120

Qy 121 GATTATAAGATTAATTAATAATGCTCGGGGAAATGCTAGTGAATACCTTGGTTCACT 180
Db 121 GATTATAAGATTAATTAATAATGCTCGGGGAAATGCTAGTGAATACCTTGGTTCACT 180

Qy 181 GAAAGTACTTTAGCGGACAGATGAGCTAAGCGCGCAATGATATAGTAGGTAAATTA 240
Db 181 GAAAGTACTTTAGCGGACAGATGAGCTAAGCGCGCAATGATATAGTAGGTAAATTA 240

Qy 241 CTATCAGGTTTAAAGGTCCTTGTGGCCGATAGTGAATGCTTATATCTCACTTAT 300
Db 241 CTATCAGGTTTAAAGGTCCTTGTGGCCGATAGTGAATGCTTATATCTCACTTAT 300

Qy 301 GATATTTCTGTGGCTTTCAGGGGAAAGAGTCAATGCGGAAATTTTATGGAACAAAGTAGAA 360
Db 301 GATATTTCTGTGGCTTTCAGGGGAAAGAGTCAATGCGGAAATTTTATGGAACAAAGTAGAA 360

Qy 361 GAACTCATTAATCAAAAATAGCAGAAATGCAAGGAATAAAGCGCTTTTCGGAATTAGAA 420
Db 361 GAACTCATTAATCAAAAATAGCAGAAATGCAAGGAATAAAGCGCTTTTCGGAATTAGAA 420

Qy 421 GGATTAAGTAAATTAACCAATTAATCTAACTGCGCTTGAAGATGCGGAAGAAATCC- 479
Db 421 GGATTAAGTAAATTAACCAATTAATCTAACTGCGCTTGAAGATGCGGAAGAAATCCA 480

Qy 480 -- AATATGGTTTCAAGAGCTTACAGATGTCGGAATTCGAATTTGAAATCCTGGATAGTTTA 537
Db 481 TTAAAATGCTAGAGCTTACAGATGTCGGAATTCGAATTTGAAATCCTGGATAGTTTA 540

Qy 538 TTATGCAATATATGCAATCTTTTAAAGTGAACAAATTTTAAAGTACCAATTCCTTACTGTA 597
Db 541 TTATGCAATATATGCAATCTTTTAAAGTGAACAAATTTTAAAGTACCAATTCCTTACTGTA 600

Qy 598 TATGCAATGGCAGCCACCTTCAATTTACTGTTATTAAGAGCGCTCAATTTTGGAGAA 657
Db 601 TATGCAATGGCAGCCACCTTCAATTTACTGTTATTAAGAGCGCTCAATTTTGGAGAA 660

Qy 658 GAATGGGATGGTCAACACTACTATTAATACTATTAATGATGCTCAAAATGAACTTACT 717
Db 661 GAATGGGATGGTCAACACTACTATTAATACTATTAATGATGCTCAAAATGAACTTACT 720

Qy 718 GCAGAAATTTCTGATCACTGTGTAAAGTGTATGAACTGGTTTACGAAATTTAAAGGC 777
Db 721 GCAGAAATTTCTGATCACTGTGTAAAGTGTATGAACTGGTTTACGAAATTTAAAGGC 780

Qy 778 ACAGCGCTTAAACAAATGGGTGATATAACCAATTCGCTAGAGAAATGACATGGCGGTT 837
Db 781 ACAGCGCTTAAACAAATGGGTGATATAACCAATTCGCTAGAGAAATGACATGGCGGTT 840

Qy 838 TTAGATGTTGTTGCAATTTCCCAATTAATGACACGCACTGACCAATGCCAATGGAAACGAA 897
Db 841 TTAGATGTTGTTGCAATTTCCCAATTAATGACACGCACTGACCAATGGCAATGGAAACGAA 900

Qy 898 GCAACAACTAAACAGGAAGTATATACAGATCCACTGGCGCGGTAAACGTTGCTTCAAT 957
Db 901 GCAACAACTAAACAGGAAGTATATACAGATCCACTGGCGCGGTAAACGTTGCTTCAAT 960

Qy 958 GGTTCCTGATGACAAAGCACCTTCTTTGGAGTGTATGAATCATCCGTTATTCGACCA 1017
Db 961 GGTTCCTGATGACAAAGCACCTTCTTTGGAGTGTATGAATCATCCGTTATTCGACCA 1020

RESULT 9
ABK87239
ID ABK87239 standard; DNA; 2022 BP.
XX

Qy 1018 CCCCATGATTATTGATTATATAACCGGACTCACAGTGTATACAAATCAAGAAGCAATTTCT 1077
Db 1021 CCCCATGATTATTGATTATATAACCGGACTCACAGTGTATACAAATCAAGAAGCAATTTCT 1080

Qy 1078 TCCGCTCCGTATATAAGCAATTTGGCTGGTCAATCAAAATAGCTACATCGTCTCAGTAGG 1137
Db 1081 TCCGCTCCGTATATAAGCAATTTGGCTGGTCAATCAAAATAGCTACATCGTCTCAGTAGG 1140

Qy 1138 GGTAGTAATCTTCAACAAATGATGTAATCAAAATCAAAATCTACACAGCACTAGTACTTT 1197
Db 1141 GGTAGTAATCTTCAACAAATGATGTAATCAAAATCAAAATCTACACAGCACTAGTACTTT 1200

Qy 1198 GATTTTACGAATTAATGATTAATTTCAAGACTCTATCAAAAGGATGCACTCTCTGATATT 1257
Db 1201 GATTTTACGAATTAATGATTAATTTCAAGACTCTATCAAAAGGATGCACTCTCTGATATT 1260

Qy 1258 GTTTACCTCGTTATACGTATATATTTTGGAAATGCCAGAAATCGAGTTTTCATGGTA 1317
Db 1261 GTTTACCTCGTTATACGTATATATTTTGGAAATGCCAGAAATCGAGTTTTCATGGTA 1320

Qy 1318 AACCAATTTGAATTAATACCAAGAAAGAGCTTAAAGTATAATCCAGTTTCCAAAGATATTATA 1377
Db 1321 AACCAATTTGAATTAATACCAAGAAAGAGCTTAAAGTATAATCCAGTTTCCAAAGATATTATA 1380

Qy 1378 GCGAGTACAAGAGATTCCGAATTTAGAAATTTACCTCCAGAAACTTTCAGATCAACCAATTAAT 1437
Db 1381 GCGAGTACAAGAGATTCCGAATTTAGAAATTTACCTCCAGAAACTTTCAGATCAACCAATTAAT 1440

Qy 1438 GAGTCATATAGCCATAGATTAATGTCATATCAAGATATTTCCGCGACGGGTAACTACTACC 1497
Db 1441 GAGTCATATAGCCATAGATTAATGTCATATCAAGATATTTCCGCGACGGGTAACTACTACC 1500

Qy 1498 GGATTAAGTACCTGTATTTTCTTGGACACATCGAAGTCGAGATTTTAAACCAATCAATATAT 1557
Db 1501 GGATTAAGTACCTGTATTTTCTTGGACACATCGAAGTCGAGATTTTAAACCAATCAATATAT 1560

Qy 1558 TCAGATAAAATCACTCAAAATTCGGCCCGTTAAATGTTGGGATAATTTACCGTTTGTTCGA 1617
Db 1561 TCAGATAAAATCACTCAAAATTCGGCCCGTTAAATGTTGGGATAATTTACCGTTTGTTCGA 1620

Qy 1618 GTGGTAAAGGACCAAGGACATACAGAGGGGATTTATACAGTATAATAGAAAGTACTGGT 1677
Db 1621 GTGGTAAAGGACCAAGGACATACAGAGGGGATTTATACAGTATAATAGAAAGTACTGGT 1680

Qy 1678 TCTGTAGGAAACCTTATTTCTAGCTCGATGCGCTAGCAATTTAGAAAGGACGAGGAATAT 1737
Db 1681 TCTGTAGGAAACCTTATTTCTAGCTCGATGCGCTAGCAATTTAGAAAGGACGAGGAATAT 1740

Qy 1738 CGTGTAAAGACTGAGATATGCTACTGATGAGATATTTGATTTGATGATGATGATGCTCAG 1797
Db 1741 CGTGTAAAGACTGAGATATGCTACTGATGAGATATTTGATTTGATGATGATGATGCTCAG 1800

Qy 1798 ATTGAGATGCCAAAACCAATGAACCCAGGTAGGATCTGACATCTTAAACTTTTAAAGTT 1857
Db 1801 ATTGAGATGCCAAAACCAATGAACCCAGGTAGGATCTGACATCTTAAACTTTTAAAGTT 1860

Qy 1858 GCAGATGCTATCAACCAATTAATTTAGCAACAGATAGTTTCCCTAGCATTTGAAACATAT 1917
Db 1861 GCAGATGCTATCAACCAATTAATTTAGCAACAGATAGTTTCCCTAGCATTTGAAACATAT 1920

Qy 1918 TTAGGTGAAGACCCCTTAATTTCAACATTTCTGTTAGTTTACGTTGACCGAATTCGAATTC 1977
Db 1921 TTAGGTGAAGACCCCTTAATTTCAACATTTCTGTTAGTTTACGTTGACCGAATTCGAATTC 1980

Qy 1978 ATCCCAGTAGATGAGACATATGAACGGGAACAA 2010
Db 1981 ATCCCAGTAGATGAGACATATGAACGGGAATAA 2013

AC ABK87239;
XX 07-OCT-2002 (first entry)
XX Bacillus thuringiensis NSRG.N1218-1 mutant gene sequence.
DE Pesticidal; spraying; dusting; broadcasting; seed coating; insect pest;
XX Colorado potato beetle; western corn rootworm; southern corn rootworm;
KW insect target range; endotoxin; Cry1218; gene; mutant; ds.
XX Bacillus thuringiensis.
OS Synthetic.
XX WO200234774-A2.
XX 02-MAY-2002.
XX 24-OCT-2001; 2001WO-US45468.
PF 24-OCT-2000; 2000US-242838P.
XX 23-OCT-2001; 2001US-0032717.
PR (DUPO) DU PONT DE NEMOURS & CO E I.
XX Abad AR, Duck NB, Feng X, Flannagan RD, Kahn TW, Sims LE;
XX WPI; 2002-519178/55.
XX P-F5DB; AU99260.
DR New isolated pesticidal polypeptide useful for impacting insect pest
XX e.g. Colorado potato beetle -
XX Claim 23; Page 118-121; 176pp; English.
XX The present invention relates to a new pesticidal polypeptide. The
CC invention is useful for impacting an insect pest by applying the
CC the molecules of the invention to the environment of the insect pest by
CC spraying, dusting, broadcasting, or seed coating, where the insect pest
CC is selected from Colorado potato beetle, western corn rootworm or
CC southern corn rootworm. The invention is also useful for increasing
CC insect target range and for producing transgenic microorganisms and
CC plants that express the pesticidal polypeptide. The invention is also
CC useful for producing transformed plants and in transforming any organism
CC to produce the pesticidal polypeptide of the invention. The present
CC nucleic acid sequence encodes a Bacillus thuringiensis mutant Cry1218
CC endotoxin protein.
XX Sequence 2022 BP; 692 A; 351 C; 398 G; 581 T; 0 other;
SQ Query Match 54.9%; Score 1986.4; DB 24; Length 2022;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 2009; Conservative 0; Mismatches 1; Indels 12; Gaps 1;
QY 1 ATGAGTCCAAATATCAAAATGAATATGAATATATAGATCGGACACCTTCTCTCTGTA 60
DB 1 ATGAGTCCAAATATCAAAATGAATATGAATATATAGATCGGACACCTTCTCTCTGTA 60
QY 61 TCCAATGATCTAACAGATACCTTTTGGCAATGAGGCCAACAAATGCGCTACAAATATG 120
DB 61 TCCAATGATCTAACAGATACCTTTTGGCAATGAGGCCAACAAATGCGCTACAAATATG 120
QY 121 GATTATAAAGATTATTTAAATAATGCTGCGGAAATGCTAGTGAATACCCCTGGTTCACTT 180
DB 121 GATTATAAAGATTATTTAAATAATGCTGCGGAAATGCTAGTGAATACCCCTGGTTCACTT 180
QY 181 GAAGTACTTGTTCGCGGACAAAGATGACAGCTAAGCCGCAATTCATATAGTAAATTA 240
DB 181 GAAGTACTTGTTCGCGGACAAAGATGACAGCTAAGCCGCAATTCATATAGTAAATTA 240
QY 241 CTATCAGGTTTAGGGTCCCAATTTGTTGGCCGATAGTACTTATATCTCAACTTATT 300
DB 241 CTATCAGGTTTAGGGTCCCAATTTGTTGGCCGATAGTACTTATATCTCAACTTATT 300

QY 301 GATATTTCTGTGGCCTTCAGGGGAAAAGAGTCAATGGGAAAATTTTTATGGAACAAGTAGAA 360
DB 301 GATATTTCTGTGGCCTTCAGGGGAAAAGAGTCAATGGGAAAATTTTTATGGAACAAGTAGAA 360
QY 361 GAACCTCATTAATCAAAAATAGCAGCAATATGCAAGCAATAAAGCGCTTTTCGGAATTAGAA 420
DB 361 GAACCTCATTAATCAAAAATAGCAGCAATATGCAAGCAATAAAGCGCTTTTCGGAATTAGAA 420
QY 421 CGATTAGGTAATAATTAACCAATTTATCTTAACCTGCGCTTGAAGCAATGCGCAAGAAATCCA 480
DB 421 CGATTAGGTAATAATTAACCAATTTATCTTAACCTGCGCTTGAAGCAATGCGCAAGAAATCCA 480
QY 481 AATGTTTCAAGA-----GCCTTACGAGATGTCGAAATCGATTTGAAATCCTG 528
DB 481 AATGTTTCAAGAATGTTCCCGGCGCTTACGAGATGTCGAAATCGATTTGAAATCCTG 540
QY 529 GATAGTTTATTTACGCAATATATGCAATCTTTTAGAGTGACAAATTTTGAAGTACCAATTC 588
DB 541 GATAGTTTATTTACGCAATATATATGCAATCTTTTAGAGTGACAAATTTTGAAGTACCAATTC 600
QY 589 CTCTACTGTATATGCAATGGCAGCCCAACCTTCAATTTACTGTTTAAAGGACGCGTCAATT 648
DB 601 CTCTACTGTATATGCAATGGCAGCCCAACCTTCAATTTACTGTTTAAAGGACGCGTCAATT 660
QY 649 TTTGGAGAAATGGGATGTCACCACTACTATTAATAACTATTTATGATCGTCAAAATG 708
DB 661 TTTGGAGAAATGGGATGTCACCACTACTATTAATAACTATTTATGATCGTCAAAATG 720
QY 709 AAACCTTACTGCAATATTTCTGATCACTGTGTAAAGTGTATGAACTGTTTGAAGCAAA 768
DB 721 AAACCTTACTGCAATATTTCTGATCACTGTGTAAAGTGTATGAACTGTTTGAAGCAAA 780
QY 769 TTTAAAAGGCAAGCGCTAAACCAATGGGTTGACTATAACCAATTCGTTAGAGAAATGACA 828
DB 781 TTTAAAAGGCAAGCGCTAAACCAATGGGTTGACTATAACCAATTCGTTAGAGAAATGACA 840
QY 829 CTGGCGGTTTTAGATGTTGTTGCTATTTCCCAATTTATGACACACGACGACGACGTAATG 888
DB 841 CTGGCGGTTTTAGATGTTGTTGCTATTTCCCAATTTATGACACACGACGACGACGTAATG 900
QY 889 GAAACGAAAGCAACTAAACAGGGAATATATACAGTCCCTGCGCGGTTAAACGTTG 948
DB 901 GAAACGAAAGCAACTAAACAGGGAATATATACAGTCCCTGCGCGGTTAAACGTTG 960
QY 949 TCTTCAATTTGTTCTGTTGATGACAAAGCACCTTCTTTCCGAGTGTAGTAATCATCGTT 1008
DB 961 TCTTCAATTTGTTCTGTTGATGACAAAGCACCTTCTTTCCGAGTGTAGTAATCATCGTT 1020
QY 1009 ATTTCGACCAACCCATGTTATTTGATTATATAACGGGACTCACAGTGTATACCAATCAAGA 1068
DB 1021 ATTTCGACCAACCCATGTTATTTGATTATATAACGGGACTCACAGTGTATACCAATCAAGA 1080
QY 1069 AGCATTTCTTCGCTGCTATATAGACATTTGGGCTGTCATCAATAAGTACCAATCGT 1128
DB 1081 AGCATTTCTTCGCTGCTATATAGACATTTGGGCTGTCATCAATAAGTACCAATCGT 1140
QY 1129 GTTCAGTAGGGTAGTAATCTTCAACAAATGTATGGAATCAATAAATCTACACGACT 1188
DB 1141 GTTCAGTAGGGTAGTAATCTTCAACAAATGTATGGAATCAATAAATCTACACGACT 1200
QY 1189 AGTACCTTTGATTTTACGAATTTATGATATTTACAGACTCTATCAAGGATGAGTACTC 1248
DB 1201 AGTACCTTTGATTTTACGAATTTATGATATTTACAGACTCTATCAAGGATGAGTACTC 1260
QY 1249 CTGTATTTGTTTACCTGTTTATAGTATATTTTGGAAATGCCAAGTCCGAGTTT 1308
DB 1261 CTGTATTTGTTTACCTGTTTATAGTATATTTTGGAAATGCCAAGTCCGAGTTT 1320
QY 1309 TTTCTGTGTAACCAATTTGAATATACCAAGAGCGTTAAAGTATATATCCAGTTTCCAA 1368
DB 1321 TTTCTGTGTAACCAATTTGAATATATACCAAGAGCGTTAAAGTATATATCCAGTTTCCAA 1380
QY 1369 GATATTATAGCGAGTACAAGAGATTTCGGAATTAGAATTACCTCCAGAACTTCAGATCAA 1428

Db 1381 GATATATTACGAGTACAGAGATTCGGAAATTAGATTTACCTCCAGAACTTCAGATCAA 1440
QY 1429 CCAAAATTATGAGTCATATAGCCATAGATTTATGTCATATCAAAATGATTTCCGCGACGGGT 1488
Db 1441 CCAATTTATGATGATATAGCCATAGATTTATGTCATATCAAAATGATTTCCGCGACGGGT 1500
QY 1489 AACACTACCGGATTTAGTACCTGTTATTTCTTTGGACACATCGAATGCGAGATTTAAACAAT 1548
Db 1501 AACACTACCGGATTTAGTACCTGTTATTTCTTTGGACACATCGAATGCGAGATTTAAACAAT 1560
QY 1549 ACAATATATTCAGATAAAATCACTCAAAATTTCCGCGCGTTAAATGTTGGGATAATTTACCG 1608
Db 1561 ACAATATATTCAGATAAAATCACTCAAAATTTCCGCGCGTTAAATGTTGGGATAATTTACCG 1620
QY 1609 TTTGTTCCAGTGTAAAGACACAGGACATACAGGAGGAGTTTATTCAGATATAATAGA 1668
Db 1621 TTTGTTCCAGTGTAAAGACACAGGACATACAGGAGGAGTTTATTCAGATATAATAGA 1680
QY 1669 AGTACTGTTCTGTAGGAACCTTTATTTCTAGCTCGATATGCGCTAGCATTTAGAAAAAGCA 1728
Db 1681 AGTACTGTTCTGTAGGAACCTTTATTTCTAGCTCGATATGCGCTAGCATTTAGAAAAAGCA 1740
QY 1729 GCGAAATATCGTTAGACATGAGATATGCTACTGATCGAGATATTTGATGATGTAAC 1788
Db 1741 GCGAAATATCGTTAGACATGAGATATGCTACTGATCGAGATATTTGATGATGTAAC 1800
QY 1789 GATGCTCAGATTCAGATGCGCAAAACCAATGAACCCAGTGGAGGATCTGACATCTAAACT 1848
Db 1801 GATGCTCAGATTCAGATGCGCAAAACCAATGAACCCAGTGGAGGATCTGACATCTAAACT 1860
QY 1849 TTTAAAGTTGCGATGCTATCACAACTAAATTTAGCAACAGATAGTTGCTAGCATTTG 1908
Db 1861 TTTAAAGTTGCGATGCTATCACAACTAAATTTAGCAACAGATAGTTGCTAGCATTTG 1920
QY 1909 AAACATAATTTAGTGAGACCTTAATTTCAACATATCTGATATAGTTTACGTTGACCGA 1968
Db 1921 AAACATAATTTAGTGAGACCTTAATTTCAACATATCTGATATAGTTTACGTTGACCGA 1980
QY 1969 ATCGAATTCATCCAGTAGATGAGACATATGAGCGCAACAA 2010
Db 1981 ATCGAATTCATCCAGTAGATGAGACATATGAGCGCAACAA 2022

RESULT 10
ID ABK87244 standard; DNA; 2022 BP.
XX AC ABK87244;
XX DT 07-OCT-2002 (first entry)
XX DE Bacillus thuringiensis LKMS.N1218-1 mutant gene sequence.
XX KW Pesticidal; spraying; dusting; broadcating; seed coating; insect pest;
XX KW Colorado potato beetle; western corn rootworm; southern corn rootworm;
XX KW insect target range; endotoxin; Cry1218; gene; mutant; ds.
XX OS Bacillus thuringiensis.
XX OS Synthetic.
XX PN WO200234774-A2.
XX PD 02-MAY-2002.
XX PF 24-OCT-2001; 2001WO-US45468.
XX PR 24-OCT-2000; 2000US-242838P.
XX PR 23-OCT-2001; 2001US-0032717.
XX PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX PI Abad AR, Duck NB, Feng X, Flannagan RD, Kahn TW, Sims LE;

XX WPI; 2002-519178/55.
DR P-PSDB; AAU99265.
XX New isolated pesticidal polypeptide useful for impacting insect pest
PT e.g. Colorado potato beetle -
XX Claim 23; Page 135-138; 176pp; English.
XX The present invention relates to a new pesticidal polypeptide. The
CC invention is useful for impacting an insect pest by applying the
CC the molecules of the invention to the environment of the insect pest by
CC spraying, dusting, broadcating, or seed coating, where the insect pest
CC is selected from Colorado potato beetle, western corn rootworm or
CC southern corn rootworm. The invention is also useful for increasing
CC insect target range and for producing transgenic microorganisms and
CC plants that express the pesticidal polypeptide. The invention is also
CC useful for producing transformed plants and in transforming any organism
CC to produce the pesticidal polypeptide of the invention. The present
CC nucleic acid sequence encodes a Bacillus thuringiensis mutant Cry1218
CC endotoxin protein.
XX Sequence 2022 BP; 695 A; 349 C; 395 G; 583 T; 0 other;
SQ Query Match 54.9%; Score 1986.4; DB 24; Length 2022;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 2009; Conservative 0; Mismatches 1; Indels 12; Gaps 1;
QY 1 ATGAGTCCAAATATCAAAATGAATGAAATTTATGATGCGACACCTTCTACTTCTGTA 60
Db 1 ATGAGTCCAAATATCAAAATGAATGAAATTTATGATGCGACACCTTCTACTTCTGTA 60
QY 61 TCCAATGATTTCTAACAGATACCTTTTGGCAATGAGCCCAAAATGCGTACAAAATATG 120
Db 61 TCCAATGATTTCTAACAGATACCTTTTGGCAATGAGCCCAAAATGCGTACAAAATATG 120
QY 121 GATTAATAAGATTTATTAATAATGTTCTGGCGGAAATGCTAGTGAATACCTTGGTTACCT 180
Db 121 GATTAATAAGATTTATTAATAATGTTCTGGCGGAAATGCTAGTGAATACCTTGGTTACCT 180
QY 181 GAAGTACTTGTAGCGGACAAAGATGAGCTAAGCGCGCAATTCATATAGTAAATTA 240
Db 181 GAAGTACTTGTAGCGGACAAAGATGAGCTAAGCGCGCAATTCATATAGTAAATTA 240
QY 241 CTATCAGGTTTAGGGTCCCATTTGTTGGCCGATAGTGGTCTTATCTCACTTATT 300
Db 241 CTATCAGGTTTAGGGTCCCATTTGTTGGCCGATAGTGGTCTTATCTCACTTATT 300
QY 301 GATATTCTGTGGCTTCAGGGGAAAAGAGTCAATGGGAAATTTTATGGAAACAAGTAGAA 360
Db 301 GATATTCTGTGGCTTCAGGGGAAAAGAGTCAATGGGAAATTTTATGGAAACAAGTAGAA 360
QY 361 GAATCATTAAATCAAAATAATGAGAAATATGCAAGGAATAAAGCGCTTTCGGAATTAAGA 420
Db 361 GAATCATTAAATCAAAATAATGAGAAATATGCAAGGAATAAAGCGCTTTCGGAATTAAGA 420
QY 421 GGATTAAGTAAATTAATTAACCAATTTATCTAACTGCGCTTGAAGTGGGAGAAATCCA 480
Db 421 GGATTAAGTAAATTAATTAACCAATTTATCTAACTGCGCTTGAAGTGGGAGAAATCCA 480
QY 481 -----AATGTTCAAGAGCGCTTACGAGATGTCGAAATCGATTTGAAATCCTG 528
Db 481 TTAATAATGTCATANTGTTCAAGAGCGCTTACGAGATGTCGAAATCGATTTGAAATCCTG 540
QY 529 GATAGTTTATTTACGCAATATATGCGCATCTTTTAGAGTGAACAAATTTTGAAGTACCATTC 588
Db 541 GATAGTTTATTTACGCAATATATGCGCATCTTTTAGAGTGAACAAATTTTGAAGTACCATTC 600
QY 589 CTTACTGTATATGCAATGCGCAACCTTCACTTCTTATTAAGGACGGTCAATT 648
Db 601 CTTACTGTATATGCAATGCGCAACCTTCACTTCTTATTAAGGACGGTCAATT 660
QY 649 TTTGGAGAAATGGGATGTTGTCACAACTACTATTATAACTATTATATGATCGTCAATG 708

Db 661 TTTGGAGAAGATGGGATGTCACAACTACTATTATAACTATTATGATCGTCAAAATG 720
Qy 709 AAACCTTACTGAGATATTTCTGATCAGTCTGTGTAAAGTGGTATGAACCTGGTTAGCAAAA 768
Db 721 AAACCTTACTGAGATATTTCTGATCAGTCTGTGTAAAGTGGTATGAACCTGGTTAGCAAAA 780
Qy 769 TTTAAAGGACAGAGCGCTAAACAAATGGGTGACTATAACCAATTCGGTAGAGAAATGACA 828
Db 781 TTTAAAGGACAGAGCGCTAAACAAATGGGTGACTATAACCAATTCGGTAGAGAAATGACA 840
Qy 829 CTGGCGGTTTGTAGTGTGTGCAATTTATCCAAATATGACACAGCGAGTACCAATG 888
Db 841 CTGGCGGTTTGTAGTGTGTGCAATTTATCCCAATATGACACAGCGAGTACCAATG 900
Qy 889 GAAACGAAAGCACAACTAACAGGGAAGTATATACAGATCCACTGGGCGCGGTAAACGTG 948
Db 901 GAAACGAAAGCACAACTAACAGGGAAGTATATACAGATCCACTGGGCGCGGTAAACGTG 960
Qy 949 TCTTCAATTTGGTTCCTGGTATGACAAAGCACCTTCTTTGGAGTGTAGTAATCATCCGTT 1008
Db 961 TCTTCAATTTGGTTCCTGGTATGACAAAGCACCTTCTTTGGAGTGTAGTAATCATCCGTT 1020
Qy 1009 ATTCGACACACCCATGTAATTTGATATATTAACGGGACTCACAGTGTATACAAATCAAGA 1068
Db 1021 ATTCGACACACCCATGTAATTTGATATATTAACGGGACTCACAGTGTATACAAATCAAGA 1080
Qy 1069 AGCAATTTCTCGGCTGCTATATAGACATTTGGGCTGTGCATCAATAAGCTTACCATGTT 1128
Db 1081 AGCAATTTCTCGGCTGCTATATAGACATTTGGGCTGTGCATCAATAAGCTTACCATGTT 1140
Qy 1129 GTCAGTAGGGTGTAACTCTCAACAAATGTATGAACCTTAATCAAAATCTACACAGCACT 1188
Db 1141 GTCAGTAGGGTGTAACTCTCAACAAATGTATGAACCTTAATCAAAATCTACACAGCACT 1200
Qy 1189 AGTACCTTTTGATTTTACGAATTTATGATATTTTACAGACTCTATCAAGAGTCCAGTACTC 1248
Db 1201 AGTACCTTTTGATTTTACGAATTTATGATATTTTACAGACTCTATCAAGAGTCCAGTACTC 1260
Qy 1249 CTTGATATTTGTTACCTCGTTTATAGTATATATTTTGGGATGCCAGAGTCCAGTTT 1308
Db 1261 CTTGATATTTGTTACCTCGTTTATAGTATATATTTTGGGATGCCAGAGTCCAGTTT 1320
Qy 1309 TTTATGTTAAACCAATTTGAATTAATACAGAAAGCTTAAAGTATAATCCAGTTTCCAAA 1368
Db 1321 TTTATGTTAAACCAATTTGAATTAATACAGAAAGCTTAAAGTATAATCCAGTTTCCAAA 1380
Qy 1369 GATATTTATAGCGAGTACAGAGATTTCCGAATTTAGAAATTTACCTCCAGAAATTTAGATCAA 1428
Db 1381 GATATTTATAGCGAGTACAGAGATTTCCGAATTTAGAAATTTACCTCCAGAAATTTAGATCAA 1440
Qy 1429 CCAATTTATAGTATATAGCATAGATTTATGTCATATACAAAGTATTTCCCGGAGCGGT 1488
Db 1441 CCAATTTATAGTATATAGCATAGATTTATGTCATATACAAAGTATTTCCCGGAGCGGT 1500
Qy 1489 AACCTACCGGATTTAGTACTGTTTCTTTCGACACATCCGAAGTCCAGATTTAAACAT 1548
Db 1501 AACCTACCGGATTTAGTACTGTTTCTTTCGACACATCCGAAGTCCGAATTTAAACAT 1560
Qy 1549 ACAATATATTCAGATAAAATCACTCAAATTTCCGCGGTTAAATTTGGGATTAATTTACCG 1608
Db 1561 ACAATATATTCAGATAAAATCACTCAAATTTCCGCGGTTAAATTTGGGATTAATTTACCG 1620
Qy 1609 TTTGTTCCAGTGTAAAGGACAGACATACAGAGGGGATTTATTAAGTATATAGTA 1668
Db 1621 TTTGTTCCAGTGTAAAGGACAGACATACAGAGGGGATTTATTAAGTATATAGTA 1680
Qy 1669 AGTACTGTTCTGTAGGACCTTATTTCTAGCTCCGATATGGCTAGCATTTAGAAAAGCA 1728
Db 1681 AGTACTGTTCTGTAGGACCTTATTTCTAGCTCCGATATGGCTAGCATTTAGAAAAGCA 1740
Qy 1729 GGGAAATATCGTGTAGAGCTGAGATATGCTACTGATCGAGATTTGTTATGATGTAAAC 1788

Db 1741 GGGAAATATCGTGTAGAGCTGAGATATGCTACTGATGACAGATATTTGTTATGATGTAAAC 1800
Qy 1789 GATGCTCAGATTTAGTGCAGAACCAATGAACCCAGGTGAGGATCTGACATCTTAAAACT 1848
Db 1801 GATGCTCAGATTTAGTGCAGAACCAATGAACCCAGGTGAGGATCTGACATCTTAAAACT 1860
Qy 1849 TTTAAAGTTCAGATGCTATCACAACTTAAATTTAGCAACAGATAGTTGCTAGCAATTG 1908
Db 1861 TTTAAAGTTCAGATGCTATCACAACTTAAATTTAGCAACAGATAGTTGCTAGCAATTG 1920
Qy 1909 AAACATATTTAGTGAAGACCCCTTAATTTCAACATATCTGGTATAGTTTACGTTGACCGA 1968
Db 1921 AAACATATTTAGTGAAGACCCCTTAATTTCAACATATCTGGTATAGTTTACGTTGACCGA 1980
Qy 1969 ATCGAATTTCAATCCAGTAGATGAGACATATGAAGCGGAACAA 2010
Db 1981 ATCGAATTTCAATCCAGTAGATGAGACATATGAAGCGGAATAA 2022

RESULT 11

ABK87256

ID ABK87256 standard; DNA; 2022 BP.

XX ABK87256;

DT 07-OCT-2002 (first entry)

DE Bacillus thuringiensis LRNS.N1218-1 mutant gene sequence.

XX Pesticidal; spraying; dusting; broadcasting; seed coating; insect pest;
KW Colorado potato beetle; western corn rootworm; southern corn rootworm;
KW insect target range; endotoxin; Cry1218; gene; mutant; ds.
XX Bacillus thuringiensis.

OS Synthetic.

FN WO200234774-A2.

PD 02-MAY-2002.

XX 24-OCT-2001; 2001WO-US45468.

PF 24-OCT-2000; 2000US-242838P.

PR 23-OCT-2001; 2001US-0032717.

PA (DUPO) DU PONT DE NEMOURS & CO E I.

XX Abad AR, Duck NB, Feng X, Flannagan RD, Kahn TW, Sims LE;

PI WPI; 2002-519178/55.

XX P-PSDB; RAU99271.

DR DR

XX New isolated pesticidal polypeptide useful for impacting insect pest

PT e.g. Colorado potato beetle

XX Claim 23; Page 160-162; 176pp; English.

PS The present invention relates to a new pesticidal polypeptide. The

XX invention is useful for impacting an insect pest by applying the

CC the molecules of the invention to the environment of the insect pest by

CC spraying, dusting, broadcasting, or seed coating, where the insect pest

CC is selected from Colorado potato beetle, western corn rootworm or

CC southern corn rootworm. The invention is also useful for increasing

CC insect target range and for producing transgenic microorganisms and

CC plants that express the pesticidal polypeptide. The invention is also

CC useful for producing transformed plants and in transforming any organism

CC to produce the pesticidal polypeptide of the invention. The present

CC nucleic acid sequence encodes a Bacillus thuringiensis mutant Cry1218

XX endotoxin protein.

SQ Sequence 2022 BP; 694 A; 349 C; 396 G; 583 T; 0 other;

XX Query Match 54.9%; Score 1986.4; DB 24; Length 2022;

Best Local Similarity 99.4%; Pred. No. 0;
Matches 2009; Conservative 0; Mismatches 1; Indels 12; Gaps 1;

```
QY 1 ATGAGTCCAAATATCAAAATGAATGAATGAATATAGATGCGACACCTCTTCTCTCTGTA 60
DB 1 ATGAGTCCAAATATCAAAATGAATGAATGAATATAGATGCGACACCTCTCTCTCTGTA 60
QY 61 TCAATGATTTCTAACAGATACCCCTTTTGGCAATGAGCAAAATGCGCTCAAAAATATG 120
DB 61 TCAATGATTTCTAACAGATACCCCTTTTGGCAATGAGCAAAATGCGCTCAAAAATATG 120
QY 121 GATTATAAGATTTATTAATAATGTCGCGGGAATGCTAGTGAATACCTCGTTCACCT 180
DB 121 GATTATAAGATTTATTAATAATGTCGCGGGAATGCTAGTGAATACCTCGTTCACCT 180
QY 181 GAAATGATTTGTTAGCGGCAAGATGAGCTAAGCGCGCAATTCATATAGTAGTAAATTA 240
DB 181 GAAATGATTTGTTAGCGGCAAGATGAGCTAAGCGCGCAATTCATATAGTAGTAAATTA 240
QY 241 CTATCAGGTTTAGGGTCCCAATTTGTTGGCCGATAGTGAATCTTATATCTCAACTTAT 300
DB 241 CTATCAGGTTTAGGGTCCCAATTTGTTGGCCGATAGTGAATCTTATATCTCAACTTAT 300
QY 301 GATATCTGTGGCTTCAGGGGAAAGAGTCAATGGGAAATTTTATGGAACAAAGTAGAA 360
DB 301 GATATCTGTGGCTTCAGGGGAAAGAGTCAATGGGAAATTTTATGGAACAAAGTAGAA 360
QY 361 GAACTCATTAATCAAAAATAGCAGAAATAGCAAGGAAATGAAGGCGCTTTCGGAAATTAG 420
DB 361 GAACTCATTAATCAAAAATAGCAGAAATAGCAAGGAAATGAAGGCGCTTTCGGAAATTAG 420
QY 421 GGAATGAGTAATTAATCAAAATATATCTAACTGCGCTTGAAGAAATGGAAGAAATCCA 480
DB 421 GGAATGAGTAATTAATCAAAATATATCTAACTGCGCTTGAAGAAATGGAAGAAATCCA 480
QY 481 -----AATGGTTCAAGAGCCTTACGAGATGTGCGAAATCGAATTTGAAATCCTG 528
DB 481 TTAAGAAATGCTAAATGGTTCAAGAGCCTTACGAGATGTGCGAAATCGAATTTGAAATCCTG 540
QY 529 GATAGTTTATTTACGCAATATATGCCATCTTTTAGATGACAAATTTTGAAGTACCATT 588
DB 541 GATAGTTTATTTACGCAATATATGCCATCTTTTAGATGACAAATTTTGAAGTACCATT 600
QY 589 CTTACTGTATATGCAATGCGAGCAACCTTCATTTACTGTATTAAGAGACGGTCAAT 648
DB 601 CTTACTGTATATGCAATGCGAGCAACCTTCATTTACTGTATTAAGAGACGGTCAAT 660
QY 649 TTTGGAGAAATGCGGATGGTCAACAACTATTAATTAATTAATTAATTAATTAATTAAT 708
DB 661 TTTGGAGAAATGCGGATGGTCAACAACTATTAATTAATTAATTAATTAATTAATTAAT 720
QY 709 AAACCTTACTGCAAGATATTTCTGATCTCTGTAAAGTGTATGAATCTGTTAGCAAAA 768
DB 721 AAACCTTACTGCAAGATATTTCTGATCTCTGTAAAGTGTATGAATCTGTTAGCAAAA 780
QY 769 TTAAGAGGCAAGCGCTAAACAAATGGGTTGACTATAACCAATTCGGTGAAGAAATGACA 828
DB 781 TTAAGAGGCAAGCGCTAAACAAATGGGTTGACTATAACCAATTCGGTGAAGAAATGACA 840
QY 829 CTGGCGGTTTATAGATGTTGTCATTTATTTCCAAATTTATGACACACGACGTACCCAATG 888
DB 841 CTGGCGGTTTATAGATGTTGTCATTTATTTCCAAATTTATGACACACGACGTACCCAATG 900
QY 889 GAAACGAAAGCAACCTAACAGGGGAAGTATATACAGATCCACTGGGCGCGGTAAACGTTG 948
DB 901 GAAACGAAAGCAACCTAACAGGGGAAGTATATACAGATCCACTGGGCGCGGTAAACGTTG 960
QY 949 TCTTCAATTTGGTTTCTGGTATGACAAAGCACCTTCTTTGGAGTGTAGATCATCCGTT 1008
DB 961 TCTTCAATTTGGTTTCTGGTATGACAAAGCACCTTCTTTGGAGTGTAGATCATCCGTT 1020
QY 1009 ATTTCGACCAACCCCATGATTTTGAATATATAACCGGAGTCCACAGTGTATACAAATCAAGA 1068
DB 1009 ATTTCGACCAACCCCATGATTTTGAATATATAACCGGAGTCCACAGTGTATACAAATCAAGA 1068
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RESULT 12
ABK87258
ID ABK87258 standard; DNA; 2013 BP.
XX
AC ABK87258;
XX

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DB 1021 ATTTCGACCAACCCCATGATTTTGAATATATAACCGGAGTCCACAGTGTATACAAATCAAGA 1080
QY 1069 AGCATTTCTTCGCTCGCTATATAGACATTCGGCTGGTCACTCAATTAAGCTTACCATCGT 1128
DB 1081 AGCATTTCTTCGCTCGCTATATAGACATTCGGCTGGTCACTCAATTAAGCTTACCATCGT 1140
QY 1129 GTCAGTAGGGGTAGTAATCTTCAACAAATGATGGAATCTAAATCAAAATCTTACACAGCACT 1188
DB 1141 GTCAGTAGGGGTAGTAATCTTCAACAAATGATGGAATCTAAATCAAAATCTTACACAGCACT 1200
QY 1189 AGTACCTTTGATTTTACGAATTTATGATATTTACAGACTCTATCAAAAGGATGCGTACTC 1248
DB 1201 AGTACCTTTGATTTTACGAATTTATGATATTTACAGACTCTATCAAAAGGATGCGTACTC 1260
QY 1249 CTTGATATTTGTTTACCTCGTTATACGTATATATTTTGGGAATGCCAGAGTTCGAGTTT 1308
DB 1261 CTTGATATTTGTTTACCTCGTTATACGTATATATTTTGGGAATGCCAGAGTTCGAGTTT 1320
QY 1309 TTCATGGTAAACCAATTTGAATTAATACCAAGAAAGAGCTTTAAAGTATAAATCCAGTTTCCAAA 1368
DB 1321 TTCATGGTAAACCAATTTGAATTAATACCAAGAAAGAGCTTTAAAGTATAAATCCAGTTTCCAAA 1380
QY 1369 GATATATAGCGAGTACAAAGAGATTCGGAATTTAGAAATTTACCTCCAGAAACTTTCAGATCAA 1428
DB 1381 GATATATAGCGAGTACAAAGAGATTCGGAATTTAGAAATTTACCTCCAGAAACTTTCAGATCAA 1440
QY 1429 CCAAATTTAGCTCATATAGCCATAGTTATCTCATATCACAAGTATTTCCCGGCGGCT 1488
DB 1441 CCAAATTTAGCTCATATAGCCATAGTTATCTCATATCACAAGTATTTCCCGGCGGCT 1500
QY 1489 AACACTTACCGGATTTAGTACTGTATTTCTTGGACACATCGAAGTGCAGATTTTAAACAAT 1548
DB 1501 AACACTTACCGGATTTAGTACTGTATTTCTTGGACACATCGAAGTGCAGATTTTAAACAAT 1560
QY 1549 ACAATATATTCAGATTAATAATCACTCAAAATTCGGCGCTTAAATTTGGGATTAATTTACCG 1608
DB 1561 ACAATATATTCAGATTAATAATCACTCAAAATTCGGCGCTTAAATTTGGGATTAATTTACCG 1620
QY 1609 TTTGTTCCAGTGGTAAAGGACAGGACATACAGAGGGGATTTATACAGTATATATAGA 1668
DB 1621 TTTGTTCCAGTGGTAAAGGACAGGACATACAGAGGGGATTTATACAGTATATATAGA 1680
QY 1669 AGTACTGTTCTGTAGGAACCTTATTTCTAGCTCGATATGGCTAGCATTAGAAAAAGCA 1728
DB 1681 AGTACTGTTCTGTAGGAACCTTATTTCTAGCTCGATATGGCTAGCATTAGAAAAAGCA 1740
QY 1729 GGGAAATATCGGTGAAGTACGATATGCTACTGATGAGATATTTGATTTGCAATGTAAC 1788
DB 1741 GGGAAATATCGGTGAAGTACGATATGCTACTGATGAGATATTTGATTTGCAATGTAAC 1800
QY 1789 GATGCTCAGATTCAGATGCGCAAAACCAATGAAACCGGAGGATCTGACATCTAAATCT 1848
DB 1801 GATGCTCAGATTCAGATGCGCAAAACCAATGAAACCGGAGGATCTGACATCTAAATCT 1860
QY 1849 TTTAAAGTTGCGAGATGCTATCAACCAATTTAAATTTAGCAACAGATAGTTTCGCTAGCATTTG 1908
DB 1861 TTTAAAGTTGCGAGATGCTATCAACCAATTTAAATTTAGCAACAGATAGTTTCGCTAGCATTTG 1920
QY 1909 AAACATAATTTAGGTGAAGACCTTAATTAATCAACATTTACTGGTATAGTTTACGTTGACCGA 1968
DB 1921 AAACATAATTTAGGTGAAGACCTTAATTAATCAACATTTACTGGTATAGTTTACGTTGACCGA 1980
QY 1969 ATCGAATTCATCCAGTAGATGAGACATATGAAGCGGAAACAA 2010
DB 1981 ATCGAATTCATCCAGTAGATGAGACATATGAAGCGGAAACAA 2022
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07-OCT-2002 (first entry)
 Bacillus thuringiensis LRMS.R1218-1 mutant gene sequence.
 Pesticidal; spraying; dusting; broadcasing; seed coating; insect pest;
 Colorado potato beetle; western corn rootworm; southern corn rootworm;
 insect target range; endotoxin; Cry1218; gene; mutant; ds.
 Bacillus thuringiensis.
 Synthetic.
 WO200234774-A2.
 02-MAY-2002.
 24-OCT-2001; 2001WO-US45468.
 24-OCT-2000; 2000US-242838P.
 23-OCT-2001; 2001US-0032717.
 (DUPO) DU PONT DE NEMOURS & CO E I.
 Abad AR, Duck NB, Feng X, Flannagan RD, Kahn TW, Sims LE;
 WPI; 2002-519178/55.
 P-PSDB; RAU99273.
 New isolated pesticidal polypeptide useful for impacting insect pest
 e.g. Colorado potato beetle -
 Claim 23; Page 168-170; 176pp; English.
 The present invention relates to a new pesticidal polypeptide. The
 invention is useful for impacting an insect pest by applying the
 molecules of the invention to the environment of the insect pest by
 spraying, dusting, broadcasing, or seed coating, where the insect pest
 is selected from Colorado potato beetle, western corn rootworm or
 southern corn rootworm. The invention is also useful for increasing
 insect target range and for producing transgenic microorganisms and
 plants that express the pesticidal polypeptide. The invention is also
 useful for producing transformed plants and in transforming any organism
 to produce the pesticidal polypeptide of the invention. The present
 nucleic acid sequence encodes a Bacillus thuringiensis mutant Cry1218
 endotoxin protein.
 Sequence 2013 BP; 691 A; 348 C; 394 G; 580 T; 0 other;
 Query Match 54.8%; Score 1985.8; DB 24; Length 2013;
 Best Local Similarity 99.5%; Pred. No. 0;
 Matches 2003; Conservative 0; Mismatches 7; Indels 3; Gaps 1;
 1 ATGAGTCCAAATTAATCAAAATGAATGAAATATGAAATATGAGTGGACACCTTCTACTTCTGTA 60
 1 ATGAGTCCAAATTAATCAAAATGAATGAAATATGAAATATGAGTGGACACCTTCTACTTCTGTA 60
 61 TCCAAATGATTTTAAATTAATGTTGGGGAATGCTAGTGAATGCTAGTGAATGCTAGTGAATGCT 120
 61 TCCAAATGATTTTAAATTAATGTTGGGGAATGCTAGTGAATGCTAGTGAATGCTAGTGAATGCT 120
 121 GATTATAAGATTTTAAATTAATGTTGGGGAATGCTAGTGAATGCTAGTGAATGCTAGTGAATGCT 180
 121 GATTATAAGATTTTAAATTAATGTTGGGGAATGCTAGTGAATGCTAGTGAATGCTAGTGAATGCT 180
 181 GAAGTACTGTTAGCGGACAAAGATGAGTGAATGCTAGTGAATGCTAGTGAATGCTAGTGAATGCT 240
 181 GAAGTACTGTTAGCGGACAAAGATGAGTGAATGCTAGTGAATGCTAGTGAATGCTAGTGAATGCT 240
 241 CTATCAGGTTTATAGGTTTCCCATTTGTTGGGCGATAGTGAATGCTAGTGAATGCTAGTGAATGCT 300
 241 CTATCAGGTTTATAGGTTTCCCATTTGTTGGGCGATAGTGAATGCTAGTGAATGCTAGTGAATGCT 300
 301 GATATTCTGTGGCTTCAGGGGAAAAGAGTCAATGCGAAATTTTATGCGAAACAAAGTAGAA 360
 |||||

Db 301 GATATTCTGTGGCTTCAGGGGAAAAGAGTCAATGCGAAATTTTATGCGAAACAAAGTAGAA 360
 Qy 361 GAACTCATTAATCAAAAATAGCAGAAATATGCAAGGAATTAAGCGCTTTTCGGAATTAGAA 420
 Db 361 GAACTCATTAATCAAAAATAGCAGAAATATGCAAGGAATTAAGCGCTTTTCGGAATTAGAA 420
 Qy 421 GGATTAGTAATAATACCAATTAATCTAACTCGCTTGAAGAAATGGGAAGAAATCC- 479
 Db 421 GGATTAGTAATAATACCAATTAATCTAACTCGCTTGAAGAAATGGGAAGAAATCCCA 480
 Qy 480 --AAATGGTTCAAGAGCTTACGAGATGTCGAAATCGATTTGAAATCCTCGATAGTTTA 537
 Db 481 TTAAGAAATGCTAGAGCGCTTACGAGATGTCGAAATCGATTTGAAATCCTCGATAGTTTA 540
 Qy 538 TTTAGGCAATATATATGCGCATCTTTTAGAGTGAACAAATTTGAAATGTCCTTACTCTGA 597
 Db 541 TTTAGGCAATATATATGCGCATCTTTTAGAGTGAACAAATTTGAAATGTCCTTACTCTGA 600
 Qy 598 TATGCAATGGCAGCAACCTTTCATTTTACTGTTTATTAAGGACGCGTCAATTTTGGAGAA 657
 Db 601 TATGCAATGGCAGCAACCTTTCATTTACTGTTTATTAAGGACGCGTCAATTTTGGAGAA 660
 Qy 658 GAATGGGGATGGTCAACAACTACTATTAATTAATCTATTAATGATGTCGTAATGAAATCTTACT 717
 Db 661 GAATGGGGATGGTCAACAACTACTATTAATTAATCTATTAATGATGTCGTAATGAAATCTTACT 720
 Qy 718 GCAGAAATATCTGATCACTGTGTAAGTGGTATGAACCTGTTTAGCAAAATTTAAAGGC 777
 Db 721 GCAGAAATATCTGATCACTGTGTAAGTGGTATGAACCTGTTTAGCAAAATTTAAAGGC 780
 Qy 778 ACAGCGCTAAACAAATGGTGTGACTATAACCAATTTCCGTAGAGAAATGACACTGCGCGTT 837
 Db 781 ACAGCGCTAAACAAATGGTGTGACTATAACCAATTTCCGTAGAGAAATGACACTGCGCGTT 840
 Qy 838 TTAGATGTTGTTGCAATTTATCCCAATTTATGACACACGACGTCCTCAATGAAACGAAA 897
 Db 841 TTAGATGTTGTTGCAATTTATCCCAATTTATGACACACGACGTCCTCAATGAAACGAAA 900
 Qy 898 GCACAACCTAAACAAGGAGTATATACAGATCCATGCGCGGCTAAACGTCCTCAAT 957
 Db 901 GCACAACCTAAACAAGGAGTATATACAGATCCATGCGCGGCTAAACGTCCTCAAT 960
 Qy 958 GGTTCCTCGTATGACAAAGCACCTTCTTTCCGAGTGTAGTAATCATCCGTTTATTCGACCA 1017
 Db 961 GGTTCCTCGTATGACAAAGCACCTTCTTTCCGAGTGTAGTAATCATCCGTTTATTCGACCA 1020
 Qy 1018 CCCCATGTTTGTGATTTATTAACCGGACTCAAGTGTATACAAATCAAGAACGATTTCT 1077
 Db 1021 CCCCATGTTTGTGATTTATTAACCGGACTCAAGTGTATACAAATCAAGAACGATTTCT 1080
 Qy 1078 TCCGCTCGCTATTAAGACATTTGGCTGTCATCAATAAGCTACCATCGTGTCTAGTAGG 1137
 Db 1081 TCCGCTCGCTATTAAGACATTTGGCTGTCATCAATAAGCTACCATCGTGTCTAGTAGG 1140
 Qy 1138 GGTAGTAATCTTCAACAAATGTATGGAATCAATCAAAATCTACACAGCACTAGTAGTCTT 1197
 Db 1141 GGTAGTAATCTTCAACAAATGTATGGAATCAATCAAAATCTACACAGCACTAGTAGTCTT 1200
 Qy 1198 GATTTTACGAATTAATGATTTTACAAAGCTCTATCAAAAGGATGCAAGTCTCTGATATT 1257
 Db 1201 GATTTTACGAATTAATGATTTTACAAAGCTCTATCAAAAGGATGCAAGTCTCTGATATT 1260
 Qy 1258 GTTTTACCTCGTGTATACGTTATATTTTTTGGAAATGCGAGAGTGGTGTTCATGTA 1317
 Db 1261 GTTTTACCTCGTGTATACGTTATATTTTTTGGAAATGCGAGAGTGGTGTTCATGTA 1320
 Qy 1318 AACCAATTAATTAATACCAAGAAAGCTTTAAAGTATATATCCAGTTTCCAAAGATATTATA 1377
 Db 1321 AACCAATTAATTAATACCAAGAAAGCTTTAAAGTATATATCCAGTTTCCAAAGATATTATA 1380
 Qy 1378 GCGAGTACAAGAGATTCCGAATTTAGAAATTAATCTCAGAAATCTTCAGATCAACCAATTAAT 1437
 Db 1381 GCGAGTACAAGAGATTCCGAATTTAGAAATTAATCTCAGAAATCTTCAGATCAACCAATTAAT 1440
 |||||

QY 1438 GAGTCATATAGCCATAGATTATGTCTATATCACAGTATTCCGCGACGGGTAACTACC 1497
 DB 1441 GAGTCATATAGCCATAGATTATGTCTATATCACAGTATTCCGCGACGGGTAACTACC 1500
 QY 1498 GGATTAGTACCTGTTATTTCTTGGACACATCGAAGTCGAGATTTAAACATACATATAT 1557
 DB 1501 GGATTAGTACCTGTTATTTCTTGGACACATCGAAGTCGAGATTTAAACATACATATAT 1560
 QY 1558 TCAGATAAATCACTCAAAATCCGCGCGTTAAATGTTGGATAATTTACCGTTTGTCCA 1617
 DB 1561 TCAGATAAATCACTCAAAATCCGCGCGTTAAATGTTGGATAATTTACCGTTTGTCCA 1620
 QY 1618 GTGTAAGAAGCACGAGACATACAGAGGGGATTTATACAGTATATATAGAGTACTGGT 1677
 DB 1621 GTGTAAGAAGCACGAGACATACAGAGGGGATTTATACAGTATATATAGAGTACTGGT 1680
 QY 1678 TCTGTAGGAACCTTATTTCTAGCTGATATGCGCTAGCATTTAGAAAAGCGAGGAATAT 1737
 DB 1681 TCTGTAGGAACCTTATTTCTAGCTGATATGCGCTAGCATTTAGAAAAGCGAGGAATAT 1740
 QY 1738 CGTGTAGACTGAGATATGCTACTGATGACATATTTGATTTGCTATTAACGATCTCAG 1797
 DB 1741 CGTGTAGACTGAGATATGCTACTGATGACATATTTGATTTGCTATTAACGATCTCAG 1800
 QY 1798 ATTCAGATGCCAAAACAAATGAACCCAGGTGAGGATCTGACATCTTAAACTTTTAAAGTT 1857
 DB 1801 ATTCAGATGCCAAAACAAATGAACCCAGGTGAGGATCTGACATCTTAAACTTTTAAAGTT 1860
 QY 1858 GCAGATGCTATCACAACTTAAATTTAGCAACAGATGTTGCTAGCATTTGAAACATAT 1917
 DB 1861 GCAGATGCTATCACAACTTAAATTTAGCAACAGATGTTGCTAGCATTTGAAACATAT 1920
 QY 1918 TTAGTGAAGACCCCTAATTCACATATCTGCTATGTTTACGTTGACCGAATCGAATTC 1977
 DB 1921 TTAGTGAAGACCCCTAATTCACATATCTGCTATGTTTACGTTGACCGAATCGAATTC 1980
 QY 1978 ATCCAGTAGATGAGACATATGAAGCGGAACAA 2010
 DB 1981 ATCCAGTAGATGAGACATATGAAGCGGAATAA 2013

RESULT 13
 ABK87243
 ID ABK87243 standard; DNA; 1860 BP.
 AC ABK87243;
 XX
 XX
 DT 07-OCT-2002 (first entry)
 XX
 DE Bacillus thuringiensis Cry1218-49PDV truncated gene sequence.
 XX
 KW Pesticidal; spraying; dusting; broadcasting; seed coating; insect pest;
 KW Colorado potato beetle; western corn rootworm; southern corn rootworm;
 KW insect target range; endotoxin; Cry1218; gene; ds.
 XX
 OS Bacillus thuringiensis.
 XX
 XX WO200234774-A2.
 PN
 XX
 PD 02-MAY-2002.
 XX
 PF 24-OCT-2001; 2001WO-US45468.
 XX
 PR 24-OCT-2000; 2000US-242838P.
 PR 23-OCT-2001; 2001US-0032717.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO B I.
 XX
 PI Abad AR, Duck NB, Peng X, Flannagan RD, Kahn TW, Sims LE;
 XX WPI; 2002-519178/55.
 DR P-PSDB; AAU99264.
 DR

XX New isolated pesticidal polypeptide useful for impacting insect pest
 PT e.g. Colorado potato beetle -
 XX Claim 20; Page 131-134; 176pp; English.
 PS The present invention relates to a new pesticidal polypeptide. The
 CC invention is useful for impacting an insect pest by applying the
 CC molecules of the invention to the environment of the insect pest by
 CC spraying, dusting, broadcasting, or seed coating, where the insect pest
 CC is selected from Colorado potato beetle, western corn rootworm or
 CC southern corn rootworm. The invention is also useful for increasing
 CC insect target range and for producing transgenic microorganisms and
 CC plants that express the pesticidal polypeptide. The invention is also
 CC useful for producing transformed plants and in transforming any organism
 CC to produce the pesticidal polypeptide of the invention. The present
 CC nucleic acid sequence encodes a *Bacillus thuringiensis* wild-type
 CC Cry1218 endotoxin protein.
 XX
 SQ Sequence 1860 BP; 626 A; 325 C; 372 G; 537 T; 0 other;
 Query Match 51.0%; Score 1848.4; DB 24; Length 1860;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1849; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 142 ATGTCTCGGGGAATGCTAGTGAATACCTGGTTCACCTGAAGTACTTGTAGCGGACAA 201
 DB 10 ATGTCTCGGGGAATGCTAGTGAATACCTGGTTCACCTGAAGTACTTGTAGCGGACAA 69
 QY 202 GATGCAGCTAAGGCCGCAATTTGATATAGTAGTAAATTTATCTATCAGGTTTAGGGGTCCCA 261
 DB 70 GATGCAGCTAAGGCCGCAATTTGATATAGTAGTAAATTTATCTATCAGGTTTAGGGGTCCCA 129
 QY 262 TTTGTTGGGCGGATAGTACTTTTATCTCAACTTATGATATCTTGTGSCCTTCAGGG 321
 DB 130 TTTGTTGGGCGGATAGTACTTTTATCTCAACTTATGATATCTTGTGSCCTTCAGGG 189
 QY 322 GAAAGAGTCAATGGGAAATTTTATGGACCAAGTAGAAGTCAATTAATCAAAAAATA 381
 DB 190 GAAAGAGTCAATGGGAAATTTTATGGACCAAGTAGAAGTCAATTAATCAAAAAATA 249
 QY 382 GCAGATATGCAAGGAATAAAGCGCTTTCGGAATTTAGAGGATTTAGGTAATTAATACCAA 441
 DB 250 GCAGATATGCAAGGAATAAAGCGCTTTCGGAATTTAGAGGATTTAGGTAATTAATACCAA 309
 QY 442 TTATATCTAACTGCGCTTGAAGAAATGGGAAGAAAATCCAAATGGTTCAGAGCGCTTACGA 501
 DB 310 TTATATCTAACTGCGCTTGAAGAAATGGGAAGAAAATCCAAATGGTTCAGAGCGCTTACGA 369
 QY 502 GATGTGGGAATCGATTTGAAATCCTGGATAGTTTATTTACGCAATATATGCCATCTTTT 561
 DB 370 GATGTGGGAATCGATTTGAAATCCTGGATAGTTTATTTACGCAATATATGCCATCTTTT 429
 QY 562 AGAGTGACAAATTTTGAAGTACCAATCTTCTGTATATCAATGGCAGCGCAACCTTCAT 621
 DB 430 AGAGTGACAAATTTTGAAGTACCAATCTTCTGTATATCAATGGCAGCGCAACCTTCAT 489
 QY 622 TTAAGTGTATTAAGGACGCGTCAATTTTGGAGAGAAGATGGGGATGGTCAACAACTACT 681
 DB 490 TTAAGTGTATTAAGGACGCGTCAATTTTGGAGAGAAGATGGGGATGGTCAACAACTACT 549
 QY 682 ATTAATACTATTTATGATCGTCAAACTTACTGCGAATATTTCTGATCACTGTGTA 741
 DB 550 ATTAATACTATTTATGATCGTCAAACTTACTGCGAATATTTCTGATCACTGTGTA 609
 QY 742 AAGTGTATGAAACTGTTTGTAGCAAAATTAAGGACGCGCTAAACAACTGGGTGAC 801
 DB 610 AAGTGTATGAAACTGTTTGTAGCAAAATTAAGGACGCGCTAAACAACTGGGTGAC 669
 QY 802 TATAACCAATTCGTTAGAGAAATGACACTGGCGGTTTTAGATGTTGTCATTTATTTCCCA 861
 DB 670 TATAACCAATTCGTTAGAGAAATGACACTGGCGGTTTTAGATGTTGTCATTTATTTCCCA 729

QY 322 GAAAAGAGTCATGGGAAATTTTATGGAAACAAGTAGAAGAACTCATTAATCAAAAATA 381
DB 181 GAAAAGAGTCATGGGAAATTTTATGGAAACAAGTAGAAGAACTCATTAATCAAAAATA 240
QY 382 GCAGATATGCAAGGAATAAGCGCTTTTCGGAATTTAGAGGATAGGTAAATAATTCGAA 441
DB 241 GCAGATATGCAAGGAATAAGCGCTTTTCGGAATTTAGAGGATAGGTAAATAATTCGAA 300
QY 442 TTATATCTAACTGCGCTTGAAGATGGGAAGAAAATCC--AAATGGTTCAAGAGCCTTA 498
DB 301 TTATATCTAACTGCGCTTGAAGATGGGAAGAAAATCCATTAATAAATGCTTAGAGCCTTA 360
QY 499 CGAGATGCGGAATTCGATTTGAATCTCGATATGTTTATTCGCAATATATGCCATCT 558
DB 361 CGAGATGCGGAATTCGATTTGAATCTCGATATGTTTATTCGCAATATATGCCATCT 420
QY 559 TTTAGAGTGCAAAATTTTGAAGTACCATTCTTACTCTATATGCAATGGCGCAACCTT 618
DB 421 TTTAGAGTGCAAAATTTTGAAGTACCATTCTTACTCTATATGCAATGGCGCAACCTT 480
QY 619 CATTTACTGTTTATTAAGGACGCGTCAATTTTGGAGAAGAAATGGGGATGGTCAACCACT 678
DB 481 CATTTACTGTTTATTAAGGACGCGTCAATTTTGGAGAAGAAATGGGGATGGTCAACCACT 540
QY 679 ACTATTAATTAATATGATCGTCAATGAATGAACCTTACTGCAGAATATCTGATCACTGT 738
DB 541 ACTATTAATTAATATGATCGTCAATGAATGAACCTTACTGCAGAATATCTGATCACTGT 600
QY 739 GTAAAGTGATGAACTGCTTTAGCAAAATTAAGGCAAGCGGCTTAACATGGGTT 798
DB 601 GTAAAGTGATGAACTGCTTTAGCAAAATTAAGGCAAGCGGCTTAACATGGGTT 660
QY 799 GACTATAACCAATTCGCTAGAGAAATGACACTGGCGGTTTATGATGTTTGTGCAATATTC 858
DB 661 GACTATAACCAATTCGCTAGAGAAATGACACTGGCGGTTTATGATGTTTGTGCAATATTC 720
QY 859 CCAAAATATGACACACGACGTACCCAAATGGAACGAAAGCAACCTTAAAGGGAAGTA 918
DB 721 CCAAAATATGACACACGACGTACCCAAATGGAACGAAAGCAACCTTAAAGGGAAGTA 780
QY 919 TATACAGATCCACTGGGCGGGTAAAGTGTCTTCAATTTGGTTCCTGCTATGACAAAGCA 978
DB 781 TATACAGATCCACTGGGCGGGTAAAGTGTCTTCAATTTGGTTCCTGCTATGACAAAGCA 840
QY 979 CCTTCTTTGCGAGTGATAGAAATCATCGTTTATTCGACACCCCATGTATTTGATTATATA 1038
DB 841 CCTTCTTTGCGAGTGATAGAAATCATCGTTTATTCGACACCCCATGTATTTGATTATATA 900
QY 1039 ACGGACTCACAGTGATATACAAATCAAGAAAGCAATTTCTTCGCTGCTATATAAGACAT 1098
DB 901 ACGGACTCACAGTGATATACAAATCAAGAAAGCAATTTCTTCGCTGCTATATAAGACAT 960
QY 1099 TGGGCTGGTTCATCAATTAAGTACCTACCTGTCGATAGGAGGTAGTATCTTCAACAAATG 1158
DB 961 TGGGCTGGTTCATCAATTAAGTACCTACCTGTCGATAGGAGGTAGTATCTTCAACAAATG 1020
QY 1159 TATGGAATCAATCAAAATCTACACAGCACTAGTACCTTTGATTTTACGAATTTATGATTT 1218
DB 1021 TATGGAATCAATCAAAATCTACACAGCACTAGTACCTTTGATTTTACGAATTTATGATTT 1080
QY 1219 TACAAGCTCTATCAAGAGTACGATGCTCTTGAATTTGTTTACCTGGTATATACGTAT 1278
DB 1081 TACAAGCTCTATCAAGAGTACGATGCTCTTGAATTTGTTTACCTGGTATATACGTAT 1140
QY 1279 ATATTTTGGATGCGAAGTGCAGTCTTTTCAATGTTAAACCAATTTGAATATATACAGA 1338
DB 1141 ATATTTTGGATGCGAAGTGCAGTCTTTTCAATGTTAAACCAATTTGAATATATACAGA 1200
QY 1339 AAGACGTTAAAGTATATATCCAGTTTCCAAAGATATATAGCGAGTACAGAGATTTGGAA 1398
DB 1201 AAGACGTTAAAGTATATATCCAGTTTCCAAAGATATATAGCGAGTACAGAGATTTGGAA 1260
QY 1399 TTAGAAATTAACCTCCAGAAATCTTCAAGATCAACCAAAATTTATGATCATATAGCCATAGATTA 1458

DB 1261 TTAGAATTAACCTCCAGAAATCTTCAAGATCAACCAAAATTTATGATCATATAGCCATAGATTA 1320
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DB 1321 TGTCAATATCAACAGTATTCCTCGGAGGGGTAAACACTACCGGATTTAGTCTGTTTCT 1380
QY 1519 TGGACACATCGAAGTGCAGATTTTAAACAATACATAATATTTTCAAGATAAAATCACTCAAAAT 1578
DB 1381 TGGACACATCGAAGTGCAGATTTTAAACAATACATAATATTTCAAGATAAAATCACTCAAAAT 1440
QY 1579 CCGCGCTTAAATGTTGGGATAATTTACCGTTTGTTCAGTGTGTAAAGGACAGGACAT 1638
DB 1441 CCGCGCTTAAATGTTGGGATAATTTACCGTTTGTTCAGTGTGTAAAGGACAGGACAT 1500
QY 1639 ACAGGAGGGGATTTATACAGTATATAGAACTACTGTTCTGTAGGAACCTTATTTCTA 1698
DB 1501 ACAGGAGGGGATTTATACAGTATATAGAACTACTGTTCTGTAGGAACCTTATTTCTA 1560
QY 1699 GCTCGATATGGCTAGCATTTAGAAAAAGCAGGGAATATCGTGTAAAGCTGAGATATGCT 1758
DB 1561 GCTCGATATGGCTAGCATTTAGAAAAAGCAGGGAATATCGTGTAAAGCTGAGATATGCT 1620
QY 1759 ACTGATGCGAGATTTGATTTGCATGTAAACGATGCTCAGATTCAGATGCGCAAAACAATG 1818
DB 1621 ACTGATGCGAGATTTGATTTGCATGTAAACGATGCTCAGATTCAGATGCGCAAAACAATG 1680
QY 1819 AACCCAGGTGAGGATCTGACATCTTAAACCTTTTAAAGTTGCAGATGCTATCACAACATTA 1878
DB 1681 AACCCAGGTGAGGATCTGACATCTTAAACCTTTTAAAGTTGCAGATGCTATCACAACATTA 1740
QY 1879 AATTTAGCAACAGATAGTTGCTAGCATTTGAAACATAAATTTAGGTGAAGACCTTAATTC 1938
DB 1741 AATTTAGCAACAGATAGTTGCTAGCATTTGAAACATAAATTTAGGTGAAGACCTTAATTC 1800
QY 1939 ACATTAATCTGGTATAGTTTACGTTGACCGAATCGAATTCATCCAGTATAGTA 1991
DB 1801 ACATTAATCTGGTATAGTTTACGTTGACCGAATCGAATTCATCCAGTATAGTA 1853

RESULT 15
ABK87249
ID ABK87249 standard; DNA; 1863 BP.
XX
AC ABK87249;
XX
DT 07-OCT-2002 (first entry)
XX
DE Bacillus thuringiensis NGSR.N49PDV mutant gene sequence.
XX
KW Pesticidal; spraying; dusting; broadcasing; seed coating; insect pest;
KW Colorado potato beetle; western corn rootworm; southern corn rootworm;
KW insect target range; endotoxin; Cry12I8; gene; mutant; ds.
XX
OS Bacillus thuringiensis.
OS Synthetic.
XX
PN WO200234774-A2.
XX
PD 02-MAY-2002.
XX
PF 24-OCT-2001; 2001WO-US45468.
XX
PR 24-OCT-2000; 2000US-242838P.
XX
PR 23-OCT-2001; 2001US-0032717.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Abad AR, Duck NB, Feng X, Flannagan RD, Kahn TW, Sims LE;
XX WPI; 2002-519178/55.
DR P-P8DB; AAU99268.
XX

PT New isolated pesticidal polypeptide useful for impacting insect pest
XX e.g. Colorado potato beetle -

PS Claim 27; Page 147-150; 176pp; English.

XX The present invention relates to a new pesticidal polypeptide. The
CC invention is useful for impacting an insect pest by applying the
CC the molecules of the invention to the environment of the insect pest by
CC spraying, dusting, broadcasting, or seed coating, where the insect pest
CC is selected from Colorado potato beetle, western corn rootworm or
CC southern corn rootworm. The invention is also useful for increasing
CC insect target range and for producing transgenic microorganisms and
CC plants that express the pesticidal polypeptide. The invention is also
CC useful for producing transformed plants and in transforming any organism
CC to produce the pesticidal polypeptide of the invention. The present
CC nucleic acid sequence encodes a *Bacillus thuringiensis* mutant Cry1218
CC endotoxin protein.

XX Sequence 1863 BP; 627 A; 325 C; 373 G; 538 T; 0 other;

Query Match 50.4%; Score 1826.4; DB 24; Length 1863;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1849; Conservative 0; Mismatches 1; Indels 12; Gaps 1;

QY	142	ATGTCGCGGAAATGCTAGTCAATACCTCGTTCACCTGAAGTACTTGTGTAGCGGACAA	201
DB	1	ATGTCGCGGAAATGCTAGTCAATACCTCGTTCACCTGAAGTACTTGTGTAGCGGACAA	60
QY	202	GATCAGCTAAGCGCGCAATTTGATATAGTAAATTAATTAATTAATTAATTAATTAATTA	261
DB	61	GATCAGCTAAGCGCGCAATTTGATATAGTAAATTAATTAATTAATTAATTAATTAATTA	120
QY	262	TTTCTGGCGGATAGTGAAGTCTTATATCTCACTTATGATATCTGCGCTTCAGGG	321
DB	121	TTTCTGGCGGATAGTGAAGTCTTATATCTCACTTATGATATCTGCGCTTCAGGG	180
QY	322	GAAGAAGTCAATGGGAAATTTTATGGAACAAGTAGAAGAACTCATTAATCAAAAATA	381
DB	181	GAAGAAGTCAATGGGAAATTTTATGGAACAAGTAGAAGAACTCATTAATCAAAAATA	240
QY	382	GCAGAAATGCAAGGAATAAAGCGCTTTTCGGAATTTAGAAGATTAGGTAATTAATTA	441
DB	241	GCAGAAATGCAAGGAATAAAGCGCTTTTCGGAATTTAGAAGATTAGGTAATTAATTA	300
QY	442	TTATATCTAATCTGCTGAGAGATGGAAGAAATCCAAATGCTTCAAG- - - - -	492
DB	301	TTATATCTAATCTGCTGAGAGATGGAAGAAATCCAAATGCTTCAAGAAATGCTTCC	360
QY	493	---GCCTTACGAGATGTCGGAATTCGATTTGAAATCCTGGATAGTTTATTAACGCAATAT	549
DB	361	CGGCGCTTACGAGATGTCGGAATTCGATTTGAAATCCTGGATAGTTTATTAACGCAATAT	420
QY	550	ATGCCATCTTTTAGAGTGCACAAATTTTGAAGTACCATTTCTTACTGTATATGCAATGCA	609
DB	421	ATGCCATCTTTTAGAGTGCACAAATTTTGAAGTACCATTTCTTACTGTATATGCAATGCA	480
QY	610	GCCAACTTCAATTTACTGTTATTAAGACCGCTCAATTTTGGAGAAGATGGGGTGG	669
DB	481	GCCAACTTCAATTTACTGTTATTAAGACCGCTCAATTTTGGAGAAGATGGGGTGG	540
QY	670	TCAACAACTACTATTAATAATCTATATGATCGTCAAAATGAACTTACTGCGAATATTTCT	729
DB	541	TCAACAACTACTATTAATAATCTATATGATCGTCAAAATGAACTTACTGCGAATATTTCT	600
QY	730	GATCACTGTGTAAGTGTATGAATCTGGTTTATGCAAAATTAATAAGGACGAGCGCTAAA	789
DB	601	GATCACTGTGTAAGTGTATGAATCTGGTTTATGCAAAATTAATAAGGACGAGCGCTAAA	660
QY	790	CAATGGGTTGACTATAACCAATTCGTAGAGAAATGACACTGCGCGTTTATGATGTTGTT	849
DB	661	CAATGGGTTGACTATAACCAATTCGTAGAGAAATGACACTGCGCGTTTATGATGTTGTT	720
QY	850	GCAATTTTCCCAATTTATGACACACGCGTACCCCAATGGAATCGAAATTCATCCAGTAGAT	909

DB	721	GCATTTATTCCTCAATTTATGACACACGCGCTACCCCAATGGAACGAAAGCACAACTAACCA	780
QY	910	AGGGAAGTATATACAGATCCACTGGGCGGTAAGAGTGCTTCAATTTGCTTCTCGGTAT	969
DB	781	AGGGAAGTATATACAGATCCACTGGGCGGTAAGAGTGCTTCAATTTGCTTCTCGGTAT	840
QY	970	GACAAAGCACCTTCTTTTCGGAGTGATAGATCATCCGTTATTTCGACCAACCCCAATGTTAT	1029
DB	841	GACAAAGCACCTTCTTTTCGGAGTGATAGATCATCCGTTATTTCGACCAACCCCAATGTTAT	900
QY	1030	GATTATATAACCGGACTCAAGTGTTATACAAATCAAGAAAGCAATTTCTTCGCTCGCTAT	1089
DB	901	GATTATATAACCGGACTCAAGTGTTATACAAATCAAGAAAGCAATTTCTTCGCTCGCTAT	960
QY	1090	ATAAGACATTTGGCTGCTCATCAATTAAGCTACCATCGTCTAGTAGGGGTGTAATCTTT	1149
DB	961	ATAAGACATTTGGCTGCTCATCAATTAAGCTACCATCGTCTAGTAGGGGTGTAATCTTT	1020
QY	1150	CAACAAATGTATGGAACCTAATCAAAATCTACACAGCACTAGTACCTTTGATTTTACGAAT	1209
DB	1021	CAACAAATGTATGGAACCTAATCAAAATCTACACAGCACTAGTACCTTTGATTTTACGAAT	1080
QY	1210	TATGATATTTCAAGACTCTATCAAGGATGCGAGTACTCTTGATATTTGTTTACCTGGT	1269
DB	1081	TATGATATTTCAAGACTCTATCAAGGATGCGAGTACTCTTGATATTTGTTTACCTGGT	1140
QY	1270	TATAGTATATATTTTGGAAATGCGAAGTCTGAGTTTTCATGTTAAACCAATTTGAAT	1329
DB	1141	TATAGTATATATTTTGGAAATGCGAAGTCTGAGTTTTCATGTTAAACCAATTTGAAT	1200
QY	1330	AATACCAAGAAAGCGTTTAAAGTATTAATCAAGTTTCCAAAGATATTAAGCGAGTACAAGA	1389
DB	1201	AATACCAAGAAAGCGTTTAAAGTATTAATCAAGTTTCCAAAGATATTAAGCGAGTACAAGA	1260
QY	1390	GATTTCGGAATTTAGAAATTTACCTCCAGAAATTTTCAGATCAACCAATTTATGAGTCAATAGC	1449
DB	1261	GATTTCGGAATTTAGAAATTTACCTCCAGAAATTTTCAGATCAACCAATTTATGAGTCAATAGC	1320
QY	1450	CATGATATTTGTCATATCAAGTATTTCCGCGACGGGTAAACACTACCGGATTTAGTACCT	1509
DB	1321	CATGATATTTGTCATATCAAGTATTTCCGCGACGGGTAAACACTACCGGATTTAGTACCT	1380
QY	1510	GTATTTTCTTGGACACATCGAAGTGACAGTTTAAACCAATTAATTAATTCAGATAAATC	1569
DB	1381	GTATTTTCTTGGACACATCGAAGTGACAGTTTAAACCAATTAATTAATTCAGATAAATC	1440
QY	1570	ACTCAAAATTCGCGCGTTAAATTTGGGATAATTTTACCGTTTGTTCAGTGGTAAAGGA	1629
DB	1441	ACTCAAAATTCGCGCGTTAAATTTGGGATAATTTTACCGTTTGTTCAGTGGTAAAGGA	1500
QY	1630	CCAGGACATACAGAGGGGATTTATTAAGTATTAAGAGTACTGTTCTGTAGGAAC	1689
DB	1501	CCAGGACATACAGAGGGGATTTATTAAGTATTAAGAGTACTGTTCTGTAGGAAC	1560
QY	1690	TTATTTCTAGCTGATATGGCTAGCAATTAAGAAACGAGGGAATATCGTGTAGGACTG	1749
DB	1561	TTATTTCTAGCTGATATGGCTAGCAATTAAGAAACGAGGGAATATCGTGTAGGACTG	1620
QY	1750	AGATATGCTACTGATGACAGATATTTGATTTGATGCAATTAAGCAATGCTCAGATTCAGATGCA	1809
DB	1621	AGATATGCTACTGATGACAGATATTTGATTTGATGCAATTAAGCAATGCTCAGATTCAGATGCA	1680
QY	1810	AAAACAAATGAACCCAGGTAGGATCTGACATCTTAAACCTTTTAAAGTTGCGAGATGCTATC	1869
DB	1681	AAAACAAATGAACCCAGGTAGGATCTGACATCTTAAACCTTTTAAAGTTGCGAGATGCTATC	1740
QY	1870	ACACATTTAAATTTAGCAACAGATAGTTTCGTAGCTAGCAATTAATTTAGGTGAAGAC	1929
DB	1741	ACACATTTAAATTTAGCAACAGATAGTTTCGTAGCTAGCAATTAATTTAGGTGAAGAC	1800
QY	1930	CCTAATTTCAACATTTATCTGGTATAGTTTACGTTGACCGAATTCGAATTCATCCAGTAGAT	1989

Db 1801 CCTAATTCAACATTATCTGGTATAGTTTACGTTGACCGAATCGAATTCATCCAGTAGAT 1860

Qy 1990 GA 1991

Db 1861 TA 1862

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